

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.**

PCT

WORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 6 : C07K 1/00, 16/00, C07H 21/04, C12N 15/00	A1	(11) International Publication Number: WO 97/30070 (43) International Publication Date: 21 August 1997 (21.08.97)
(21) International Application Number: PCT/US97/02318 (22) International Filing Date: 19 February 1997 (19.02.97) (30) Priority Data: 60/011,888 20 February 1996 (20.02.96) US (71) Applicant (for all designated States except US): SMITHKLINE BEECHAM CORPORATION [US/US]; Corporate Intellectual Property, UW2220, 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406-0939 (US). (72) Inventors; and (75) Inventors/Applicants (for US only): BLACK, Michael, Terrence [GB/US]; 502 Milhouse Way, Chester Springs, PA 19425 (US). BURNHAM, Martin, Karl, Russel [US/US]; 2927 Tanglewood Lane, Norristown, PA 19403 (US). HODGSON, John, Edward [GB/GB]; 260 Lapp Road, Malvern, PA 19355 (GB). KNOWLES, David, Justin, Charles [GB/GB]; Downsvew House, Redhill, Surrey RH1 6LY (GB). NICHOLAS, Richard, Oakley [GB/GB]; 355 Carmen Drive, Collegeville, PA 19426 (GB). PRATT, Julie, M. [GB/GB]; 77 Highfield Drive, Wigston, Leicester LE8 1NP (GB). REICHARD, Raymond, Winfield [US/US]; 2091 Clover Mill Road, Quakertown, PA 18951 (US). ROSENBERG, Martin [US/US]; 241 Mingo Road,	Royersford, PA 19468 (US). WARD, Judith, M. [GB/GB]; Carmela Cottage, 19 Cotmandene, Dorking, Surrey RH4 2BT (GB). (74) Agents: GIMMI, Edward, R. et al.; SmithKline Beecham Corporation, Corporate Intellectual Property, UW2220, 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406-0939 (US). (81) Designated States: JP, US, European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE). Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i>	
(54) Title: NOVEL COMPOUNDS (57) Abstract <p>This invention relates to newly identified Staphylococcal polynucleotides, polypeptides encoded by such polynucleotides, the uses of such polynucleotides and polypeptides, as well as the production of such polynucleotides and polypeptides and recombinant host cells transformed with the polynucleotides. This invention also relates to inhibiting the biosynthesis or action of such polynucleotides or polypeptides and to the use of such inhibitors in therapy.</p> <p style="text-align: center;">P 553 S. ID# 513</p>		

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AM	Armenia	GB	United Kingdom	MW	Malawi
AT	Austria	GE	Georgia	MX	Mexico
AU	Australia	GN	Guinea	NE	Niger
BB	Barbados	GR	Greece	NL	Netherlands
BE	Belgium	HU	Hungary	NO	Norway
BF	Burkina Faso	IE	Ireland	NZ	New Zealand
BG	Bulgaria	IT	Italy	PL	Poland
BJ	Benin	JP	Japan	PT	Portugal
BR	Brazil	KE	Kenya	RO	Romania
BY	Belarus	KG	Kyrgyzstan	RU	Russian Federation
CA	Canada	KP	Democratic People's Republic of Korea	SD	Sudan
CF	Central African Republic			SE	Sweden
CG	Congo	KR	Republic of Korea	SG	Singapore
CH	Switzerland	KZ	Kazakhstan	SI	Slovenia
CI	Côte d'Ivoire	LI	Liechtenstein	SK	Slovakia
CM	Cameroon	LK	Sri Lanka	SN	Senegal
CN	China	LR	Liberia	SZ	Swaziland
CS	Czechoslovakia	LT	Lithuania	TD	Chad
CZ	Czech Republic	LU	Luxembourg	TG	Togo
DE	Germany	LV	Latvia	TJ	Tajikistan
DK	Denmark	MC	Monaco	TT	Trinidad and Tobago
EE	Estonia	MD	Republic of Moldova	UA	Ukraine
ES	Spain	MG	Madagascar	UG	Uganda
FI	Finland	ML	Mali	US	United States of America
FR	France	MN	Mongolia	UZ	Uzbekistan
GA	Gabon	MR	Mauritania	VN	Viet Nam

NOVEL COMPOUNDS

Field of the Invention:

This invention relates to newly identified polynucleotides, particularly Staphylococcal polynucleotides, polypeptides encoded by such polynucleotides, the uses of
5 such polynucleotides and polypeptides, as well as the production of such polynucleotides and polypeptides and recombinant host cells transformed with the polynucleotides. This invention also relates to activating or inhibiting the biosynthesis or action of such polynucleotides or polypeptides and to the use of such activators or inhibitors in therapy.

Background of the Invention:

10 The Staphylococci make up a medically important genera of microbes. They are known to produce two types of disease, invasive and toxigenic. Invasive infections are characterized generally by abscess formation effecting both skin surfaces and deep tissues. *Staphylococcus aureus* (*S. aureus*) is the second leading cause of bacteremia in cancer patients. Osteomyelitis, septic arthritis, septic thrombophlebitis and acute bacterial
15 endocarditis are also relatively common. There are at least three clinical conditions resulting from the toxigenic properties of Staphylococci. The manifestation of these diseases result from the actions of exotoxins as opposed to tissue invasion and bacteremia. These conditions include: Staphylococcal food poisoning, scalded skin syndrome and toxic shock syndrome.

20 While certain Staphylococcal proteins associated with pathogenicity have been identified, e.g., coagulase, hemolysins, leucocidins and exo and enterotoxins, very little is known concerning the temporal expression of such genes during infection and disease progression in a mammalian host. Discovering the sets of genes the bacterium is likely to be expressing at the different stages of infection, particularly when an infection is established,
25 provides critical information for the screening and characterization of novel antibacterials which can interrupt pathogenesis. In addition to providing a fuller understanding of known proteins, such an approach will identify previously unrecognized targets.

Brief Description of the Invention:

This invention provides novel protein from *Staphylococcus aureus* WCUH29,
30 characterized in that it comprises the amino acid sequence given herein or a fragment, analogue or derivative thereof.

Also provided by the invention is an isolated polypeptide comprising an acid sequence selected from the group consisting of SEQ ID NO:1 through SEQ ID NO:623, or any combination of these SEQ ID NOS (SEQ ID NOS:1 through 623).

Further provided by the invention is an isolated nucleic acid (herein also "polynucleotide") encoding one of the amino acid sequences of SEQ ID NO:1 through SEQ ID NO:623, or an isolated polynucleotide sequence selected from the group consisting of SEQ ID NO:624 through 1165, or any combination of these SEQ ID NOS (SEQ ID NOS:624 through 1165), or any polynucleotide sequences capable of hybridizing therewith under stringent conditions.

In accordance with another aspect of the present invention, there are provided polynucleotides (DNA or RNA) which encode such polypeptides.

In particular the invention provides polynucleotides having the DNA sequences given herein.

The invention also relates to novel oligonucleotides derived from the sequences given herein which can act as PCR primers in the process herein described to determine whether or not the gene identified herein, particularly a *Staphylococcus aureus* gene, in whole or in part is expressed in infected tissue. It is recognized that such sequences will also have utility in diagnosis of the stage of infection and type of infection the pathogen has attained. The proteins so identified are also useful as targets in screens designed to identify antimicrobial compounds.

Detailed Description of the Invention:

Each of the polynucleotide sequences provided herein, particularly the DNA sequences, may be used in the discovery and development of antibacterial compounds. Because each of the sequences contains an open reading frame (ORF) or putative gene with an appropriate initiation and termination codons, the encoded protein upon expression can be used as a target for the screening of antimicrobial compounds, such as drugs. Additionally, the DNA sequences encoding the amino terminal regions of the encoded protein can be used to construct antisense or ribozyme sequences to control the expression of the coding sequence of interest. Furthermore, many of the sequences disclosed herein also provide regions upstream and downstream from the encoding sequence. These sequences are useful as a source of regulatory elements for the control of bacterial gene expression. Such sequences are conveniently isolated by restriction enzyme action or synthesized chemically and introduced, for example, into promoter identification strains. These strains contain a reporter structural gene sequence located downstream from a restriction site such that if an active promoter is inserted, the reporter gene will be expressed.

Although each of the sequences may be employed as described above, this invention also provides several means for identifying particularly useful target genes. The first of these approaches entails searching appropriate databases for sequence matches in related organisms. Thus, if a homologue exists, the Staphylococcal-like form of this gene would likely play an analogous role. For example, a Staphylococcal protein identified as homologous to a cell surface protein in another organism would be useful as a vaccine candidate. To the extent such homologies have been identified for the sequences disclosed herein they are reported along with the coding sequence.

Recently techniques have become available to evaluate temporal gene expression in bacteria, particularly as it applies to viability under laboratory and infection conditions. A number of methods can be used to identify genes which are essential to survival *per se*, or essential to the establishment/maintenance of an infection. Identification of an ORF unknown by one of these methods yields additional information about its function and permits the selection of such an ORF for further development as a screening target. Briefly, these approaches include:

1) Signature Tagged Mutagenesis (STM)

This technique is described by Hensel *et al.*, Science 269: 400-403(1995), the contents of which is incorporated by reference for background purposes. Signature tagged mutagenesis identifies genes necessary for the establishment/maintenance of infection in a given infection model.

The basis of the technique is the random mutagenesis of target organism by various means (e.g., transposons) such that unique DNA sequence tags are inserted in close proximity to the site of mutation. The tags from a mixed population of bacterial mutants and bacteria recovered from an infected hosts are detected by amplification, radiolabeling and hybridization analysis. Mutants attenuated in virulence are revealed by absence of the tag from the pool of bacteria recovered from infected hosts.

2) In Vivo Expression Technology (IVET)

This technique is described by Camilli *et al.*, Proc. Nat'l. Acad. Sci. USA 91:2634-2638 (1994), the contents of which is incorporated by reference for background purposes. IVET identifies genes up-regulated during infection when compared to laboratory cultivation, implying an important role in infection. ORF identified by this technique are implied to have a significant role in infection establishment/maintenance.

In this technique random chromosomal fragments of target organism are cloned upstream of a promoter-less recombinase gene in a plasmid vector. This construct is

introduced into the target organism which carries an antibiotic resistance gene flanked by resolvase sites. Growth in the presence of the antibiotic removes from the population those fragments cloned into the plasmid vector capable of supporting transcription of the recombinase gene and therefore have caused loss of antibiotic resistance. The resistant pool is introduced into a host and at various times after infection bacteria may be recovered and assessed for the presence of antibiotic resistance. The chromosomal fragment carried by each antibiotic sensitive bacterium should carry a promoter or portion of a gene normally upregulated during infection. Sequencing upstream of the recombinase gene allows identification of the up regulated gene.

3) Differential display

This technique is described by Chuang *et al.*, *J. Bacteriol.* 175:2026-2036 (1993), the contents of which is incorporated by reference for background purposes. This method identifies those genes which are expressed in an organism by identifying mRNA present using randomly-primed RT-PCR. By comparing pre-infection and post infection profiles, genes up and down regulated during infection can be identified and the RT-PCR product sequenced and matched to ORF 'unknowns'.

4) Generation of conditional lethal mutants by transposon mutagenesis.

This technique, described by de Lorenzo, V. *et al.*, *Gene* 123:17-24 (1993); Neuwald, A. F. *et al.*, *Gene* 125: 69-73(1993); and Takiff, H. E. *et al.*, *J. Bacteriol.* 174:1544-1553(1992), the contents of which is incorporated by reference for background purposes, identifies genes whose expression are essential for cell viability.

In this technique transposons carrying controllable promoters, which provide transcription outward from the transposon in one or both directions, are generated. Random insertion of these transposons into target organisms and subsequent isolation of insertion mutants in the presence of inducer of promoter activity ensures that insertions which separate promoter from coding region of a gene whose expression is essential for cell viability will be recovered. Subsequent replica plating in the absence of inducer identifies such insertions, since they fail to survive. Sequencing of the flanking regions of the transposon allows identification of site of insertion and identification of the gene disrupted. Close monitoring of the changes in cellular processes/morphology during growth in the absence of inducer yields information on likely function of the gene. Such monitoring could include flow cytometry (cell division, lysis, redox potential, DNA replication), incorporation of radiochemically labeled precursors into DNA, RNA, protein, lipid,

peptidoglycan, monitoring reporter enzyme gene fusions which respond to known cellular stresses.

5) Generation of conditional lethal mutants by chemical mutagenesis.

This technique is described by Beckwith, J., Methods in Enzymology 204:

5 3-18(1991), the contents of which are incorporated herein by reference for background purposes. In this technique random chemical mutagenesis of target organism, growth at temperature other than physiological temperature (permissive temperature) and subsequent replica plating and growth at different temperature (e.g. 42°C to identify ts, 25°C to identify cs) are used to identify those isolates which now fail to grow (conditional mutants). As
10 above close monitoring of the changes upon growth at the non-permissive temperature yields information on the function of the mutated gene. Complementation of conditional lethal mutation by library from target organism and sequencing of complementing gene allows matching with unknown ORF.

Each of these techniques may have advantages or disadvantage depending on the
15 particular application. The skilled artisan would choose the approach that is the most relevant with the particular end use in mind. For example, some genes might be recognized as essential for infection but in reality are only necessary for the initiation of infection and so their products would represent relatively unattractive targets for antibacterials developed to cure established and chronic infections.

20 In yet another variation, a suitably labelled oligonucleotide probe which anneals specifically to the bacterial ribosomal RNA in Northern blots of bacterial RNA preparations from infected tissue is employed. Using the more abundant ribosomal RNA as a hybridization target greatly facilitates the optimization of a protocol to purify bacterial RNA of a suitable size for RT-PCR from infected tissue.

25 Use of the of these technologies when applied to the ORFs of the present invention enables identification of bacterial proteins expressed during infection, inhibitors of which would have utility in anti-bacterial therapy.

S. aureus WCUH 29 has been deposited at the National Collection of Industrial and Marine Bacteria Ltd. (NCIMB), Aberdeen, Scotland under number NCIMB 40771 on 11
30 September 1995.

The nucleotide sequences disclosed herein can be obtained by synthetic chemical techniques known in the art or can be obtained from *S. aureus* WCUH 29 by probing a DNA preparation with probes constructed from the particular sequences disclosed herein. Alternatively, oligonucleotides derived from a disclosed sequence can act as PCR primers

in a process of PCR-based cloning of the sequence from a bacterial genomic source. It is recognized that such sequences will also have utility in diagnosis of the stage of infection and type of infection the pathogen has attained.

To obtain the polynucleotide encoding the protein using the DNA sequence given
5 herein typically a library of clones of chromosomal DNA of *S. aureus* WCUH29 in *E. coli*
or some other suitable host is probed with a radiolabelled oligonucleotide, preferably a
17mer or longer, derived from the partial sequence. Clones carrying DNA identical to that
of the probe can then be distinguished using high stringency washes. By sequencing the
individual clones thus identified with sequencing primers designed from the original
10 sequence it is then possible to extend the sequence in both directions to determine the full
gene sequence. Conveniently such sequencing is performed using denatured double
stranded DNA prepared from a plasmid clone. Suitable techniques are described by
Maniatis, T., Fritsch, E.F. and Sambrook, J. in MOLECULAR CLONING, A Laboratory
Manual, 2nd edition, 1989, Cold Spring Harbor Laboratory (see: Screening By
15 Hybridization 1.90 and Sequencing Denatured Double-Stranded DNA Templates 13.70).

A polynucleotide of the present invention may be in the form of RNA or in the
form of DNA, which DNA includes cDNA, genomic DNA, and synthetic DNA. The DNA
may be double-stranded or single-stranded, and if single stranded may be the coding strand
or non-coding (anti-sense) strand. The coding sequence which encodes the polypeptide
20 may be identical to the coding sequence shown or may be a different coding sequence
which coding sequence, as a result of the redundancy or degeneracy of the genetic code,
encoding the same polypeptide.

The present invention includes variants of the hereinabove described
polynucleotides which encode fragments, analogues and derivatives of the polypeptide
25 characterized by the deduced amino acid sequence given herein. The variant of the
polynucleotide may be a naturally occurring allelic variant of the polynucleotide or a non-
naturally occurring variant of the polynucleotide. In addition to the standard A, G, C, T/U
representations for nucleic acid bases, the term "N" is also used in certain polynucleotides
of the invention. "N" means that any of the four DNA or RNA bases may appear at such a
30 designated position in the DNA or RNA sequence, except that in preferred embodiments N
cannot be a base that when taken in combination with adjacent nucleotide positions, when
read in the correct reading frame, would have the effect of generating a premature
termination codon in such reading frame.

Thus, the present invention includes polynucleotides encoding the same polypeptide characterized by the deduced amino acid sequence given herein as well as variants of such polynucleotides which variants encode for a fragment, derivative or analogue of the polypeptide. Such nucleotide variants include deletion variants, substitution variants and addition or insertion variants.

The polynucleotide may have a coding sequence which is a naturally occurring allelic variant of the coding sequence characterized by the DNA sequence disclosed herein. As known in the art, an allelic variant is an alternate form of a polynucleotide sequence which may have a substitution, deletion or addition of one or more nucleotides, which does not substantially alter the function of the encoded polypeptide.

The polynucleotide which encodes for the mature polypeptide, may include only the coding sequence for the mature polypeptide or the coding sequence for the mature polypeptide and additional coding sequence such as a leader or secretory sequence or a proprotein sequence.

Thus, the term "polynucleotide encoding a polypeptide" encompasses a polynucleotide which includes only coding sequence for the polypeptide as well as a polynucleotide which includes additional coding and/or non-coding sequence.

The present invention therefore includes polynucleotides, wherein the coding sequence for the mature polypeptide may be fused in the same reading frame to a polynucleotide sequence which aids in expression and secretion of a polypeptide from a host cell, for example, a leader sequence which functions as a secretory sequence for controlling transport of a polypeptide from the cell. The polypeptide having a leader sequence is a preprotein and may have the leader sequence cleaved by the host cell to form the mature form of the polypeptide. The polynucleotides may also encode for a proprotein which is the mature protein plus additional 5' amino acid residues. A mature protein having a prosequence is a proprotein and is an inactive form of the protein. Once the prosequence is cleaved an active mature protein remains.

Thus, for example, the polynucleotide of the present invention may encode for a mature protein, or for a protein having a prosequence or for a protein having both a prosequence and a presequence (leader sequence). Further, the amino acid sequences provided herein show a methionine residue at the NH₂-terminus. It is appreciated, however, that during post-translational modification of the peptide, this residue may be deleted. Accordingly, this invention contemplates the use of both the methionine-containing and the methionineless amino terminal variants of each protein disclosed herein.

The polynucleotides of the present invention may also have the coding sequence fused in frame to a marker sequence at either the 5' or 3' terminus of the gene which allows for purification of the polypeptide of the present invention. The marker sequence may be a hexa-histidine tag supplied by the pQE series of vectors (supplied commercially by Quiagen Inc.) to provide for purification of the polypeptide fused to the marker in the case of a bacterial host.

The present invention further relates to polynucleotides which hybridize to the hereinabove-described sequences if there is at least 50% or 60% and preferably at least 70%, 80% or 90% identity between the sequences. The present invention particularly relates to Staphylococcal polynucleotides which hybridize under stringent conditions to the hereinabove-described polynucleotides. As herein used, the term "stringent conditions" means hybridization will occur only if there is at least 95% and preferably at least 97% identity between the sequences. The polynucleotides which hybridize to the hereinabove described polynucleotides in a preferred embodiment encode polypeptides which retain substantially the same biological function or activity as the polypeptide characterized by the deduced amino acid sequence given herein.

The deposit referred to herein will be maintained under the terms of the Budapest Treaty on the International Recognition of the Deposit of Micro-organisms for purposes of Patent Procedure. These deposits are provided merely as convenience to those of skill in the art and are not an admission that a deposit is required under 35 U.S.C. §112. The sequence of the polynucleotides contained in the deposited material, as well as the amino acid sequence of the polypeptides encoded thereby, are incorporated herein by reference and are controlling in the event of any conflict with any description of sequences herein. A license may be required to make, use or sell the deposited material, and no such license is hereby granted.

The terms "fragment," "derivative" and "analogue" when referring to the polypeptide characterized by the deduced amino acid sequence herein, means a polypeptide which retains essentially the same biological function or activity as such polypeptide. Thus, an analogue includes a proprotein which can be activated by cleavage of the proprotein portion to produce an active mature polypeptide.

The polypeptide of the present invention may be a recombinant polypeptide, a natural polypeptide or a synthetic polypeptide, preferably a recombinant polypeptide.

The fragment, derivative or analogue of the polypeptide characterized by the deduced amino acid sequence herein may be (i) one in which one or more of the amino acid

residues are substituted with a conserved or non-conserved amino acid residue (preferably a conserved amino acid residue) and such substituted amino acid residue may or may not be one encoded by the genetic code, or (ii) one in which one or more of the amino acid residues includes a substituent group, or (iii) one in which the polypeptide is fused with another compound, such as a compound to increase the half-life of the polypeptide (for example, polyethylene glycol), or (iv) one in which the additional amino acids are fused to the polypeptide, such as a leader or secretory sequence or a sequence which is employed for purification of the polypeptide or a proprotein sequence. Such fragments, derivatives and analogues are deemed to be within the scope of those skilled in the art from the teachings herein.

The polypeptides and polynucleotides of the present invention are preferably provided in an isolated form, and preferably are purified to homogeneity.

The term "isolated" means that the material is removed from its original environment (e.g., the natural environment if it is naturally occurring). For example, a naturally-occurring polynucleotide or polypeptide present in a living animal is not isolated, but the same polynucleotide or polypeptide, separated from some or all of the coexisting materials in the natural system, is isolated. Such polynucleotides could be part of a vector and/or such polynucleotides or polypeptides could be part of a composition, and still be isolated in that such vector or composition is not part of its natural environment.

The present invention also relates to vectors which include polynucleotides of the present invention, host cells which are genetically engineered with vectors of the invention and the production of polypeptides of the invention by recombinant techniques.

In accordance with yet a further aspect of the present invention, there is therefore provided a process for producing the polypeptide of the invention by recombinant techniques by expressing a polynucleotide encoding said polypeptide in a host and recovering the expressed product. Alternatively, the polypeptides of the invention can be synthetically produced by conventional peptide synthesizers.

Host cells are genetically engineered (transduced or transformed or transfected) with the vectors of this invention which may be, for example, a cloning vector or an expression vector. The vector may be, for example, in the form of a plasmid, a cosmid, a phage, etc. The engineered host cells can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants or amplifying the genes. The culture conditions, such as temperature, pH and the like, are those previously

used with the host cell selected for expression, and will be apparent to the ordinarily skilled artisan.

Suitable expression vectors include chromosomal, nonchromosomal and synthetic DNA sequences, e.g., bacterial plasmids; phage DNA; baculovirus; yeast plasmids; vectors
5 derived from combinations of plasmids and phage DNA. However, any other vector may be used as long as it is replicable and viable in the host.

The appropriate DNA sequence may be inserted into the vector by a variety of procedures. In general, the DNA sequence is inserted into an appropriate restriction endonuclease site(s) by procedures known in the art.

10 The DNA sequence in the expression vector is operatively linked to an appropriate expression control sequence(s) (promoter) to direct mRNA synthesis. As representative examples of such promoters, there may be mentioned: LTR or SV40 promoter, the *E. coli* *lac* or *trp*, the phage lambda P_L promoter and other promoters known to control expression of genes in eukaryotic or prokaryotic cells or their viruses. The expression vector also
15 contains a ribosome binding site for translation initiation and a transcription terminator. The vector may also include appropriate sequences for amplifying expression.

In addition, the expression vectors preferably contain one or more selectable marker genes to provide a phenotypic trait for selection of transformed host cells such as dihydrofolate reductase or neomycin resistance for eukaryotic cell culture, or such as
20 tetracycline or ampicillin resistance in *E. coli*.

The gene can be placed under the control of a promoter, ribosome binding site (for bacterial expression) and, optionally, an operator (collectively referred to herein as "control" elements), so that the DNA sequence encoding the desired protein is transcribed into RNA in the host cell transformed by a vector containing this expression construction. The coding
25 sequence may or may not contain a signal peptide or leader sequence. The polypeptides of the present invention can be expressed using, for example, the *E. coli* *tac* promoter or the protein A gene (*spa*) promoter and signal sequence. Leader sequences can be removed by the bacterial host in post-translational processing. See, e.g., U.S. Patent Nos. 4,431,739; 4,425,437; 4,338,397. Promoter regions can be selected from any desired gene using CAT
30 (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are PKK232-8 and PCM7. Particular named bacterial promoters include *lacI*, *lacZ*, T3, T7, *gpt*, lambda P_R, P_L and *trp*. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and

mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art.

In addition to control sequences, it may be desirable to add regulatory sequences which allow for regulation of the expression of the protein sequences relative to the growth of the host cell. Regulatory sequences are known to those of skill in the art, and examples include those which cause the expression of a gene to be turned on or off in response to a chemical or physical stimulus, including the presence of a regulatory compound. Other types of regulatory elements may also be present in the vector, for example, enhancer sequences.

An expression vector is constructed so that the particular coding sequence is located in the vector with the appropriate regulatory sequences, the positioning and orientation of the coding sequence with respect to the control sequences being such that the coding sequence is transcribed under the "control" of the control sequences (i.e., RNA polymerase which binds to the DNA molecule at the control sequences transcribes the coding sequence). Modification of the coding sequences may be desirable to achieve this end. For example, in some cases it may be necessary to modify the sequence so that it may be attached to the control sequences with the appropriate orientation; i.e., to maintain the reading frame. The control sequences and other regulatory sequences may be ligated to the coding sequence prior to insertion into a vector, such as the cloning vectors described above. Alternatively, the coding sequence can be cloned directly into an expression vector which already contains the control sequences and an appropriate restriction site.

Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, e.g., the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an N-terminal identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed recombinant product.

The vector containing the appropriate DNA sequence as hereinabove described, as well as an appropriate promoter or control sequence, may be employed to transform an appropriate host to permit the host to express the protein.

More particularly, the present invention also includes recombinant constructs comprising one or more of the sequences as broadly described above. The constructs comprise a vector, such as a plasmid or viral vector, into which a sequence of the invention has been inserted, in a forward or reverse orientation. In a preferred aspect of this
5 embodiment, the construct further comprises regulatory sequences, including, for example, a promoter, operably linked to the sequence. Large numbers of suitable vectors and promoters are known to those of skill in the art, and are commercially available. The following vectors are provided by way of example. Bacterial: pET-3 vectors (Stratagene), pQE70, pQE60, pQE-9 (Qiagen), pbs, pD10, phagescript, psiX174, pbluescript SK, pbsks,
10 pNH8A, pNH16a, pNH18A, pNH46A (Stratagene); ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pBlueBacIII (Invitrogen), pWLNEO, pSV2CAT, pOG44, pXT1, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia). However, any other plasmid or vector may be used as long as they are replicable and viable in the host.

15 Examples of recombinant DNA vectors for cloning and host cells which they can transform include the bacteriophage λ (*E. coli*), pBR322 (*E. coli*), pACYC177 (*E. coli*), pKT230 (gram-negative bacteria), pGV1106 (gram-negative bacteria), pLAFR1 (gram-negative bacteria), pME290 (non-*E. coli* gram-negative bacteria), pHV14 (*E. coli* and *Bacillus subtilis*), pBD9 (*Bacillus*), pIJ61 (*Streptomyces*), pUC6 (*Streptomyces*), YIp5
20 (*Saccharomyces*), a baculovirus insect cell system, YCp19 (*Saccharomyces*). See, generally, "DNA Cloning": Vols. I & II, Glover *et al.* ed. IRL Press Oxford (1985) (1987) and; T. Maniatis *et al.* ("Molecular Cloning" Cold Spring Harbor Laboratory (1982).

In some cases, it may be desirable to add sequences which cause the secretion of the polypeptide from the host organism, with subsequent cleavage of the secretory signal.

25 Polypeptides can be expressed in host cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, *et al.*, Molecular Cloning: A Laboratory Manual, Second Edition, Cold
30 Spring Harbor, N.Y., (1989), the disclosure of which is hereby incorporated by reference.

Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced by appropriate means (e.g., temperature shift or chemical induction) and cells are cultured for an additional period.

Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents, such methods are well known to those skilled in the art.

Depending on the expression system and host selected, the polypeptide of the present invention may be produced by growing host cells transformed by an expression vector described above under conditions whereby the polypeptide of interest is expressed. The polypeptide is then isolated from the host cells and purified. If the expression system secretes the polypeptide into growth media, the polypeptide can be purified directly from the media. If the polypeptide is not secreted, it is isolated from cell lysates or recovered from the cell membrane fraction. Where the polypeptide is localized to the cell surface, whole cells or isolated membranes can be used as an assayable source of the desired gene product. Polypeptide expressed in bacterial hosts such as *E. coli* may require isolation from inclusion bodies and refolding. Where the mature protein has a very hydrophobic region which leads to an insoluble product of overexpression, it may be desirable to express a truncated protein in which the hydrophobic region has been deleted. The selection of the appropriate growth conditions and recovery methods are within the skill of the art.

The polypeptide can be recovered and purified from recombinant cell cultures by methods including ammonium sulphate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps.

Depending upon the host employed in a recombinant production procedure, the polypeptides of the present invention may be glycosylated or may be non-glycosylated. Polypeptides of the invention may also include an initial methionine amino acid residue.

A "replicon" is any genetic element (e.g., plasmid, chromosome, virus) that functions as an autonomous unit of DNA replication *in vivo*; i.e., capable of replication under its own control.

A "vector" is a replicon, such as a plasmid, phage, or cosmid, to which another DNA segment may be attached so as to bring about the replication of the attached segment.

A "double-stranded DNA molecule" refers to the polymeric form of deoxyribonucleotides (bases adenine, guanine, thymine, or cytosine) in a double-stranded helix, both relaxed and supercoiled. This term refers only to the primary and secondary structure of the molecule, and does not limit it to any particular tertiary forms. Thus, this term includes double-stranded DNA found, *inter alia*, in linear DNA molecules (e.g., restriction fragments), viruses, plasmids, and chromosomes. In discussing the structure of particular double-stranded DNA molecules, sequences may be described herein according to the normal convention of giving only the sequence in the 5' to 3' direction along the nontranscribed strand of DNA (i.e., the strand having the sequence homologous to the mRNA).

A DNA "coding sequence of" or a "nucleotide sequence encoding" a particular protein, is a DNA sequence which is transcribed and translated into a polypeptide when placed under the control of appropriate regulatory sequences.

A "promoter sequence" is a DNA regulatory region capable of binding RNA polymerase in a cell and initiating transcription of a downstream (3' direction) coding sequence. For purposes of defining the present invention, the promoter sequence is bound at the 3' terminus by a translation start codon (e.g., ATG, GTG) of a coding sequence and extends upstream (5' direction) to include the minimum number of bases or elements necessary to initiate transcription at levels detectable above background. Within the promoter sequence will be found a transcription initiation site (conveniently defined by mapping with nuclease S1), as well as protein binding domains (consensus sequences) responsible for the binding of RNA polymerase. Eukaryotic promoters will often, but not always, contain "TATA" boxes and "CAT" boxes. Prokaryotic promoters contain Shine-Dalgarno sequences in addition to the -10 and -35 consensus sequences.

DNA "control sequences" refers collectively to promoter sequences, ribosome binding sites, polyadenylation signals, transcription termination sequences, upstream regulatory domains, enhancers, and the like, which collectively provide for the expression (i.e., the transcription and translation) of a coding sequence in a host cell.

A control sequence "directs the expression" of a coding sequence in a cell when RNA polymerase will bind the promoter sequence and transcribe the coding sequence into mRNA, which is then translated into the polypeptide encoded by the coding sequence.

A "host cell" is a cell which has been transformed or transfected, or is capable of transformation or transfection by an exogenous DNA sequence.

A cell has been "transformed" by exogenous DNA when such exogenous DNA has been introduced inside the cell membrane. Exogenous DNA may or may not be integrated (covalently linked) into chromosomal DNA making up the genome of the cell. In prokaryotes and yeasts, for example, the exogenous DNA may be maintained on an episomal element, such as a plasmid. With respect to eukaryotic cells, a stably transformed or transfected cell is one in which the exogenous DNA has become integrated into the chromosome so that it is inherited by daughter cells through chromosome replication. This stability is demonstrated by the ability of the eukaryotic cell to establish cell lines or clones comprised of a population of daughter cell containing the exogenous DNA.

10 A "clone" is a population of cells derived from a single cell or common ancestor by mitosis. A "cell line" is a clone of a primary cell that is capable of stable growth *in vitro* for many generations.

15 A "heterologous" region of a DNA construct is an identifiable segment of DNA within or attached to another DNA molecule that is not found in association with the other molecule in nature.

In accordance with yet a further aspect of the present invention, there is provided the use of a polypeptide of the invention for therapeutic or prophylactic purposes, for example, as an antibacterial agent or a vaccine.

20 In accordance with another aspect of the present invention, there is provided the use of a polynucleotide of the invention for therapeutic or prophylactic purposes, in particular genetic immunization.

In accordance with yet another aspect of the present invention, there are provided inhibitors to such polypeptides, useful as antibacterial agents. In particular, there are provided antibodies against such polypeptides.

25 Another aspect of the invention is a pharmaceutical composition comprising the above polypeptide, polynucleotide or inhibitor of the invention and a pharmaceutically acceptable carrier.

In a particular aspect the invention provides the use of an inhibitor of the invention as an antibacterial agent.

30 The invention further relates to the manufacture of a medicament for such uses.

The polypeptide may be used as an antigen for vaccination of a host to produce specific antibodies which have anti-bacterial action.

The polypeptides or cells expressing them can be used as an immunogen to produce antibodies thereto. These antibodies can be, for example, polyclonal or monoclonal

antibodies. The term antibodies also includes chimeric, single chain, and humanized or -
simianized antibodies, as well as Fab fragments, or the product of an Fab expression library.
Various procedures known in the art may be used for the production of such antibodies and
fragments.

- 5 Antibodies generated against the polypeptides of the present invention can be
obtained by direct injection of the polypeptides into an animal or by administering the
polypeptides to an animal, preferably a nonhuman. The antibody so obtained will then bind
the polypeptides itself. In this manner, even a sequence encoding only a fragment of the
polypeptides can be used to generate antibodies binding the whole native polypeptides.
10 Such antibodies can then be used to isolate the polypeptide from tissue expressing that
polypeptide.

Polypeptide derivatives include antigenically or immunologically equivalent
derivatives which form a particular aspect of this invention.

- 15 The term 'antigenically equivalent derivative' as used herein encompasses a
polypeptide or its equivalent which will be specifically recognized by certain antibodies
which, when raised to the protein or polypeptide according to the present invention,
interfere with the interaction between pathogen and mammalian host.

- 20 The term 'immunologically equivalent derivative' as used herein encompasses a
peptide or its equivalent which when used in a suitable formulation to raise antibodies in a
vertebrate, the antibodies act to interfere with the interaction between pathogen and
mammalian host.

- In particular derivatives which are slightly longer or slightly shorter than the native
protein or polypeptide fragment of the present invention may be used. In addition,
polypeptides in which one or more of the amino acid residues are modified may be used.
25 Such peptides may, for example, be prepared by substitution, addition, or rearrangement of
amino acids or by chemical modification thereof. All such substitutions and modifications
are generally well known to those skilled in the art of peptide chemistry.

- The polypeptide, such as an antigenically or immunologically equivalent derivative
or a fusion protein thereof is used as an antigen to immunize a mouse or other animal such
30 as a rat or chicken. The fusion protein may provide stability to the polypeptide. The
antigen may be associated, for example by conjugation, with an immunogenic carrier
protein for example bovine serum albumin (BSA) or keyhole limpet haemocyanin (KLH).
Alternatively a multiple antigenic peptide comprising multiple copies of the protein or

polypeptide, or an antigenically or immunologically equivalent polypeptide thereof may be sufficiently antigenic to improve immunogenicity so as to obviate the use of a carrier.

For preparation of monoclonal antibodies, any technique which provides antibodies produced by continuous cell line cultures can be used. Examples include the hybridoma technique (Kohler and Milstein, Nature, 256:495-497(1975)), the trioma technique, the human B-cell hybridoma technique (Kozbor et al., Immunology Today 4:72(1983)), and the EBV-hybridoma technique to produce human monoclonal antibodies (Cole, et al., 1985, in Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, Inc., pp. 77-96).

Techniques described for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce single chain antibodies to immunogenic polypeptide products of this invention.

Using the procedure of Kohler and Milstein (supra, (1975)), antibody-containing cells from the immunized mammal are fused with myeloma cells to create hybridoma cells secreting monoclonal antibodies.

The hybridomas are screened to select a cell line with high binding affinity and favorable cross reaction with other staphylococcal species using one or more of the original polypeptide and/or the fusion protein. The selected cell line is cultured to obtain the desired Mab.

Hybridoma cell lines secreting the monoclonal antibody are another aspect of this invention.

Alternatively phage display technology could be utilized to select antibody genes with binding activities towards the polypeptide either from repertoires of PCR amplified v-genes of lymphocytes from humans screened for possessing anti-Fbp or from naive libraries (McCafferty, J. et al., Nature 348:552-554(1990), and Marks, J. et al., Biotechnology 10:779-783(1992)). The affinity of these antibodies can also be improved by chain shuffling (Clackson, T. et al., Nature 352:624-628(1991)).

The antibody should be screened again for high affinity to the polypeptide and/or fusion protein.

As mentioned above, a fragment of the final antibody may be prepared.

The antibody may be either intact antibody of M_r approx 150,000 or a derivative of it, for example a Fab fragment or a Fv fragment as described in Skerra, A and Pluckthun, A., Science 240:1038-1040 (1988). If two antigen binding domains are present each domain may be directed against a different epitope - termed 'bispecific' antibodies.

The antibody of the invention may be prepared by conventional means for example by established monoclonal antibody technology (Kohler, G. and Milstein, C. (supra, (1975) or using recombinant means e.g. combinatorial libraries, for example as described in Huse, W.D. *et al.*, Science 246:1275-1281 (1989).

5 Preferably the antibody is prepared by expression of a DNA polymer encoding said antibody in an appropriate expression system such as described above for the expression of polypeptides of the invention. The choice of vector for the expression system will be determined in part by the host, which may be a prokaryotic cell, such as *E. coli* (preferably strain B) or *Streptomyces sp.* or a eukaryotic cell, such as a mouse C127, mouse myeloma,
10 human HeLa, Chinese hamster ovary, filamentous or unicellular fungi or insect cell. The host may also be a transgenic animal or a transgenic plant (for example, as described in Hiatt, A. *et al.*, Nature 340:76-78(1989). Suitable vectors include plasmids, bacteriophages, cosmids and recombinant viruses, derived from, for example, baculoviruses and vaccinia.

15 The Fab fragment may also be prepared from its parent monoclonal antibody by enzyme treatment, for example using papain to cleave the Fab portion from the Fc portion.

20 Preferably the antibody or derivative thereof is modified to make it less immunogenic in the patient. For example, if the patient is human the antibody may most preferably be 'humanized'; where the complementarity determining region(s) of the hybridoma-derived antibody has been transplanted into a human monoclonal antibody, for example as described in Jones, P. *et al.*, Nature 321:522-525 (1986), or Tempest *et al.*, Biotechnology 9:266-273 (1991).

The modification need not be restricted to one of 'humanization'; other primate sequences (for example Newman, R. *et al.*, Biotechnology 10:1455-1460 (1992)) may also be used.

25 The humanized monoclonal antibody, or its fragment having binding activity, form a particular aspect of this invention.

This invention provides a method of screening compounds, for example, drugs to identify those which activate or preferably interfere with the proteins selected as targets herein, which method comprises measuring the activation or interference of the activity of the protein by a test compound or drug. For example if the protein selected has a catalytic activity, after suitable purification and formulation the activity of the enzyme can be followed by its ability to convert its natural substrates. By incorporating different chemically synthesized test compounds or natural products into such an assay of enzymatic activity one is able to detect those additives which compete with the natural substrate or otherwise inhibit enzymatic activity.

10 The invention also relates to inhibitors identified thereby.

The use of a polynucleotide of the invention in genetic immunization will preferably employ a suitable delivery method such as direct injection of plasmid DNA into muscles (Wolff *et al.*, Hum. Mol. Genet. 1:363 (1992); Manthorpe *et al.*, Hum. Gene Ther. 4:419 (1993)), delivery of DNA complexed with specific protein carriers (Wu *et al.*, J. Biol. Chem. 264:16985 (1989)), coprecipitation of DNA with calcium phosphate (Benvenisty & Reshef, Proc. Nat'l Acad. Sci. USA, 83:9551 (1986)), encapsulation of DNA in various forms of liposomes (Kaneda *et al.*, Science 243:375 (1989)), particle bombardment (Tang *et al.*, Nature 356:152 (1992)); Eisenbraun *et al.*, DNA Cell Biol. 12:791 (1993)) and *in vivo* infection using cloned retroviral vectors (Seeger *et al.*, Proc. Nat'l Acad. Sci. USA 81:5849 (1984)). Suitable promoters for muscle transfection include CMV, RSV, SRa, actin, MCK, alpha globin, adenovirus and dihydrofolate reductase.

In therapy or as a prophylactic, the active agent i.e., the polypeptide, polynucleotide or inhibitor of the invention, may be administered to a patient as an injectable composition, for example as a sterile aqueous dispersion, preferably isotonic.

25 Alternatively the composition may be formulated for topical application for example in the form of ointments, creams, lotions, eye ointments, eye drops, ear drops, mouthwash, impregnated dressings and sutures and aerosols, and may contain appropriate conventional additives, including, for example, preservatives, solvents to assist drug penetration, and emollients in ointments and creams. Such topical formulations may also contain compatible conventional carriers, for example cream or ointment bases, and ethanol or oleyl alcohol for lotions. Such carriers may constitute from about 1% to about 98% by weight of the formulation; more usually they will constitute up to about 80% by weight of the formulation.

For administration to human patients, it is expected that the daily dosage level of the active agent will be from 0.01 to 10 mg/kg, typically around 1 mg/kg. The physician in any event will determine the actual dosage which will be most suitable for an individual patient and will vary with the age, weight and response of the particular patient. The above dosages are exemplary of the average case. There can, of course, be individual instances where higher or lower dosage ranges are merited, and such are within the scope of this invention.

A vaccine composition is conveniently in injectable form. Conventional adjuvants may be employed to enhance the immune response.

A suitable unit dose for vaccination is 0.5-5 μ g/kg of antigen, and such dose is preferably administered 1-3 times and with an interval of 1-3 weeks.

Within the indicated dosage range, no adverse toxicological effects are expected with the compounds of the invention which would preclude their administration to suitable patients.

15 EXAMPLES

In order to facilitate understanding of the following non-limiting examples certain frequently occurring methods and/or terms will be described.

"Plasmids" are designated by a lower case p preceded and/or followed by capital letters and/or numbers. The starting plasmids herein are either commercially available, publicly available on an unrestricted basis, or can be constructed from available plasmids in accord with published procedures. In addition, equivalent plasmids to those described are known in the art and will be apparent to the ordinarily skilled artisan.

"Digestion" of DNA refers to catalytic cleavage of the DNA with a restriction enzyme that acts only at certain sequences in the DNA. The various restriction enzymes used herein are commercially available and their reaction conditions, cofactors and other requirements were used as would be known to the ordinarily skilled artisan. For analytical purposes, typically 1 μ g of plasmid or DNA fragment is used with about 2 units of enzyme in about 20 μ l of buffer solution. For the purpose of isolating DNA fragments for plasmid construction, typically 5 to 50 μ g of DNA are digested with 20 to 250 units of enzyme in a larger volume. Appropriate buffers and substrate amounts for particular restriction enzymes are specified by the manufacturer. Incubation times of about 1 hour at 37 C are ordinarily used, but may vary in accordance with the supplier's instructions. After digestion the reaction is electrophoresed directly on a polyacrylamide gel to isolate the desired fragment.

Size separation of the cleaved fragments is performed using 8 percent polyacrylamide gel described by Goeddel, D. *et al.*, (1980) *Nucleic Acids Res.*, 8:4057.

"Oligonucleotides" refers to either a single stranded polydeoxynucleotide or two complementary polydeoxynucleotide strands which may be chemically synthesized. Such synthetic oligonucleotides have no 5' phosphate and thus will not ligate to another oligonucleotide without adding a phosphate with an ATP in the presence of a kinase. A synthetic oligonucleotide will ligate to a fragment that has not been dephosphorylated.

"Ligation" refers to the process of forming phosphodiester bonds between two double stranded nucleic acid fragments (Maniatis, T., *et al.*, *supra*, p. 146). Unless otherwise provided, ligation may be accomplished using known buffers and conditions with 10 units to T4 DNA ligase ("ligase") per 0.5 μ g of approximately equimolar amounts of the DNA fragments to be ligated.

Example 1

Isolation of DNA coding for a Novel Protein from *S. Aureus* WCUH 29

The polynucleotide having the DNA sequence given herein can be obtained from a library of clones of chromosomal DNA of *S.aureus* WCUH 29 in *E.coli*. Libraries may be prepared by routine methods, for example:

Methods 1 and 2.

Total cellular DNA is isolated from *Staphylococcus aureus* strain WCUH29 (NCIMB 40771) according to standard procedures and size-fractionated by either of two methods.

Method 1.

Total cellular DNA is mechanically sheared by passage through a needle in order to size-fractionate according to standard procedures. DNA fragments of up to 11 kbp in size are rendered blunt by treatment with exonuclease and DNA polymerase, and *EcoRI* linkers added. Fragments are ligated into the vector Lambda ZapII that has been cut with *EcoRI*, the library packaged by standard procedures and *E.coli* infected with the packaged library. The library is amplified by standard procedures.

Method 2.

Total cellular DNA is partially hydrolyzed with a combination of four restriction enzymes (*RsaI*, *PaeI*, *AluI* and *Bsh1235I*) and size-fractionated according to standard procedures. *EcoRI* linkers are ligated to the DNA and the fragments then ligated into the vector Lambda ZapII that have been cut with *EcoRI*, the library packaged by standard

procedures, and *E.coli* infected with the packaged library. The library is amplified by standard procedures.

Example 2

The determination of expression during infection of a gene from *Staphylococcus aureus* WCUH29

Necrotic fatty tissue from a four day groin infection of *Staphylococcus aureus* WCUH29 in the mouse is efficiently disrupted and processed in the presence of chaotropic agents and RNAase inhibitor to provide a mixture of animal and bacterial RNA. The optimal conditions for disruption and processing to give stable preparations and high yields of bacterial RNA are followed by the use of hybridization to a radiolabelled oligonucleotide specific to *Staphylococcus aureus* 16S RNA on Northern blots. The RNase free, DNase free, DNA and protein free preparations of RNA obtained are suitable for Reverse Transcription PCR (RT-PCR) using unique primer pairs designed from the sequence of each gene of *Staphylococcus aureus* WCUH29.

a) Isolation of tissue infected with *Staphylococcal aureus* WCUH29 from a mouse animal model of infection

10 ml. volumes of sterile nutrient broth (No.2 Oxoid) are seeded with isolated, individual colonies of *Staphylococcus aureus* WCUH29 from an agar culture plate.

The cultures are incubated aerobically (static culture) at 37 degrees C for 16-20 hours. 4 week old mice (female, 18g-22g, strain MF1) are each infected by subcutaneous injection of 0.5ml. of this broth culture of *Staphylococcus aureus* WCUH29 (diluted in broth to approximately 10⁸ cfu/ml.) into the anterior, right lower quadrant (groin area). Mice should be monitored regularly during the first 24 hours after infection, then daily until termination of study. Animals with signs of systemic infection, i.e. lethargy, ruffled appearance, isolation from group, should be monitored closely and if signs progress to moribundancy, the animal should be culled immediately.

Visible external signs of lesion development will be seen 24-48h after infection. Examination of the abdomen of the animal will show the raised outline of the abscess beneath the skin. The localized lesion should remain in the right lower quadrant, but may occasionally spread to the left lower quadrant, and superiorly to the thorax. On occasions, the abscess may rupture through the overlying skin layers. The affected animal should be culled immediately and the tissues sampled if possible. Failure to cull the animal may result in the necrotic skin tissue overlying the abscess being sloughed off, exposing the abdominal muscle wall.

Approximately 96h after infection, animals are killed using carbon dioxide asphyxiation. To minimize delay between death and tissue processing /storage, mice should be killed individually rather than in groups. The dead animal is placed onto its back and the fur swabbed liberally with 70% alcohol. An initial incision using scissors is made through the skin of the abdominal left lower quadrant, travelling superiorly up to, then across the thorax. The incision is completed by cutting inferiorly to the abdominal lower right quadrant. Care should be taken not to penetrate the abdominal wall. Holding the skin flap with forceps, the skin is gently pulled away from the abdomen. The exposed abscess, which covers the peritoneal wall but generally does not penetrate the muscle sheet completely, is excised, taking care not to puncture the viscera.

The abscess/muscle sheet and other infected tissue, such as the necrotic pads of fatty tissue in the abdominal lower right and left quadrants may require cutting in sections, prior to flash-freezing in liquid nitrogen, thereby allowing easier storage in plastic collecting vials.

b) Isolation of *Staphylococcus aureus* WCUH29 RNA from infected tissue samples

4-6 infected tissue samples(each approx 0.5-0.7g) in 2ml screw-cap tubes are removed from -80°C storage into a dry ice ethanol bath. In a microbiological safety cabinet the samples are disrupted individually whilst the remaining samples are kept cold in the dry ice ethanol bath. To disrupt the bacteria within the tissue sample 1ml of TRIzol Reagent (Gibco BRL, Life Technologies) is added followed by enough 0.1mm zirconia/silica beads to almost fill the tube, the lid is replaced taking care not to get any beads into the screw thread so as to ensure a good seal and eliminate aerosol generation. The sample is then homogenized in a Mini-BeadBeater Type BX-4 (Biospec Products). Necrotic fatty tissue is treated for 100 seconds at 5000 rpm in order to achieve bacterial lysis. *In vivo* grown bacteria require longer treatment than *in vitro* grown *S.aureus* WCUH29 which are disrupted by a 30 second bead-beat.

After bead-beating the tubes are chilled on ice before opening in a fume-hood as heat generated during disruption may degrade the TRIzol and release cyanide.

200 microlitres of chloroform is then added and the tubes shaken by hand for 15 seconds to ensure complete mixing. After 2-3 minutes at room temperature the tubes are spun down at 12,000 x g, 4 °C for 15 minutes and RNA extraction is then continued according to the method given by the manufacturers of TRIzol Reagent i.e.:- The aqueous phase, approx 0.6 ml, is transferred to a sterile eppendorf tube and 0.5 ml of isopropanol is added. After 10 minutes at room temperature the samples are spun at 12,000 x g, 4 °C for 10

minutes. The supernatant is removed and discarded then the RNA pellet is washed with 1 ml 75% ethanol. A brief vortex is used to mix the sample before centrifuging at 7,500 x g, 4 °C for 5 minutes. The ethanol is removed and the RNA pellet dried under vacuum for no more than 5 minutes. Samples are then resuspended by repeated pipetting in 100
5 microlitres of DEPC treated water, followed by 5-10 minutes at 55 °C. Finally, after at least 1 minute on ice, 200 units of Rnasin (Promega) is added. RNA preparations are stored at -80 °C for up to one month. For longer term storage the RNA precipitate can be stored at the wash stage of the protocol in 75% ethanol for at least one year at -20 °C.

10 Quality of the RNA isolated is assessed by running samples on 1% agarose gels. 1x TBE gels stained with ethidium bromide are used to visualize total RNA yields. To demonstrate the isolation of bacterial RNA from the infected tissue 1 x MOPS, 2.2M formaldehyde gels are run and vacuum blotted to Hybond-N (Amersham). The blot is then hybridized with a ³²P labelled oligonucleotide probe specific to 16s rRNA of *S.aureus* (K.
15 Greisen, *et al.*, *J. Clin. Microbiol.* 32 335-351(1994)). An oligonucleotide of the sequence: 5'-gctcctaaaaggttactccacggc-3' [SEQ ID NO:1166] is used as a probe. The size of the hybridizing band is compared to that of control RNA isolated from *in vitro* grown *S.aureus* WCUH29. Correct sized bacterial 16s rRNA bands can be detected in total RNA samples which show extensive degradation of the mammalian RNA when visualized on TBE gels.

20 **c) The removal of DNA from Staphylococcus aureus WCUH29 derived RNA**

DNA was removed from 73 microlitre samples of RNA by a 15 minute treatment on ice with 3 units of DNaseI, amplification grade (Gibco BRL, Life Technologies) in the buffer supplied with the addition of 200 units of Rnasin (Promega) in a final volume of 90 microlitres.

25 The DNase was inactivated and removed by treatment with TRIzol LS Reagent (Gibco BRL, Life Technologies) according to the manufacturers protocol. DNase treated RNA was resuspended in 73 microlitres of DEPC treated water with the addition of Rnasin as described in Method 1.

d) The preparation of cDNA from RNA samples derived from infected tissue

30 10 microlitre samples of DNase treated RNA are reverse transcribed using a SuperScript Preamplification System for First Strand cDNA Synthesis kit (Gibco BRL, Life Technologies) according to the manufacturers instructions. 1 nanogram of random hexamers is used to prime each reaction. Controls without the addition of SuperScriptII reverse

transcriptase are also run. Both +/-RT samples are treated with RNaseH before proceeding to the PCR reaction

e) The use of PCR to determine the presence of a bacterial cDNA species

PCR reactions are set up on ice in 0.2ml tubes by adding the following

5 components:

45 microlitres PCR SUPERMIX (Gibco BRL, Life Technologies).

1 microlitre 50mM MgCl₂, to adjust final concentration to 2.5mM.

1 microlitre PCR primers (optimally 18-25 basepairs designed to possess similar annealing temperatures), each primer at 10mM initial concentration.

10 2 microlitres cDNA.

PCR reactions are run on a Perkin Elmer GeneAmp PCR System 9600 as follows:

5 minutes at 95°C, then 50 cycles of 30 seconds each at 94°C, 42°C and 72°C followed by 3 minutes at 72°C and then a hold temperature of 4°C.

15 10 microlitre aliquots are then run out on 1% 1 x TBE gels stained with ethidium bromide with PCR product sizes estimated by comparison to a 100 bp DNA Ladder (Gibco BRL, Life Technologies).

RT/PCR controls may include +/- reverse transcriptase reactions, 16s rRNA primers or DNA specific primer pairs designed to produce PCR products from non-transcribed *S.aureus* WCUH29 genomic sequences.

20 To test the efficiency of the primer pairs they are used in DNA PCR with WCUH29 total DNA. PCR reactions are set up and run as described above using approx. 1 microgram of DNA in place of the cDNA and 35 cycles of PCR rather than 50.

Primer pairs which fail to give the predicted sized product in either DNA PCR or RT/PCR (approx 20%) are PCR failures and as such are uninformative. Of those which give the correct size product with DNA PCR three classes are distinguished in RT/PCR:

25 1. Genes which are not expressed *in vivo* reproducibly fail to give a product in RT/PCR.

2. Genes which are expressed *in vivo* reproducibly give the correct size product in RT/PCR and show a stronger signal in the +RT samples than in the -RT controls.

30 3. Genes which may be expressed *in vivo* give similar amounts of product in both +/-RT samples.

Table 1 sets forth certain information pertinent to cloning and identification of ORFs of the invention, such as reading frame direction (forward or reverse) on each polynucleotide in the Sequence Listing, a putative identity based on homology searches, the numbers of the first and last nucleic acid of the reading frame, and the number of codons in the ORF (including the stop codon). Using this information, expression vectors providing the selected protein are prepared and the protein is configured in an appropriate screen for the identification of anti-microbial agents. The SEQ ID NOS provided herewith for the amino acid (polypeptide) sequences are consecutively numbered to correlate with the information forth in Table 1, such that SEQ ID NO: 1 corresponds to the first sequence referenced in Table 1 and SEQ ID NO:623 corresponds to the last amino acid sequence referenced in Table 1. For the polynucleotide sequences SEQ ID NO:624 corresponds to the first polynucleotide sequence referenced in Table 1 and SEQ ID NO:1165 corresponds to the last sequence referenced Table 1.

Table 1

SEQ ID NO: __1__ ENCODED BY SEQ ID NO: __624__

ORF #	Start	End	Direction	Codon Length
1	64	396	F	111 codons

ORF translation from 64-396, direction F

Blastp and/or MPSearch Result:

Result: UNK

SEQ ID NO: __2__ ENCODED BY SEQ ID NO: __625__

ORF #	Start	End	Direction	Codon Length
1	127	375	F	83 codons

ORF translation from 127-375, direction F

Blastp and/or MPSearch Result:

Result: UNK

SEQ ID NO: 3 ENCODED BY SEQ ID NO: 626

5 ORF # Start End Direction Codon Length

 1 24 167 R 48 codons

ORF translation from 24-167, direction R

10

Blastp and/or MPSearch Result:

Result: UNK

15

20 SEQ ID NO: 4 ENCODED BY SEQ ID NO: 627

ORF # Start End Direction Codon Length

 1 241 378 R 46 codons

25

ORF translation from 241-378, direction R

Blastp and/or MPSearch Result:

30 Result: UNK

SEQ ID NO: 5 ENCODED BY SEQ ID NO: 628

35

ORF # Start End Direction Codon Length

 1 29 286 F 86 codons

40 ORF translation from 29-286, direction F

Blastp and/or MPSearch Result:

Result: UNK

SEQ ID NO: 6 ENCODED BY SEQ ID NO: 629

5

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	1	513	R	171 codons
---	---	-----	---	------------

10 ORF translation from 1-513, direction R

Blastp and/or MPSearch Result:

Description:

15 ESCHERICHIA COLI. PUTATIVE O-ANTIGEN TRANSPORTER.

SEQ ID NO: 7 ENCODED BY SEQ ID NO: 630

20 ORF # Start End Direction Codon Length

1	135	365	R	77 codons
---	-----	-----	---	-----------

25 ORF translation from 135-365, direction R

Blastp and/or MPSearch Result:

Result: UNK

30

SEQ ID NO: 8 ENCODED BY SEQ ID NO: 631

35 ORF # Start End Direction Codon Length

1	203	451	F	83 codons
---	-----	-----	---	-----------

40 ORF translation from 203-451, direction F

Blastp and/or MPSearch Result:

Description:

protein-methionine-S-oxide reductase (EC 1.8.4.6) - Escherichia coli

5 SEQ ID NO: __9__ ENCODED BY SEQ ID NO: __632__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	63	359	R	99 codons
---	----	-----	---	-----------

10

ORF translation from 63-359, direction R

15 Blastp and/or MPSearch Result:

Result: UNK

20 SEQ ID NO: __10__ ENCODED BY SEQ ID NO: __633__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	480	932	R	151 codons
---	-----	-----	---	------------

25

ORF translation from 480-932, direction R

30 Blastp and/or MPSearch Result:

Description:

STREPTOCOCCUS PNEUMONIAE. DNA POLYMERASE I (EC 2.7.7.7) (POL I).

35

SEQ ID NO: __11__ ENCODED BY SEQ ID NO: __634__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	265	444	R	60 codons
---	-----	-----	---	-----------

40

ORF translation from 265-444, direction R
Blastp and/or MPSearch Result:

Result: UNK

5

SEQ ID NO: _12,13_____ ENCODED BY SEQ ID NO: _635_____

ORF #	Start	End	Direction	Codon Length
1	28	258	F	77 codons
2	368	634	F	89 codons

10

15 ORF translation from 28-258, direction F

Blastp and/or MPSearch Result:

20 Result: UNK

ORF translation from 368-634, direction F

25 Blastp and/or MPSearch Result:

Result: UNK

30 SEQ ID NO: __14_____ ENCODED BY SEQ ID NO: __636_____

ORF #	Start	End	Direction	Codon Length
1	19	291	R	91 codons

35

ORF translation from 19-291, direction R

40 Blastp and/or MPSearch Result:

Description:

BACILLUS SUBTILIS. TECHOIC ACID BIOSYNTHESIS PROTEIN F.

5 SEQ ID NO: __15__ ENCODED BY SEQ ID NO: __637__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	93	224	R	44 codons
---	----	-----	---	-----------

10

ORF translation from 93-224, direction R

15 Blastp and/or MPSearch Result:

Result: UNK

20 SEQ ID NO: __16__ ENCODED BY SEQ ID NO: __638__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	141	386	F	82 codons
---	-----	-----	---	-----------

25

ORF translation from 141-386, direction F

30 Blastp and/or MPSearch Result:

Result: UNK

35

SEQ ID NO: __17__ ENCODED BY SEQ ID NO: __639__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

2	32	274	R	81 codons
---	----	-----	---	-----------

40

ORF translation from 32-274, direction R

Blastp and/or MPSearch Result:

Result: UNK

5

SEQ ID NO: __18__ ENCODED BY SEQ ID NO: __640__

	ORF #	Start	End	Direction	Codon Length
10	1	348	602	F	85 codons

ORF translation from 348-602, direction F

15

Blastp and/or MPSearch Result:

Result: UNK

20

SEQ ID NO: __19__ ENCODED BY SEQ ID NO: __641__

	ORF #	Start	End	Direction	Codon Length
25	2	159	305	F	49 codons

ORF translation from 159-305, direction F

30

Blastp and/or MPSearch Result:

Description:

35 ATP/GTP-binding protein

SEQ ID NO: __20__ ENCODED BY SEQ ID NO: __642__

	ORF #	Start	End	Direction	Codon Length
40	1	28	306	F	93 codons

ORF translation from 28-306, direction F

5 Blastp and/or MPSearch Result:

Result: UNK

10

SEQ ID NO: __21__ ENCODED BY SEQ ID NO: __643__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

15	1	44	415	R	124 codons
----	---	----	-----	---	------------

ORF translation from 44-415, direction R

20

Blastp and/or MPSearch Result:

Result: UNK

25

SEQ ID NO: __22__ ENCODED BY SEQ ID NO: __644__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

30	2	154	372	R	73 codons
----	---	-----	-----	---	-----------

ORF translation from 154-372, direction R

35

Blastp and/or MPSearch Result:

Result: UNK

40

SEQ ID NO: __23__ ENCODED BY SEQ ID NO: __645__

ORF #	Start	End	Direction	Codon Length
2	313	411	F	33 codons

5

ORF translation from 313-411, direction F

Blastp and/or MPSearch Result:

10

Result: UNK

15 SEQ ID NO: _24_____ ENCODED BY SEQ ID NO: _646_____

ORF #	Start	End	Direction	Codon Length
1	192	380	F	63 codons

20

ORF translation from 192-380, direction F

25 Blastp and/or MPSearch Result:

Result: UNK

30

SEQ ID NO: _25_____ ENCODED BY SEQ ID NO: _647_____

ORF #	Start	End	Direction	Codon Length
1	39	275	F	79 codons

35

ORF translation from 39-275, direction F

40

Blastp and/or MPSearch Result:

Description:

THERMOTOGA MARITIMA. PHOSPHOGLYCERATE KINASE (EC 2.7.2.3).

5 SEQ ID NO: 26 ENCODED BY SEQ ID NO: 648

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	83	250	R	56 codons
---	----	-----	---	-----------

10

ORF translation from 83-250, direction R

15 Blastp and/or MPSearch Result:

Result: UNK

20

SEQ ID NO: 27 ENCODED BY SEQ ID NO: 649

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	159	380	F	74 codons
---	-----	-----	---	-----------

25

ORF translation from 159-380, direction F

30

Blastp and/or MPSearch Result:

Description:

ABC transporter

35

SEQ ID NO: 28 ENCODED BY SEQ ID NO: 650

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	200	328	F	43 codons
---	-----	-----	---	-----------

40

ORF translation from 200-328, direction F

Blastp and/or MPSearch Result:

5

Description:

BACILLUS SUBTILIS. THREONYL-TRNA SYNTHETASE 1 (EC 6.1.1.3)
(THREONINE-TRNA LIGASE) (THRRS).

10

SEQ ID NO: __29__ ENCODED BY SEQ ID NO: __651__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

15	1	262	378	F	39 codons
----	---	-----	-----	---	-----------

ORF translation from 262-378, direction F

20

Blastp and/or MPSearch Result:

Result: UNK

25

SEQ ID NO: __30__ ENCODED BY SEQ ID NO: __652__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

30	1	127	438	F	104 codons
----	---	-----	-----	---	------------

ORF translation from 127-438, direction F

35

Blastp and/or MPSearch Result:

Description:

40 PSEUDOMONAS AERUGINOSA. ARGININE/ORNITHINE ANTIporter.

SEQ ID NO: __31__ ENCODED BY SEQ ID NO: __653__

5 ORF # Start End Direction Codon Length

 1 89 358 R 90 codons

10 ORF translation from 89-358, direction R

Blastp and/or MPSearch Result:

15 Result: UNK

SEQ ID NO: __32__ ENCODED BY SEQ ID NO: __654__

20 ORF # Start End Direction Codon Length

 1 131 382 F 84 codons

25 ORF translation from 131-382, direction F

Blastp and/or MPSearch Result:

30 Description:
SALMONELLA TYPHIMURIUM. HEXOSE PHOSPHATE TRANSPORT PROTEIN.

35 SEQ ID NO: __33__ ENCODED BY SEQ ID NO: __655__

40 ORF # Start End Direction Codon Length

 1 245 361 F 39 codons

ORF translation from 245-361, direction F

Blastp and/or MPSearch Result:

Result: UNK

5

SEQ ID NO: __34__ ENCODED BY SEQ ID NO: __656__

10 ORF # Start End Direction Codon Length

1 135 245 F 37 codons

15 ORF translation from 135-245, direction F

Blastp and/or MPSearch Result:

20 Result: UNK

SEQ ID NO: __35__ ENCODED BY SEQ ID NO: __657__

25

ORF # Start End Direction Codon Length

1 265 426 R 54 codons

30

ORF translation from 265-426, direction R

Blastp and/or MPSearch Result:

Result: UNK

35

SEQ ID NO: __36__ ENCODED BY SEQ ID NO: __658__

40 ORF # Start End Direction Codon Length

1 277 459 R 61 codons

ORF translation from 277-459, direction R

Blastp and/or MPSearch Result:

5

Description:

TRANSKETOLASE 1 (EC 2.2.1.1) (TK 1). - ESCHERICHIA COLI.

10 SEQ ID NO: 37 ENCODED BY SEQ ID NO: 659

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	42	326	R	95 codons
---	----	-----	---	-----------

15

ORF translation from 42-326, direction R

Blastp and/or MPSearch Result:

20

Result: UNK

25 SEQ ID NO: 38 ENCODED BY SEQ ID NO: 660

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	172	294	F	41 codons
---	-----	-----	---	-----------

30

ORF translation from 172-294, direction F

35 Blastp and/or MPSearch Result:

Result: UNK

40

SEQ ID NO: 39 ENCODED BY SEQ ID NO: 661

ORF #	Start	End	Direction	Codon Length
1	227	331	F	35 codons

5

ORF translation from 227-331, direction F

10 Blastp and/or MPSearch Result:

Result: UNK

15 SEQ ID NO: __40__ ENCODED BY SEQ ID NO: __662__

ORF #	Start	End	Direction	Codon Length
1	58	207	R	50 codons

20

ORF translation from 58-207, direction R

25 Blastp and/or MPSearch Result:

Description:

30 BACILLUS SUBTILIS. CARBAMOYL-PHOSPHATE SYNTHASE, PYRIMIDINE-SPECIFIC, LARGE CHAIN (EC 6.3.5.5) (CARBAMOYL-PHOSPHATE SYNTHETASE AMMONIA CHAIN).

35 SEQ ID NO: __41__ ENCODED BY SEQ ID NO: __663__

ORF #	Start	End	Direction	Codon Length
1	121	426	F	102 codons

40

ORF translation from 121-426, direction F

Blastp and/or MPSearch Result:

Description:

ESCHERICHIA COLI. SEQA PROTEIN.

5

SEQ ID NO: _42_ ENCODED BY SEQ ID NO: _664_

ORF #	Start	End	Direction	Codon Length
1	20	223	R	68 codons

ORF translation from 20-223, direction R

15 Blastp and/or MPSearch Result:

Result: UNK

20

SEQ ID NO: _43_ ENCODED BY SEQ ID NO: _665_

ORF #	Start	End	Direction	Codon Length
1	18	329	R	104 codons

ORF translation from 18-329, direction R

30

Blastp and/or MPSearch Result:

Result: UNK

35

SEQ ID NO: _44_ ENCODED BY SEQ ID NO: _666_

ORF #	Start	End	Direction	Codon Length
3	142	369	F	76 codons

ORF translation from 142-369, direction F

5 Blastp and/or MPSearch Result:

Result: UNK

10

SEQ ID NO: __45__ ENCODED BY SEQ ID NO: __667__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

15	2	181	369	R	63 codons
----	---	-----	-----	---	-----------

ORF translation from 181-369, direction R

20 Blastp and/or MPSearch Result:

Description:

BACILLUS SUBTILIS. PHOSPHORIBOSYLAMINOIMIDAZOLECARBOXAMIDE
FORMYLTRANSFERASE (EC 2.1.2.3) (AICAR TRANSFORMYLASE) / IMP

25 CYCLOHYDROLASE (EC 3.5.4.10) (INOSINICASE) (IMP SYNTHETASE) (ATIC).

30 SEQ ID NO: __46__ ENCODED BY SEQ ID NO: __668__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

35	1	65	268	F	68 codons
----	---	----	-----	---	-----------

ORF translation from 65-268, direction F

40 Blastp and/or MPSearch Result:

Description:

LACTOBACILLUS PLANTARUM. REP PROTEIN (REPLICATION PROTEIN).

SEQ ID NO: 47 ENCODED BY SEQ ID NO: 669

5 ORF # Start End Direction Codon Length

ORF #	Start	End	Direction	Codon Length
1	133	375	F	81 codons

10 ORF translation from 133-375, direction F

Blastp and/or MPSearch Result:

Result: UNK

15

SEQ ID NO: 48 ENCODED BY SEQ ID NO: 670

20 ORF # Start End Direction Codon Length

ORF #	Start	End	Direction	Codon Length
2	202	387	F	62 codons

25 ORF translation from 202-387, direction F

Blastp and/or MPSearch Result:

30 Description:

ATP/GTP-binding protein

SEQ ID NO: 49 ENCODED BY SEQ ID NO: 671

35 ORF # Start End Direction Codon Length

ORF #	Start	End	Direction	Codon Length
1	7	339	R	111 codons

40 ORF translation from 7-339, direction R

Blastp and/or MPSearch Result:

Description:

PSEUDOURIDYLATE SYNTHASE I (EC 4.2.1.70) (PSEUDOURIDINE SYNTHASE I)
(URACIL HYDROLYASE). - ESCHERICHIA COLI.

5 SEQ ID NO: _50_ ENCODED BY SEQ ID NO: _672_

ORF #	Start	End	Direction	Codon Length
1	51	299	F	83 codons

10

ORF translation from 51-299, direction F

15 Blastp and/or MPSearch Result:

Result: UNK

20 SEQ ID NO: _51_ ENCODED BY SEQ ID NO: _673_

ORF #	Start	End	Direction	Codon Length
1	109	378	F	90 codons

25

ORF translation from 109-378, direction F

30 Blastp and/or MPSearch Result:

Description:

ESCHERICHIA COLI. OUTER MEMBRANE PROTEIN F PRECURSOR (OUTER
MEMBRANE PROTEIN 1A, 1A, OR B).

35

SEQ ID NO: _52_ ENCODED BY SEQ ID NO: _674_

40

ORF #	Start	End	Direction	Codon Length
2	268	378	F	37 codons

ORF translation from 268-378, direction F

5

Blastp and/or MPSearch Result:

Description:

10 PROBABLE UDP-N-ACETYLGLUCOSAMINE 1-CARBOXYVINYLTRANSFERASE
(EC 2.5.1.7) (ENOYLPYRUVATE TRANSFERASE) (UDP-N-
ACETYLGLUCOSAMINE ENOLPYRUVYL TRANSFERASE). - BACILLUS
SUBTILIS.

15

SEQ ID NO: __53__ ENCODED BY SEQ ID NO: __675__

	ORF #	Start	End	Direction	Codon Length
20	1	303	437	F	45 codons

ORF translation from 303-437, direction F

25

Blastp and/or MPSearch Result:

Description:

30 UDP-N-ACETYLGLUCOSAMINE 1-CARBOXYVINYLTRANSFERASE (EC 2.5.1.7)
(ENOYLPYRUVATE TRANSFERASE) (UDP-N-ACETYLGLUCOSAMINE
ENOLPYRUVYL TRANSFERASE). - ACINETOBACTER CALCOACETICUS.

SEQ ID NO: __54__ ENCODED BY SEQ ID NO: __676__

	ORF #	Start	End	Direction	Codon Length
35	1	7	216	R	70 codons

40 ORF translation from 7-216, direction R

Blastp and/or MPSearch Result:

Result: UNK

5

SEQ ID NO: __55__ ENCODED BY SEQ ID NO: __677__

ORF #	Start	End	Direction	Codon Length
1	20	160	R	47 codons

ORF translation from 20-160, direction R

15 Blastp and/or MPSearch Result:

Description:

BACILLUS STEAROTHERMOPHILUS. GLUTAMINE TRANSPORT ATP-BINDING
PROTEIN GLNQ.

20

SEQ ID NO: __56__ ENCODED BY SEQ ID NO: __678__

ORF #	Start	End	Direction	Codon Length
1	119	328	F	70 codons

ORF translation from 119-328, direction F

30

Blastp and/or MPSearch Result:

Result: UNK

35

SEQ ID NO: __57__ ENCODED BY SEQ ID NO: __679__

40

ORF #	Start	End	Direction	Codon Length
1	32	163	R	44 codons

ORF translation from 32-163, direction R

5 Blastp and/or MPSearch Result:

Result: UNK

10 SEQ ID NO: __58__ ENCODED BY SEQ ID NO: __680__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	7	246	R	80 codons
---	---	-----	---	-----------

15

ORF translation from 7-246, direction R

20 Blastp and/or MPSearch Result:

Description:

BACILLUS SUBTILIS. ALKALINE PHOSPHATASE III PRECURSOR (EC 3.1.3.1)
(APASE III).

25

SEQ ID NO: __59__ ENCODED BY SEQ ID NO: __681__

ORF #	Start	End	Direction	Codon Length
1	45	323	R	93 codons

30

ORF translation from 45-323, direction R

35

Blastp and/or MPSearch Result:

Result: UNK

40

SEQ ID NO: __60__ ENCODED BY SEQ ID NO: __682__

ORF #	Start	End	Direction	Codon Length
2	251	355	F	35 codons

5

ORF translation from 251-355, direction F

Blastp and/or MPSearch Result:

10

Result: UNK

SEQ ID NO: __61__ ENCODED BY SEQ ID NO: __683__

15

ORF #	Start	End	Direction	Codon Length
1	24	233	R	70 codons

20

ORF translation from 24-233, direction R

Blastp and/or MPSearch Result:

25

Result: UNK

30 SEQ ID NO: __62__ ENCODED BY SEQ ID NO: __684__

ORF #	Start	End	Direction	Codon Length
1	51	302	R	84 codons

35

ORF translation from 51-302, direction R

Blastp and/or MPSearch Result:

40

Result: UNK

SEQ ID NO: 63 ENCODED BY SEQ ID NO: 685

	ORF #	Start	End	Direction	Codon Length
5	1	7	396	R	130 codons

ORF translation from 7-396, direction R

10 Blastp and/or MPSearch Result:

Description:
ABC Transporter

15

SEQ ID NO: 64 ENCODED BY SEQ ID NO: 686

	ORF #	Start	End	Direction	Codon Length
20	1	172	303	F	44 codons

25 ORF translation from 172-303, direction F

Blastp and/or MPSearch Result:

30 Description:
ALCALIGENES EUTROPHUS. MEMBRANE PROTEIN.SEQ ID NO: 65 ENCODED BY SEQ ID NO: 687

35

	ORF #	Start	End	Direction	Codon Length
	1	41	349	F	103 codons

40

1 ORF translation from 41-349, direction F

Blastp and/or MPSearch Result:

Result: UNK

5

SEQ ID NO: __66__ ENCODED BY SEQ ID NO: __688__

ORF #	Start	End	Direction	Codon Length
1	72	347	R	92 codons

15

ORF translation from 72-347, direction R

Blastp and/or MPSearch Result:

20

Description:

ESCHERICHIA COLI. IRON(III) DICITRATE TRANSPORT SYSTEM PERMEASE
PROTEIN FECD.

25

SEQ ID NO: __67__ ENCODED BY SEQ ID NO: __689__

ORF #	Start	End	Direction	Codon Length
1	65	253	F	63 codons

ORF translation from 65-253, direction F

35

Blastp and/or MPSearch Result:

Result: UNK

SEQ ID NO: __68__ ENCODED BY SEQ ID NO: __690__

40

ORF #	Start	End	Direction	Codon Length
1	114	536	F	141 codons

ORF translation from 114-536, direction F

5 Blastp and/or MPSearch Result:

Description:

BACILLUS SUBTILIS. REPLICATIVE DNA HELICASE (EC 3.6.1.-).

10

SEQ ID NO: __69__ ENCODED BY SEQ ID NO: __691__

ORF #	Start	End	Direction	Codon Length
1	46	402	R	119 codons

20

ORF translation from 46-402, direction R

Blastp and/or MPSearch Result:

Description:

25 ESCHERICHIA COLI. NICKEL TRANSPORT SYSTEM PERMEASE PROTEIN NIKC.

30

SEQ ID NO: __70__ ENCODED BY SEQ ID NO: __692__

ORF #	Start	End	Direction	Codon Length
1	227	334	F	36 codons

35

ORF translation from 227-334, direction F

40

Blastp and/or MPSearch Result:

Result: UNK

SEQ ID NO: __71__ ENCODED BY SEQ ID NO: __693__

5 ORF # Start End Direction Codon Length

ORF #	Start	End	Direction	Codon Length
1	184	342	F	53 codons

10 ORF translation from 184-342, direction F

Blastp and/or MPSearch Result:

15 Result: UNK

SEQ ID NO: __72__ ENCODED BY SEQ ID NO: __694__

20

ORF # Start End Direction Codon Length

ORF #	Start	End	Direction	Codon Length
1	17	367	R	117 codons

25

ORF translation from 17-367, direction R

Blastp and/or MPSearch Result:

30

Result: UNK

SEQ ID NO: __73__ ENCODED BY SEQ ID NO: __695__

35

ORF # Start End Direction Codon Length

ORF #	Start	End	Direction	Codon Length
1	159	317	F	53 codons

40

ORF translation from 159-317, direction F

Blastp and/or MPSearch Result:**Description:**

5 nerve growth factor {promoter} [human, Genomic, 486 nt]. ptsG protein - Staphylococcus
carnosus

10 SEQ ID NO: __74__ ENCODED BY SEQ ID NO: __696__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	2	409	F	136 codons
---	---	-----	---	------------

15

ORF translation from 2-409, direction F

20 Blastp and/or MPSearch Result:

Result: UNK

25

SEQ ID NO: __75,76__ ENCODED BY SEQ ID NO: __697__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

2	547	720	F	58 codons
3	915	1079	F	55 codons

30

ORF translation from 547-720, direction F

35

Blastp and/or MPSearch Result:

Result: UNK

40

ORF translation from 915-1079, direction F

Blastp and/or MPSearch Result:

Description:

5 ATP/GTP-binding protein

10 SEQ ID NO: __77__ ENCODED BY SEQ ID NO: __698__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	68	271	F	68 codons
---	----	-----	---	-----------

15 ORF translation from 68-271, direction F

Blastp and/or MPSearch Result:

Description:

20 BACILLUS SUBTILIS. PROBABLE ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1) (TRANSAMINASE A) (ASPAT).

25 SEQ ID NO: __78__ ENCODED BY SEQ ID NO: __699__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

2	699	797	F	33 codons
---	-----	-----	---	-----------

30

ORF translation from 699-797, direction F

Blastp and/or MPSearch Result:

35

Result: UNK

40 SEQ ID NO: __79__ ENCODED BY SEQ ID NO: __700__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

2 483 716 F 78 codons

ORF translation from 483-716, direction F

5

Blastp and/or MPSearch Result:

Result: UNK

10

SEQ ID NO: __80__ ENCODED BY SEQ ID NO: __701__

15 ORF # Start End Direction Codon Length

ORF #	Start	End	Direction	Codon Length
1	223	483	R	87 codons

20 ORF translation from 223-483, direction R

Blastp and/or MPSearch Result:

Result: UNK

25

SEQ ID NO: __81__ ENCODED BY SEQ ID NO: __702__

30 ORF # Start End Direction Codon Length

ORF #	Start	End	Direction	Codon Length
1	365	574	R	70 codons

35 ORF translation from 365-574, direction R

Blastp and/or MPSearch Result:

Description:

40 BACILLUS SUBTILIS. FERROCHELATASE (EC 4.99.1.1) (PROTOHEME FERRO-
LYASE) (HEME SYNTHETASE).

SEQ ID NO: __82__ ENCODED BY SEQ ID NO: __703__

5 ORF # Start End Direction Codon Length

 1 98 535 F 146 codons

10 ORF translation from 98-535, direction F

Blastp and/or MPSearch Result:

15 Result: UNK

SEQ ID NO: __83__ ENCODED BY SEQ ID NO: __704__

20 ORF # Start End Direction Codon Length

 2 460 726 F 89 codons

25 ORF translation from 460-726, direction F
Blastp and/or MPSearch Result:

30 Result: UNK

SEQ ID NO: __84__ ENCODED BY SEQ ID NO: __705__

35 ORF # Start End Direction Codon Length

 1 22 384 R 121 codons

40 ORF translation from 22-384, direction R

Blastp and/or MPSearch Result:

Description:

ESCHERICHIA COLI. MALONYL COA-ACYL CARRIER PROTEIN
TRANSACYLASE (EC 2.3.1.39) (MCT).

5 SEQ ID NO: __85__ ENCODED BY SEQ ID NO: __706__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	339	560	F	74 codons
---	-----	-----	---	-----------

10

ORF translation from 339-560, direction F

15 Blastp and/or MPSearch Result:

Result: UNK

20 SEQ ID NO: __86,87__ ENCODED BY SEQ ID NO: __707__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	129	419	R	97 codons
2	554	829	R	92 codons

25

ORF translation from 129-419, direction R

30

Blastp and/or MPSearch Result:

Result: UNK

35

ORF translation from 554-829, direction R

40

Blastp and/or MPSearch Result:

Result: UNK

SEQ ID NO: __88__ ENCODED BY SEQ ID NO: __708__

5 ORF # Start End Direction Codon Length

 2 159 353 R 65 codons

ORF translation from 159-353, direction R

10

Blastp and/or MPSearch Result:

Result: UNK

15

SEQ ID NO: __89,90,91__ ENCODED BY SEQ ID NO: __709__

20 ORF # Start End Direction Codon Length

 2 1212 1445 R 78 codons
 3 1456 1587 R 44 codons
 4 1705 2016 R 104 codons

25

ORF translation from 1212-1445, direction R

MDQHINILGASSDHLMLDLNGQGHYQVGDHISFSLNVEALSHSMYMKNLHKVYID
DSKID

30 TLLQNFDVKSPAMVNQY*

Blastp and/or MPSearch Result:

35 Result: UNK

ORF translation from 1456-1587, direction R

40 Blastp and/or MPSearch Result:

Result: UNK

ORF translation from 1705-2016, direction R

Blastp and/or MPSearch Result:

5

Result: UNK

SEQ ID NO: __92__ ENCODED BY SEQ ID NO: __710__

ORF #	Start	End	Direction	Codon Length
1	167	382	F	72 codons

15 ORF translation from 167-382, direction F

Blastp and/or MPSearch Result:

20 Result: UNK

SEQ ID NO: __93__ ENCODED BY SEQ ID NO: __711__

ORF #	Start	End	Direction	Codon Length
1	155	283	F	43 codons

30 ORF translation from 155-283, direction F

Blastp and/or MPSearch Result:

35 Description:

ATP-dependent Clp proteinase (EC 3.4.21.-) chain clpL - Lactococcus

SEQ ID NO: __94__ ENCODED BY SEQ ID NO: __712__

40

ORF #	Start	End	Direction	Codon Length
1	57	245	R	63 codons

ORF translation from 57-245, direction R

5

Blastp and/or MPSearch Result:

Result: UNK

10

SEQ ID NO: __95__ ENCODED BY SEQ ID NO: __713__

ORF #	Start	End	Direction	Codon Length
1	57	245	R	63 codons

ORF translation from 57-245, direction R

20

Blastp and/or MPSearch Result:

Result: UNK

25

SEQ ID NO: __96__ ENCODED BY SEQ ID NO: __714__

ORF #	Start	End	Direction	Codon Length
1	179	331	R	51 codons

35 ORF translation from 179-331, direction R

Blastp and/or MPSearch Result:

40 Result: UNK

SEQ ID NO: __97__ ENCODED BY SEQ ID NO: __715__

ORF #	Start	End	Direction	Codon Length
1	3	113	R	37 codons

5

ORF translation from 3-113, direction R

Blastp and/or MPSearch Result:

10

Description:

BACILLUS SUBTILIS. 2-OXOISOVALERATE DEHYDROGENASE BETA SUBUNIT
(EC 1.2.4.4) (BRANCHED- CHAIN ALPHA-KETO ACID DEHYDROGENASE
COMPONENT BETA CHAIN (E1)) (BCKDH E1-BETA).

15

SEQ ID NO: __98__ ENCODED BY SEQ ID NO: __716__

20

ORF #	Start	End	Direction	Codon Length
1	70	228	R	53 codons

25

ORF translation from 70-228, direction R

Blastp and/or MPSearch Result:

30

Result: UNK

35 SEQ ID NO: __99__ ENCODED BY SEQ ID NO: __717__

ORF #	Start	End	Direction	Codon Length
1	7	441	R	145 codons

40

ORF translation from 7-441, direction R

Blastp and/or MPSearch Result:

Description:

LACTOCOCCUS LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS).

ACETOLACTATE SYNTHASE LARGE SUBUNIT (EC 4.1.3.18) (AHAS)

5 (ACETOHYDROXY-ACID SYNTHASE LARGE SUBUNIT) (ALS).

10 SEQ ID NO: __100__ ENCODED BY SEQ ID NO: __718__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	279	485	F	69 codons
---	-----	-----	---	-----------

15

ORF translation from 279-485, direction F

Blastp and/or MPSearch Result:

20

Result: UNK

SEQ ID NO: __101__ ENCODED BY SEQ ID NO: __719__

25

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	517	660	R	48 codons
---	-----	-----	---	-----------

30

ORF translation from 517-660, direction R

Blastp and/or MPSearch Result:

35

Description:

BACILLUS SUBTILIS. PROTEASE SYNTHASE AND SPORULATION NEGATIVE
REGULATORY PROTEIN PAI 1.

40

SEQ ID NO: __102__ ENCODED BY SEQ ID NO: __720__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	172	402	F	77 codons
---	-----	-----	---	-----------

5

ORF translation from 172-402, direction F

Blastp and/or MPSearch Result:

10

Result: UNK

15 SEQ ID NO: __103__ ENCODED BY SEQ ID NO: __721__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	312	482	F	57 codons
---	-----	-----	---	-----------

20

ORF translation from 312-482, direction F

25 Blastp and/or MPSearch Result:

Result: UNK

30 SEQ ID NO: __104__ ENCODED BY SEQ ID NO: __722__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

2	168	404	F	79 codons
---	-----	-----	---	-----------

35

ORF translation from 168-404, direction F

40 Blastp and/or MPSearch Result:

Result: UNK

SEQ ID NO: __105__ ENCODED BY SEQ ID NO: __723__

5 ORF # Start End Direction Codon Length

1 514 933 F 140 codons

10 ORF translation from 514-933, direction F

Blastp and/or MPSearch Result:

15 Description:

THERMOTOGA MARITIMA. GLYCERALDEHYDE 3-PHOSPHATE
DEHYDROGENASE (EC 1.2.1.12) (GAPDH).

20

SEQ ID NO: __106__ ENCODED BY SEQ ID NO: __724__

ORF # Start End Direction Codon Length

25 2 632 961 R 110 codons

ORF translation from 632-961, direction R

30 Blastp and/or MPSearch Result:

Result: UNK

35

SEQ ID NO: __107__ ENCODED BY SEQ ID NO: __725__

ORF # Start End Direction Codon Length

40 1 141 323 R 61 codons

ORF translation from 141-323, direction R

Blastp and/or MPSearch Result:

Result: UNK

5

SEQ ID NO: __108,109__ ENCODED BY SEQ ID NO: __726__

ORF #	Start	End	Direction	Codon Length
1	47	943	F	299 codons
2	978	1112	F	45 codons

10

15 ORF translation from 47-943, direction F

Blastp and/or MPSearch Result:

Result: UNK

20

ORF translation from 978-1112, direction F

25 Blastp and/or MPSearch Result:

Result: UNK

30

SEQ ID NO: __110,111__ ENCODED BY SEQ ID NO: __727__

ORF #	Start	End	Direction	Codon Length
1	4	192	R	63 codons
2	224	352	R	43 codons

35

ORF translation from 4-192, direction R

40

Blastp and/or MPSearch Result:

Result: UNK

ORF translation from 224-352, direction R

5

Blastp and/or MPSearch Result:

Result: UNK

10

SEQ ID NO: __112__ ENCODED BY SEQ ID NO: __728__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

15	1	25	303	R	93 codons
----	---	----	-----	---	-----------

ORF translation from 25-303, direction R

20

Blastp and/or MPSearch Result:

Result: UNK

25

SEQ ID NO: __113__ ENCODED BY SEQ ID NO: __729__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	263	652	R	130 codons
---	-----	-----	---	------------

35 ORF translation from 263-652, direction R

Blastp and/or MPSearch Result:

Result: UNK

40

SEQ ID NO: __114__ ENCODED BY SEQ ID NO: __730__

ORF #	Start	End	Direction	Codon Length
1	84	617	R	178 codons

5

ORF translation from 84-617, direction R

Blastp and/or MPSearch Result:

10

Description:

surfactin synthetase - Bacillus subtilis

15 SEQ ID NO: __115__ ENCODED BY SEQ ID NO: __731__

ORF #	Start	End	Direction	Codon Length
1	31	213	R	61 codons

20

ORF translation from 31-213, direction R

25 Blastp and/or MPSearch Result:

Result: UNK

30

SEQ ID NO: __116__ ENCODED BY SEQ ID NO: __732__

ORF #	Start	End	Direction	Codon Length
2	533	658	F	42 codons

35

ORF translation from 533-658, direction F

40

Blastp and/or MPSearch Result:

Result: UNK

5

SEQ ID NO: __117__ ENCODED BY SEQ ID NO: __733__

	ORF #	Start	End	Direction	Codon Length
10	1	175	396	F	74 codons

ORF translation from 175-396, direction F

15

Blastp and/or MPSearch Result:

Result: UNK

20 SEQ ID NO: __118__ ENCODED BY SEQ ID NO: __734__

	ORF #	Start	End	Direction	Codon Length
25	1	3	248	R	82 codons

ORF translation from 3-248, direction R

Blastp and/or MPSearch Result:

30

Description:

ATP/GTP-binding protein

35

SEQ ID NO: __119__ ENCODED BY SEQ ID NO: __735__

	ORF #	Start	End	Direction	Codon Length
40	1	160	378	R	73 codons

ORF translation from 160-378, direction R

Blastp and/or MPSearch Result:

5 Result: UNK

SEQ ID NO: __120__ ENCODED BY SEQ ID NO: __736__

10	ORF #	Start	End	Direction	Codon Length
	1	202	546	R	115 codons

15 ORF translation from 202-546, direction R

Blastp and/or MPSearch Result:

Result: UNK

20

SEQ ID NO: __121__ ENCODED BY SEQ ID NO: __737__

25	ORF #	Start	End	Direction	Codon Length
	1	2	349	F	116 codons

30 ORF translation from 2-349, direction F

Blastp and/or MPSearch Result:

35 Result: UNK

SEQ ID NO: __122__ ENCODED BY SEQ ID NO: __738__

40	ORF #	Start	End	Direction	Codon Length
	1	1	285	F	95 codons

ORF translation from 1-285, direction F

5 Blastp and/or MPSearch Result:

Result: UNK

10 SEQ ID NO: __123,124__ ENCODED BY SEQ ID NO: __739__

	ORF #	Start	End	Direction	Codon Length
	2	487	828	R	114 codons
15	3	905	1120	R	72 codons

ORF translation from 487-828, direction R

20 Blastp and/or MPSearch Result:

Result: UNK

ORF translation from 905-1120, direction R

25 MSKLLMIGTGPVAIQLANICYLKSDYEIDMVGRASTSEKSKRLYQAYKKEKQFEVK
IQNE
AHQHLEGKFGN*

30 Blastp and/or MPSearch Result:

Description:

Putative nucleotide-binding protein

35

SEQ ID NO: __125__ ENCODED BY SEQ ID NO: __740__

	ORF #	Start	End	Direction	Codon Length
40	2	193	555	F	121 codons

ORF translation from 193-555, direction F

Blastp and/or MPSearch Result:

Result: UNK

SEQ ID NO: __126__ ENCODED BY SEQ ID NO: __741__

ORF #	Start	End	Direction	Codon Length
1	61	339	F	93 codons

ORF translation from 61-339, direction F

Blastp and/or MPSearch Result:

Result: UNK

SEQ ID NO: __127__ ENCODED BY SEQ ID NO: __742__

ORF #	Start	End	Direction	Codon Length
1	251	706	F	152 codons

ORF translation from 251-706, direction F

Blastp and/or MPSearch Result:

Description:

ESCHERICHIA COLI. NICKEL TRANSPORT SYSTEM PERMEASE PROTEIN NIKC.

SEQ ID NO: __128__ ENCODED BY SEQ ID NO: __743__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1 126 326 F 67 codons

5 ORF translation from 126-326, direction F

Blastp and/or MPSearch Result:

Result: UNK

10

SEQ ID NO: __129__ ENCODED BY SEQ ID NO: __744__

15 ORF # Start End Direction Codon Length

1 25 579 R 185 codons

ORF translation from 25-579, direction R

20

Blastp and/or MPSearch Result:

Description:

25 LACTOCOCCUS LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS). ATP
PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.17).

SEQ ID NO: __130__ ENCODED BY SEQ ID NO: __745__

30

ORF # Start End Direction Codon Length

1 641 826 F 62 codons

35

ORF translation from 641-826, direction F

Blastp and/or MPSearch Result:

40 Description:

STAPHYLOCOCCUS AUREUS. ARSENICAL PUMP MEMBRANE PROTEIN.

SEQ ID NO: __131__ ENCODED BY SEQ ID NO: __746__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

5	1	198	473	F	92 codons
---	---	-----	-----	---	-----------

ORF translation from 198-473, direction F

10 Blastp and/or MPSearch Result:

Result: UNK

15

SEQ ID NO: __132__ ENCODED BY SEQ ID NO: __747__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

20	1	95	409	R	105 codons
----	---	----	-----	---	------------

ORF translation from 95-409, direction R

25 Blastp and/or MPSearch Result:

Description:

LACALS NCBI gi: 473900NCBI gi: 473748 - *Lactococcus lactis* (strain DSM 20384, sub_species lactis) DNA.

30

SEQ ID NO: __133__ ENCODED BY SEQ ID NO: __748__

35

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	342	542	R	67 codons
---	-----	-----	---	-----------

40 ORF translation from 342-542, direction R

Blastp and/or MPSearch Result:

Result: UNK

5

SEQ ID NO: __134__ ENCODED BY SEQ ID NO: __749__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

10	2	179	598	F	140 codons
----	---	-----	-----	---	------------

ORF translation from 179-598, direction F

15

Blastp and/or MPSearch Result:

Result: UNK

20

SEQ ID NO: __135__ ENCODED BY SEQ ID NO: __750__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

25	1	179	382	R	68 codons
----	---	-----	-----	---	-----------

ORF translation from 179-382, direction R

30

Blastp and/or MPSearch Result:

Description:

Leuconostoc gelidum (strain UAL 187) leucocin A ATP-dependent

35

SEQ ID NO: __136__ ENCODED BY SEQ ID NO: __751__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

40	1	96	392	F	99 codons
----	---	----	-----	---	-----------

ORF translation from 96-392, direction F

Blastp and/or MPSearch Result:

Description:

PSEPSTD NCBI gi: 633991 NCBI gi: 473 - Pseudomonas aeruginosa (strain PAO1,) DNA.

5

SEQ ID NO: __137__ ENCODED BY SEQ ID NO: __752__

10

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	298	681	R	128 codons
---	-----	-----	---	------------

15

ORF translation from 298-681, direction R

Blastp and/or MPSearch Result:

20 Result: UNK

SEQ ID NO: __138__ ENCODED BY SEQ ID NO: __753__

25

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	153	341	F	63 codons
---	-----	-----	---	-----------

30 ORF translation from 153-341, direction F

Blastp and/or MPSearch Result:

35 Result: UNK

SEQ ID NO: __139__ ENCODED BY SEQ ID NO: __754__

40

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	38	322	F	95 codons
---	----	-----	---	-----------

ORF translation from 38-322, direction F

Blastp and/or MPSearch Result:

Description:

THERMOANAEROBACTER THERMOSULFUROGENES (CLOSTRIDIUM
THERMOSULFUROGENES). HYPOTHETICAL 35.6 KD PROTEIN IN AMYB
5'REGION (ORF1).

SEQ ID NO: __140__ ENCODED BY SEQ ID NO: __755__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	73	213	R	47 codons
---	----	-----	---	-----------

ORF translation from 73-213, direction R

Blastp and/or MPSearch Result:

Result: UNK

SEQ ID NO: __141__ ENCODED BY SEQ ID NO: __756__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	1	189	R	63 codons
---	---	-----	---	-----------

ORF translation from 1-189, direction R

Blastp and/or MPSearch Result:

Result: UNK

SEQ ID NO: __142__ ENCODED BY SEQ ID NO: __757__

ORF #	Start	End	Direction	Codon Length
2	724	966	F	81 codons

5

ORF translation from 724-966, direction F

Blastp and/or MPSearch Result:

10

Description:

ESCHERICHIA COLI. PHOTOREPAIR PROTEIN PHRA.

SEQ ID NO: __143__ ENCODED BY SEQ ID NO: __758__

15

ORF #	Start	End	Direction	Codon Length
1	353	481	F	43 codons

20

ORF translation from 353-481, direction F

Blastp and/or MPSearch Result:

25

Description:

ECOPHNAQ NCBI gi: 147192NCBI gi: 4737 - E.coli (strain B) DNA.

30

SEQ ID NO: __144__ ENCODED BY SEQ ID NO: __759__

ORF #	Start	End	Direction	Codon Length
1	144	419	F	92 codons

35

ORF translation from 144-419, direction F

40

Blastp and/or MPSearch Result:

Result: UNK

SEQ ID NO: __145__ ENCODED BY SEQ ID NO: __760__

5 ORF # Start End Direction Codon Length

1 7 312 R 102 codons

10 ORF translation from 7-312, direction R

Blastp and/or MPSearch Result:

Result: UNK

15

SEQ ID NO: __146__ ENCODED BY SEQ ID NO: __761__

20 ORF # Start End Direction Codon Length

1 89 478 F 130 codons

25 ORF translation from 89-478, direction F

Blastp and/or MPSearch Result:

30 Result: UNK

SEQ ID NO: __147__ ENCODED BY SEQ ID NO: __762__

35 ORF # Start End Direction Codon Length

1 128 382 F 85 codons

40 ORF translation from 128-382, direction F

Blastp and/or MPSearch Result:

Result: UNK

5 SEQ ID NO: __148__ ENCODED BY SEQ ID NO: __763__ ORF # Start End
Direction Codon Length

1 234 512 F 93 codons

10

ORF translation from 234-512, direction F

Blastp and/or MPSearch Result:

15

Description:

ESCHERICHIA COLI. OXYGEN-INSENSITIVE NAD(P)H NITROREDUCTASE (EC 1.-.-.-).

20

SEQ ID NO: __149__ ENCODED BY SEQ ID NO: __764__

ORF # Start End Direction Codon Length

25 1 1 432 F 144 codons

ORF translation from 1-432, direction F

30

Blastp and/or MPSearch Result:

Description:

35 PARACOCCLUS DENITRIFICANS. NADH-UBIQUINONE OXIDOREDUCTASE
CHAIN 14 (EC 1.6.5.3) (NADH DEHYDROGENASE 1, CHAIN 14) (NDH-1, CHAIN 14).

SEQ ID NO: __150__ ENCODED BY SEQ ID NO: __765__

40 ORF # Start End Direction Codon Length

1 125 394 R 90 codons

ORF translation from 125-394, direction R

Blastp and/or MPSearch Result:

5

Description:

BACILLUS STEAROTHERMOPHILUS. GLUCOSE-6-PHOSPHATE ISOMERASE A
(GPI A) (EC 5.3.1.9) (PHOSPHOGLUCOSE ISOMERASE A).

10

SEQ ID NO: __151__ ENCODED BY SEQ ID NO: __766__

ORF #	Start	End	Direction	Codon Length
2	256	426	F	57 codons

ORF translation from 256-426, direction F

20

Blastp and/or MPSearch Result:

Result: UNK

25

SEQ ID NO: __152__ ENCODED BY SEQ ID NO: __767__

ORF #	Start	End	Direction	Codon Length
1	322	717	R	132 codons

ORF translation from 322-717, direction R

35

Blastp and/or MPSearch Result:

Description:

BACRSBU NCBI gi: 642 - Bacillus subtilis (strain 168 Marburg) DNA.

40

SEQ ID NO: __153__ ENCODED BY SEQ ID NO: __768__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1 33 572 R 180 codons

5

ORF translation from 33-572, direction R

Blastp and/or MPSearch Result:

Result: UNK

10

SEQ ID NO: __154__ ENCODED BY SEQ ID NO: __769__

15

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	78	545	F	156 codons
---	----	-----	---	------------

20

ORF translation from 78-545, direction F

Blastp and/or MPSearch Result:

Result: UNK

25

SEQ ID NO: __155__ ENCODED BY SEQ ID NO: __770__

30

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	310	540	F	77 codons
---	-----	-----	---	-----------

35

ORF translation from 310-540, direction F

Blastp and/or MPSearch Result:

Description:

40

Potential ATP/GTP-binding protein

SEQ ID NO: __156__ ENCODED BY SEQ ID NO: __771__

ORF #	Start	End	Direction	Codon Length
1	220	390	F	57 codons

5

ORF translation from 220-390, direction F

10 Blastp and/or MPSearch Result:

Result: UNK

SEQ ID NO: __157__ ENCODED BY SEQ ID NO: __772__

ORF #	Start	End	Direction	Codon Length
1	104	577	F	158 codons

20 ORF translation from 104-577, direction F

Blastp and/or MPSearch Result:

25 Description:

SALMONELLA TYPHIMURIUM. L-RIBULOKINASE (EC 2.7.1.16).

30 SEQ ID NO: __158__ ENCODED BY SEQ ID NO: __773__

ORF #	Start	End	Direction	Codon Length
2	218	352	F	45 codons

35

ORF translation from 218-352, direction F

MTINLSETFANAKNEFINAVNNGEPQERQNELXGDMINXLFGGN*

40

Blastp and/or MPSearch Result:

Result: UNK

SEQ ID NO: __159__ ENCODED BY SEQ ID NO: __774__

5 ORF # Start End Direction Codon Length

ORF #	Start	End	Direction	Codon Length
1	90	401	F	104 codons

10 ORF translation from 90-401, direction F

Blastp and/or MPSearch Result:

Result: UNK

15

SEQ ID NO: __160__ ENCODED BY SEQ ID NO: __775__

20 ORF # Start End Direction Codon Length

ORF #	Start	End	Direction	Codon Length
2	296	424	R	43 codons

25 ORF translation from 296-424, direction R

Blastp and/or MPSearch Result:

30 Result: UNK

SEQ ID NO: __161__ ENCODED BY SEQ ID NO: __776__

35

ORF # Start End Direction Codon Length

ORF #	Start	End	Direction	Codon Length
1	211	378	F	56 codons

40

ORF translation from 211-378, direction F

Blastp and/or MPSearch Result:

Description:

BACILLUS SUBTILIS. AMIDOPHOSPHORIBOSYLTRANSFERASE PRECURSOR
(EC 2.4.2.14) (GLUTAMINE PHOSPHORIBOSYLPYROPHOSPHATE

5 AMIDOTRANSFERASE) (ATASE).

10 SEQ ID NO: __162__ ENCODED BY SEQ ID NO: __777__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

2	217	327	F	37 codons
---	-----	-----	---	-----------

15 ORF translation from 217-327, direction F

20 Blastp and/or MPSearch Result:

Result: UNK

25 SEQ ID NO: __163__ ENCODED BY SEQ ID NO: __778__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	33	275	R	81 codons
---	----	-----	---	-----------

30 ORF translation from 33-275, direction R

35 Blastp and/or MPSearch Result:

Description:

Potential peptidase

40 SEQ ID NO: __164__ ENCODED BY SEQ ID NO: __779__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	65	253	R	63 codons
---	----	-----	---	-----------

ORF translation from 65-253, direction R

10 Blastp and/or MPSearch Result:

Result: UNK

15

SEQ ID NO: __165__ ENCODED BY SEQ ID NO: __780__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	120	284	F	55 codons
---	-----	-----	---	-----------

ORF translation from 120-284, direction F

25

Blastp and/or MPSearch Result:

Result: UNK

30

SEQ ID NO: __166__ ENCODED BY SEQ ID NO: __781__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	191	364	F	58 codons
---	-----	-----	---	-----------

ORF translation from 191-364, direction F

Blastp and/or MPSearch Result:

40

Description:

Potential prenylated protein

SEQ ID NO: __167__ ENCODED BY SEQ ID NO: __782__

5 ORF # Start End Direction Codon Length

 1 219 551 R 111 codons

10 ORF translation from 219-551, direction R

Blastp and/or MPSearch Result:

Description:

15 SALMONELLA TYPHIMURIUM. RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE
2 BETA CHAIN (EC 1.17.4.1) (RIBONUCLEOTIDE REDUCTASE 2).

SEQ ID NO: __168__ ENCODED BY SEQ ID NO: __783__

20 ORF # Start End Direction Codon Length

 2 134 346 F 71 codons

25 ORF translation from 134-346, direction F

Blastp and/or MPSearch Result:

30 Result: UNK

SEQ ID NO: __169__ ENCODED BY SEQ ID NO: __784__

35 ORF # Start End Direction Codon Length

 1 28 333 R 102 codons

40 ORF translation from 28-333, direction R

Blastp and/or MPSearch Result:

Description:

ESCHERICHIA COLI. MOLYBDENUM COFACTOR BIOSYNTHESIS PROTEIN C.

5

SEQ ID NO: __170__ ENCODED BY SEQ ID NO: __785__

ORF #	Start	End	Direction	Codon Length
1	108	299	F	64 codons

ORF translation from 108-299, direction F

15

Blastp and/or MPSearch Result:

Description:

20 BACILLUS SUBTILIS. CTP SYNTHASE (EC 6.3.4.2) (UTP--AMMONIA LIGASE)
(CTP SYNTHETASE).

25

SEQ ID NO: __171__ ENCODED BY SEQ ID NO: __786__

ORF #	Start	End	Direction	Codon Length
1	7	141	R	45 codons

ORF translation from 7-141, direction R

35

Blastp and/or MPSearch Result:

Result: UNK

40

SEQ ID NO: __172__ ENCODED BY SEQ ID NO: __787__

ORF #	Start	End	Direction	Codon Length
1	106	390	F	95 codons

5

ORF translation from 106-390, direction F

Blastp and/or MPSearch Result:

10

Description:

VIBRIO ALGINOLYTICUS. PTS SYSTEM, SUCROSE-SPECIFIC IIBC COMPONENT
(EIIBC-SCR) (SUCROSE- PERMEASE IIBC COMPONENT)
(PHOSPHOTRANSFERASE ENZYME II, BC COMPONENT) (EC 2.7.1.69) (EII-SCR).

15

SEQ ID NO: __173__ ENCODED BY SEQ ID NO: __788__

ORF #	Start	End	Direction	Codon Length
1	17	298	R	94 codons

20

ORF translation from 17-298, direction R

25

Blastp and/or MPSearch Result:

Description:

ABC Transporter

30

SEQ ID NO: __174__ ENCODED BY SEQ ID NO: __789__

ORF #	Start	End	Direction	Codon Length
1	99	290	F	64 codons

35

ORF translation from 99-290, direction F

40

Blastp and/or MPSearch Result:

Description:

Potential prenylated protein

5

SEQ ID NO: __175__ ENCODED BY SEQ ID NO: __790__

ORF #	Start	End	Direction	Codon Length
1	68	295	F	76 codons

15

ORF translation from 68-295, direction F

Blastp and/or MPSearch Result:

Result: UNK

20 SEQ ID NO: __176__ ENCODED BY SEQ ID NO: __791__

ORF #	Start	End	Direction	Codon Length
2	135	344	R	70 codons

25

ORF translation from 135-344, direction R

MDSFVNIDGTDNLLVLKTLPGNAQSIGAILDQINWEEVLGTICGDDTCLICRSKEAS
DE
IKSRIFNLL*

30

Blastp and/or MPSearch Result:

Description:

35 BACILLUS SUBTILIS. ARGININE HYDROXIMATE RESISTANCE PROTEIN.

SEQ ID NO: __177__ ENCODED BY SEQ ID NO: __792__

ORF #	Start	End	Direction	Codon Length
1	20	358	F	113 codons

ORF translation from 20-358, direction F

5 Blastp and/or MPSearch Result:

Description:

ESCHERICHIA COLI. N-ACETYLGLUCOSAMINE-6-PHOSPHATE DEACETYLASE
(EC 3.5.1.25).

10

SEQ ID NO: __178__ ENCODED BY SEQ ID NO: __793__

ORF #	Start	End	Direction	Codon Length
1	9	131	R	41 codons

ORF translation from 9-131, direction R

20

Blastp and/or MPSearch Result:

Result: UNK

25

SEQ ID NO: __179__ ENCODED BY SEQ ID NO: __794__

ORF #	Start	End	Direction	Codon Length
1	59	334	R	92 codons

ORF translation from 59-334, direction R

35

Blastp and/or MPSearch Result:

Description:

STAPHYLOCOCCUS EPIDERMIDIS. FOSFOMYCIN RESISTANCE PROTEIN.

40

SEQ ID NO: __180__ ENCODED BY SEQ ID NO: __795__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	7	219	R	71 codons
---	---	-----	---	-----------

ORF translation from 7-219, direction R

10 Blastp and/or MPSearch Result:

Description:

PSEUDOMONAS PUTIDA. UROCANATE HYDRATASE (EC 4.2.1.49)
(UROCANASE).

SEQ ID NO: __181__ ENCODED BY SEQ ID NO: __796__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	127	315	R	63 codons
---	-----	-----	---	-----------

ORF translation from 127-315, direction R

Blastp and/or MPSearch Result:

Result: UNK

SEQ ID NO: __182__ ENCODED BY SEQ ID NO: __797__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	149	265	F	39 codons
---	-----	-----	---	-----------

ORF translation from 149-265, direction F

40 Blastp and/or MPSearch Result:

Result: UNK

5 SEQ ID NO: __183__ ENCODED BY SEQ ID NO: __798__

ORF #	Start	End	Direction	Codon Length
1	87	284	F	66 codons

10

ORF translation from 87-284, direction F

Blastp and/or MPSearch Result:

15

Result: UNK

20 SEQ ID NO: __184__ ENCODED BY SEQ ID NO: __799__

ORF #	Start	End	Direction	Codon Length
1	126	299	F	58 codons

25

ORF translation from 126-299, direction F

30 Blastp and/or MPSearch Result:

Result: UNK

35

SEQ ID NO: __185__ ENCODED BY SEQ ID NO: __800__

ORF #	Start	End	Direction	Codon Length
2	426	845	F	140 codons

40

ORF translation from 426-845, direction F

Blastp and/or MPSearch Result:

5 Description:

ESCHERICHIA COLI. TYPE I RESTRICTION ENZYME ECOR124/3 I M PROTEIN
(EC 2.1.1.72).

10

SEQ ID NO: __186__ ENCODED BY SEQ ID NO: __801__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

15	1	119	391	R	91 codons
----	---	-----	-----	---	-----------

ORF translation from 119-391, direction R

20

Blastp and/or MPSearch Result:

Result: UNK

25

SEQ ID NO: __187__ ENCODED BY SEQ ID NO: __802__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

30	1	108	548	F	147 codons
----	---	-----	-----	---	------------

ORF translation from 108-548, direction F

35 Blastp and/or MPSearch Result:

Result: UNK

40

SEQ ID NO: __188__ ENCODED BY SEQ ID NO: __803__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

2 421 816 R 132 codons

5 ORF translation from 421-816, direction R

Blastp and/or MPSearch Result:

10 Result: UNK

SEQ ID NO: __189__ ENCODED BY SEQ ID NO: __804__

15

ORF # Start End Direction Codon Length

2 427 609 R 61 codons

20

ORF translation from 427-609, direction R

Blastp and/or MPSearch Result:

25

Result: UNK

30 SEQ ID NO: __190__ ENCODED BY SEQ ID NO: __805__

ORF # Start End Direction Codon Length

1 216 356 R 47 codons

35

ORF translation from 216-356, direction R

40 Blastp and/or MPSearch Result:

Result: UNK

SEQ ID NO: __191__ ENCODED BY SEQ ID NO: __806__

5 ORF # Start End Direction Codon Length

1 369 797 F 143 codons

10 ORF translation from 369-797, direction F

Blastp and/or MPSearch Result:

Result: UNK

15

SEQ ID NO: __192__ ENCODED BY SEQ ID NO: __807__

20 ORF # Start End Direction Codon Length

1 136 411 F 92 codons

ORF translation from 136-411, direction F

25

Blastp and/or MPSearch Result:

Result: UNK

30

SEQ ID NO: __193__ ENCODED BY SEQ ID NO: __808__

35 ORF # Start End Direction Codon Length

1 4 372 R 123 codons

40 ORF translation from 4-372, direction R

Blastp and/or MPSearch Result:

Description:

BACILLUS SUBTILIS. CELL DIVISION PROTEIN FTSA.

5 SEQ ID NO: __194__ ENCODED BY SEQ ID NO: __809__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	477	692	F	72 codons
---	-----	-----	---	-----------

10

ORF translation from 477-692, direction F

Blastp and/or MPSearch Result:

15

Result: UNK

20 SEQ ID NO: __195__ ENCODED BY SEQ ID NO: __810__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

2	588	824	R	79 codons
---	-----	-----	---	-----------

25

ORF translation from 588-824, direction R

30 Blastp and/or MPSearch Result:

Result: UNK

35

SEQ ID NO: __196__ ENCODED BY SEQ ID NO: __811__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

2	203	325	F	41 codons
---	-----	-----	---	-----------

40

ORF translation from 203-325, direction F

Blastp and/or MPSearch Result:

5 Result: UNK

SEQ ID NO: __197__ ENCODED BY SEQ ID NO: __812__

10

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	23	406	R	128 codons
---	----	-----	---	------------

15

ORF translation from 23-406, direction R

Blastp and/or MPSearch Result:

20

Description:

SALMONELLA TYPHIMURIUM. VIRULENCE TRANSCRIPTIONAL
REGULATORY PROTEIN PHOP.

25

SEQ ID NO: __198__ ENCODED BY SEQ ID NO: __813__

30

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	66	359	R	98 codons
---	----	-----	---	-----------

35

ORF translation from 66-359, direction R

Blastp and/or MPSearch Result:

40 Result: UNK

SEQ ID NO: __199__ ENCODED BY SEQ ID NO: __814__

	ORF #	Start	End	Direction	Codon Length
5	2	387	602	F	72 codons

ORF translation from 387-602, direction F

10 Blastp and/or MPSearch Result:

Result: UNK

15 SEQ ID NO: __200,201__ ENCODED BY SEQ ID NO: __815__

	ORF #	Start	End	Direction	Codon Length
	1	206	538	R	111 codons
20	2	572	745	R	58 codons

ORF translation from 206-538, direction R

25

Blastp and/or MPSearch Result:

Description:

GLYCINE CLEAVAGE SYSTEM H PROTEIN. - ESCHERICHIA COLI.

30

ORF translation from 572-745, direction R

35 Blastp and/or MPSearch Result:

Result: UNK

40

SEQ ID NO: __202__ ENCODED BY SEQ ID NO: __816__

ORF #	Start	End	Direction	Codon Length
1	145	318	R	58 codons

5

ORF translation from 145-318, direction R

Blastp and/or MPSearch Result:

10

Result: UNK

15 SEQ ID NO: __203__ ENCODED BY SEQ ID NO: __817__

ORF #	Start	End	Direction	Codon Length
2	609	803	F	65 codons

20

ORF translation from 609-803, direction F

Blastp and/or MPSearch Result:

25

Result: UNK

30 SEQ ID NO: __204__ ENCODED BY SEQ ID NO: __818__

ORF #	Start	End	Direction	Codon Length
1	209	754	F	182 codons

35

ORF translation from 209-754, direction F

40 Blastp and/or MPSearch Result:

Result: UNK

SEQ ID NO: __205__ ENCODED BY SEQ ID NO: __819__

5 ORF # Start End Direction Codon Length

2 444 605 R 54 codons

ORF translation from 444-605, direction R

10

Blastp and/or MPSearch Result:

Result: UNK

15

SEQ ID NO: __206__ ENCODED BY SEQ ID NO: __820__

20 ORF # Start End Direction Codon Length

2 458 823 F 122 codons

ORF translation from 458-823, direction F

25 Blastp and/or MPSearch Result:

Result: UNK

SEQ ID NO: __207__ ENCODED BY SEQ ID NO: __821__

30

ORF # Start End Direction Codon Length

2 379 510 F 44 codons

35 ORF translation from 379-510, direction F

Blastp and/or MPSearch Result:

40 Description:

LACTOCOCCUS LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS). KETOL-
ACID REDUCTOISOMERASE (EC 1.1.1.86) (ACETOHYDROXY-ACID

ISOMEROREDUCTASE) (ALPHA-KETO-BETA-HYDROXYLACIL
REDUCTOISOMERASE).

5

SEQ ID NO: __208,209__ ENCODED BY SEQ ID NO: __822__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

10	1	241	429	F	63 codons
	3	1284	1427	F	48 codons

ORF translation from 241-429, direction F

15

Blastp and/or MPSearch Result:

Result: UNK

20

ORF translation from 1284-1427, direction F

Blastp and/or MPSearch Result:

25

Result: UNK

SEQ ID NO: __210__ ENCODED BY SEQ ID NO: __823__

30

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	88	417	F	110 codons
---	----	-----	---	------------

35 ORF translation from 88-417, direction F

Blastp and/or MPSearch Result:

Description:

40 STAPHYLOCOCCUS AUREUS, AND BACILLUS SP. REPLICATION PROTEIN.

SEQ ID NO: __211__ ENCODED BY SEQ ID NO: __824__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	254	757	R	168 codons
---	-----	-----	---	------------

5

ORF translation from 254-757, direction R

10 Blastp and/or MPSearch Result:

Result: UNK

15

SEQ ID NO: _212_ ENCODED BY SEQ ID NO: _825_

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	230	1198	R	323 codons
---	-----	------	---	------------

20

ORF translation from 230-1198, direction R

Blastp and/or MPSearch Result:

25

Description:

A/G-specific adenine glycosylase (mutY) homolog - Haemophilus

30

SEQ ID NO: _213_ ENCODED BY SEQ ID NO: _826_

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

2	725	895	F	57 codons
---	-----	-----	---	-----------

35

ORF translation from 725-895, direction F

40 Blastp and/or MPSearch Result:

Result: UNK

SEQ ID NO: __214__ ENCODED BY SEQ ID NO: __827__

5 ORF # Start End Direction Codon Length

 1 253 393 R 47 codons

10 ORF translation from 253-393, direction R

Blastp and/or MPSearch Result:

15 Result: UNK

SEQ ID NO: __215__ ENCODED BY SEQ ID NO: __828__

20 ORF # Start End Direction Codon Length

 1 245 619 F 125 codons

25 ORF translation from 245-619, direction F
Blastp and/or MPSearch Result:

Result: UNK

30 SEQ ID NO: __216__ ENCODED BY SEQ ID NO: __829__

ORF # Start End Direction Codon Length

 2 753 1049 R 99 codons

35 ORF translation from 753-1049, direction R
Blastp and/or MPSearch Result:

40 Description:
DNA helicase pcrA - Staphylococcus aureus

SEQ ID NO: __217__ ENCODED BY SEQ ID NO: __830__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

5	1	77	298	F	74 codons
---	---	----	-----	---	-----------

ORF translation from 77-298, direction F

10 Blastp and/or MPSearch Result:

Description:

crtN protein - Staphylococcus aureus

15

SEQ ID NO: __218__ ENCODED BY SEQ ID NO: __831__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

20	1	71	367	F	99 codons
----	---	----	-----	---	-----------

ORF translation from 71-367, direction F

Blastp and/or MPSearch Result:

25

Description:

crtN protein - Staphylococcus aureus

30

SEQ ID NO: __219__ ENCODED BY SEQ ID NO: __832__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

35	1	33	356	R	108 codons
----	---	----	-----	---	------------

ORF translation from 33-356, direction R

40 Blastp and/or MPSearch Result:

Result: UNK

SEQ ID NO: __220__ ENCODED BY SEQ ID NO: __833__

5 ORF # Start End Direction Codon Length

ORF #	Start	End	Direction	Codon Length
2	243	362	F	40 codons

10 ORF translation from 243-362, direction F

Blastp and/or MPSearch Result:

15 Result: UNK

SEQ ID NO: __221__ ENCODED BY SEQ ID NO: __834__

20

ORF # Start End Direction Codon Length

ORF #	Start	End	Direction	Codon Length
1	56	763	R	236 codons

25 ORF translation from 56-763, direction R

Blastp and/or MPSearch Result:

30 Description:

regulator protein - Staphylococcus xylosus

SEQ ID NO: __222__ ENCODED BY SEQ ID NO: __835__

35

ORF # Start End Direction Codon Length

ORF #	Start	End	Direction	Codon Length
1	145	312	R	56 codons

40

ORF translation from 145-312, direction R

Blastp and/or MPSearch Result:

Result: UNK

5

SEQ ID NO: __223__ ENCODED BY SEQ ID NO: __836__

	ORF #	Start	End	Direction	Codon Length
10	3	868	1131	F	88 codons

ORF translation from 868-1131, direction F

15 Blastp and/or MPSearch Result:

Result: UNK

20 SEQ ID NO: __224__ ENCODED BY SEQ ID NO: __837__

	ORF #	Start	End	Direction	Codon Length
25	1	24	368	F	115 codons

ORF translation from 24-368, direction F

30 Blastp and/or MPSearch Result:

Description:

STREPTOCOCCUS PYOGENES. STREPTOCOCCAL ACID GLYCOPROTEIN.

35

SEQ ID NO: __225__ ENCODED BY SEQ ID NO: __838__

	ORF #	Start	End	Direction	Codon Length
40	1	556	696	F	47 codons

ORF translation from 556-696, direction F

Blastp and/or MPSearch Result:

5

Result: UNK

10 SEQ ID NO: __226,227__ ENCODED BY SEQ ID NO: __839__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	316	501	F	62 codons
15	2	573	1013	F 147 codons

ORF translation from 316-501, direction F

20 Blastp and/or MPSearch Result:

Result: UNK

25 ORF translation from 573-1013, direction F

Blastp and/or MPSearch Result:

30 Result: UNK

SEQ ID NO: __228__ ENCODED BY SEQ ID NO: __840__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

2	221	460	R	80 codons
---	-----	-----	---	-----------

40 ORF translation from 221-460, direction R

Blastp and/or MPSearch Result:

Result: UNK

SEQ ID NO: __229__ ENCODED BY SEQ ID NO: __841__

5

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

2	275	712	F	146 codons
---	-----	-----	---	------------

10

ORF translation from 275-712, direction F

Blastp and/or MPSearch Result:

15

Result: UNK

SEQ ID NO: __230__ ENCODED BY SEQ ID NO: __842__

20

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	141	365	F	75 codons
---	-----	-----	---	-----------

25

ORF translation from 141-365, direction F

Blastp and/or MPSearch Result:

30

Result: UNK

35 SEQ ID NO: __231__ ENCODED BY SEQ ID NO: __843__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	89	241	F	51 codons
---	----	-----	---	-----------

40

ORF translation from 89-241, direction F

Blastp and/or MPSearch Result:

Result: UNK

5

SEQ ID NO: __232__ ENCODED BY SEQ ID NO: __844__

10 ORF # Start End Direction Codon Length

ORF #	Start	End	Direction	Codon Length
1	128	595	F	156 codons

15 ORF translation from 128-595, direction F

Blastp and/or MPSearch Result:

20 Description:
stringent response-like protein - Streptococcus equisimilis

25 SEQ ID NO: __233__ ENCODED BY SEQ ID NO: __845__

ORF # Start End Direction Codon Length

ORF #	Start	End	Direction	Codon Length
1	230	382	F	51 codons

30

ORF translation from 230-382, direction F

Blastp and/or MPSearch Result:

35

Result: UNK

SEQ ID NO: __234__ ENCODED BY SEQ ID NO: __846__

40 ORF # Start End Direction Codon Length

ORF #	Start	End	Direction	Codon Length
2	682	843	R	54 codons

ORF translation from 682-843, direction R

5 Blastp and/or MPSearch Result:

Description:

MSU10425 NCBI gi: 595400NCBI gi: 473748 - Mycobacterium smegmatis.

10 SEQ ID NO: __235__ ENCODED BY SEQ ID NO: __847__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	376	573	F	66 codons
---	-----	-----	---	-----------

15

ORF translation from 376-573, direction F

20 Blastp and/or MPSearch Result:

Description:

ESCHERICHIA COLI. GAMMA-GLUTAMYLTRANSPEPTIDASE PRECURSOR (EC 2.3.2.2).

25

SEQ ID NO: __236__ ENCODED BY SEQ ID NO: __848__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

30

1	72	272	R	67 codons
---	----	-----	---	-----------

35

ORF translation from 72-272, direction R

Blastp and/or MPSearch Result:

Description:

40 STAPHYLOCOCCUS AUREUS. FIBRONECTIN-BINDING PROTEIN PRECURSOR (FNBP).

SEQ ID NO: 237 ENCODED BY SEQ ID NO: 849

5 ORF # Start End Direction Codon Length

1 207 905 F 233 codons

10 ORF translation from 207-905, direction F

Blastp and/or MPSearch Result:

Result: UNK

15

SEQ ID NO: 238 ENCODED BY SEQ ID NO: 850

20 ORF # Start End Direction Codon Length

2 234 515 F 94 codons

25 ORF translation from 234-515, direction F

Blastp and/or MPSearch Result:

Description:

30 BACILLUS SUBTILIS. UDP-N-ACETYLMURAMOYLALANINE--D-GLUTAMATE
LIGASE (EC 6.3.2.9) (UDP-N- ACETYLMURANOYL-L-ALANYL-D-GLUTAMATE
SYNTHETASE).

35

SEQ ID NO: 239 ENCODED BY SEQ ID NO: 851

40 ORF # Start End Direction Codon Length

1 377 733 R 119 codons

ORF translation from 377-733, direction R

Blastp and/or MPSearch Result:

5 Result: UNK

SEQ ID NO: __240__ ENCODED BY SEQ ID NO: __852__

10

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	377	670	R	98 codons
---	-----	-----	---	-----------

15

ORF translation from 377-670, direction R

Blastp and/or MPSearch Result:

20 Result: UNK

25 SEQ ID NO: __241__ ENCODED BY SEQ ID NO: __853__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	132	329	F	66 codons
---	-----	-----	---	-----------

30

ORF translation from 132-329, direction F

35 Blastp and/or MPSearch Result:

Description:

Potential prenylated protein

40

SEQ ID NO: __242__ ENCODED BY SEQ ID NO: __854__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1 179 370 R 64 codons

ORF translation from 179-370, direction R

5

Blastp and/or MPSearch Result:

Result: UNK

10

SEQ ID NO: __243__ ENCODED BY SEQ ID NO: __855__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

15

1	270	875	R	202 codons
---	-----	-----	---	------------

ORF translation from 270-875, direction R

20

Blastp and/or MPSearch Result:

Result: UNK

25

SEQ ID NO: __244__ ENCODED BY SEQ ID NO: __856__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

30

1	94	216	F	41 codons
---	----	-----	---	-----------

ORF translation from 94-216, direction F

35

Blastp and/or MPSearch Result:

Result: UNK

40

SEQ ID NO: __245__ ENCODED BY SEQ ID NO: __857__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

2 261 515 F 85 codons

5 ORF translation from 261-515, direction F

Blastp and/or MPSearch Result:

10 Result: UNK

SEQ ID NO: __246__ ENCODED BY SEQ ID NO: __858__

15

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	328	597	F	90 codons
---	-----	-----	---	-----------

20

ORF translation from 328-597, direction F

Blastp and/or MPSearch Result:

25

Result: UNK

SEQ ID NO: __247__ ENCODED BY SEQ ID NO: __859__

30

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	76	543	F	156 codons
---	----	-----	---	------------

35

ORF translation from 76-543, direction F

Blastp and/or MPSearch Result:

40

Description:

BACILLUS SUBTILIS. ADENYLOSUCCINATE LYASE (EC 4.3.2.2)
(ADENYLOSUCCINASE) (ASL).

SEQ ID NO: __248__ ENCODED BY SEQ ID NO: __860__

5 ORF # Start End Direction Codon Length

1 665 982 F 106 codons

10 ORF translation from 665-982, direction F

Blastp and/or MPSearch Result:

15 Description:

membrane-associated component, branched amino acid transport system

20 SEQ ID NO: __249__ ENCODED BY SEQ ID NO: __861__

ORF # Start End Direction Codon Length

1 45 296 R 84 codons

25

ORF translation from 45-296, direction R

30 Blastp and/or MPSearch Result:

Result: UNK

35 SEQ ID NO: __250__ ENCODED BY SEQ ID NO: __862__

ORF # Start End Direction Codon Length

1 29 256 F 76 codons

40

ORF translation from 29-256, direction F

Blastp and/or MPSearch Result:

Description:

- 5 BACILLUS SUBTILIS. NAPHTHOATE SYNTHASE (EC 4.1.3.36)
(DIHYDROXYNAPHTHOIC ACID SYNTHETASE) (DHNA SYNTHETASE).

- 10 SEQ ID NO: __251__ ENCODED BY SEQ ID NO: __863__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	136	282	R	49 codons
---	-----	-----	---	-----------

15

ORF translation from 136-282, direction R

- 20 Blastp and/or MPSearch Result:

Result: UNK

- 25 SEQ ID NO: __252__ ENCODED BY SEQ ID NO: __864__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	119	442	F	108 codons
---	-----	-----	---	------------

30

ORF translation from 119-442, direction F

- 35 Blastp and/or MPSearch Result:

Description:

ESCHERICHIA COLI. MOLYBDATE-BINDING PERIPLASMIC PROTEIN
PRECURSOR.

40

SEQ ID NO: __253__ ENCODED BY SEQ ID NO: __865__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

5	1	1	204	R	68 codons
---	---	---	-----	---	-----------

ORF translation from 1-204, direction R

10

Blastp and/or MPSearch Result:

Result: UNK

15

SEQ ID NO: __254__ ENCODED BY SEQ ID NO: __866__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

20	1	324	611	F	96 codons
----	---	-----	-----	---	-----------

ORF translation from 324-611, direction F

25

Blastp and/or MPSearch Result:

Result: UNK

30

SEQ ID NO: __255__ ENCODED BY SEQ ID NO: __867__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

35	1	93	395	F	101 codons
----	---	----	-----	---	------------

40 ORF translation from 93-395, direction F

Blastp and/or MPSearch Result:

Description:

STREPTOCOCCUS PNEUMONIAE. DNA MISMATCH REPAIR PROTEIN HEXA.

5

SEQ ID NO: __256__ ENCODED BY SEQ ID NO: __868__

ORF #	Start	End	Direction	Codon Length
2	418	621	R	68 codons

ORF translation from 418-621, direction R

15

Blastp and/or MPSearch Result:

Result: UNK

20

SEQ ID NO: __257__ ENCODED BY SEQ ID NO: __869__

ORF #	Start	End	Direction	Codon Length
1	177	398	R	74 codons

ORF translation from 177-398, direction R

30 Blastp and/or MPSearch Result:

Result: UNK

35

SEQ ID NO: __258__ ENCODED BY SEQ ID NO: __870__

ORF #	Start	End	Direction	Codon Length
2	208	549	F	114 codons

ORF translation from 208-549, direction F

Blastp and/or MPSearch Result:

5

Description:

BACILLUS SUBTILIS. ELONGATION FACTOR TU (EF-TU).

10 SEQ ID NO: __259__ ENCODED BY SEQ ID NO: __871__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	171	299	F	43 codons
---	-----	-----	---	-----------

15

ORF translation from 171-299, direction F

20 Blastp and/or MPSearch Result:

Result: UNK

25

SEQ ID NO: __260__ ENCODED BY SEQ ID NO: __872__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	11	478	F	156 codons
---	----	-----	---	------------

30

ORF translation from 11-478, direction F

35 Blastp and/or MPSearch Result:

Description:

dehydrogenase/reductase-like protein

40

SEQ ID NO: __261__ ENCODED BY SEQ ID NO: __873__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1 85 393 F 103 codons

ORF translation from 85-393, direction F

5

Blastp and/or MPSearch Result:

Description:

10 BACILLUS SUBTILIS. CARBAMOYL-PHOSPHATE SYNTHASE, PYRIMIDINE-SPECIFIC, LARGE CHAIN (EC 6.3.5.5) (CARBAMOYL-PHOSPHATE SYNTHETASE AMMONIA CHAIN).

15

SEQ ID NO: __262__ ENCODED BY SEQ ID NO: __874

ORF # Start End Direction Codon Length

20 1 152 334 F 61 codons

ORF translation from 152-334, direction F

25 Blastp and/or MPSearch Result:

Result: UNK

30

SEQ ID NO: __263__ ENCODED BY SEQ ID NO: __875__

ORF # Start End Direction Codon Length

35 1 124 435 F 104 codons

ORF translation from 124-435, direction F

40

Blastp and/or MPSearch Result:

Result: UNK

SEQ ID NO: __264__ ENCODED BY SEQ ID NO: __876__

5

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	126	719	F	198 codons
---	-----	-----	---	------------

10

ORF translation from 126-719, direction F

Blastp and/or MPSearch Result:

15

Description:

EF protein - Streptococcus suis

20 SEQ ID NO: __265__ ENCODED BY SEQ ID NO: __877__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	83	361	R	93 codons
---	----	-----	---	-----------

25

ORF translation from 83-361, direction R

Blastp and/or MPSearch Result:

30

Description:

methionyl-tRNA formyltransferase (fmt) homolog - Haemophilus

35 SEQ ID NO: __266__ ENCODED BY SEQ ID NO: __878__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	131	559	R	143 codons
---	-----	-----	---	------------

40

ORF translation from 131-559, direction R

Blastp and/or MPSearch Result:

Result: UNK

5

SEQ ID NO: __267__ ENCODED BY SEQ ID NO: __879

	ORF #	Start	End	Direction	Codon Length
10	1	93	290	R	66 codons

ORF translation from 93-290, direction R

15

Blastp and/or MPSearch Result:

Description:

20 STAPHYLOCOCCUS CARNOSUS. TRANSCRIPTION ANTITERMINATION
PROTEIN NUSG.

SEQ ID NO: __268__ ENCODED BY SEQ ID NO: __880__

	ORF #	Start	End	Direction	Codon Length
25	2	166	378	R	71 codons

30 ORF translation from 166-378, direction R

Blastp and/or MPSearch Result:

35

Description:

BACILLUS SUBTILIS. FERRICHROME-BINDING PROTEIN PRECURSOR.

SEQ ID NO: __269__ ENCODED BY SEQ ID NO: __881__

40

	ORF #	Start	End	Direction	Codon Length
	2	242	523	F	94 codons

ORF translation from 242-523, direction F

5

Blastp and/or MPSearch Result:

Description:

STREPTOCOCCUS MUTANS. GTP-BINDING PROTEIN ERA HOMOLOG.

10

SEQ ID NO: __270__ ENCODED BY SEQ ID NO: __882__

15

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	38	409	F	124 codons
---	----	-----	---	------------

20

ORF translation from 38-409, direction F

Blastp and/or MPSearch Result:

25

Description:

Bacterial regulatory protein, gntR family

30 SEQ ID NO: __271__ ENCODED BY SEQ ID NO: __883__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

2	116	448	R	111 codons
---	-----	-----	---	------------

35

ORF translation from 116-448, direction R

Blastp and/or MPSearch Result:

40

Result: UNK

SEQ ID NO: __272__ ENCODED BY SEQ ID NO: __884__

5 ORF # Start End Direction Codon Length

 1 148 501 R 118 codons

ORF translation from 148-501, direction R

10

Blastp and/or MPSearch Result:

Description:

15 BACILLUS SUBTILIS. GMP SYNTHASE (GLUTAMINE-HYDROLYZING) (EC
6.3.5.2) (GLUTAMINE AMIDOTRANSFERASE).

SEQ ID NO: __273__ ENCODED BY SEQ ID NO: __885__

20

ORF # Start End Direction Codon Length

 1 71 415 F 115 codons

25

ORF translation from 71-415, direction F

Blastp and/or MPSearch Result:

30

Result: UNK

SEQ ID NO: __274__ ENCODED BY SEQ ID NO: __886__

35

ORF # Start End Direction Codon Length

 2 130 384 R 85 codons

40

ORF translation from 130-384, direction R

Blastp and/or MPSearch Result:

Description:

BACILLUS STEAROTHERMOPHILUS. N-ACETYL-GAMMA-GLUTAMYL-
PHOSPHATE REDUCTASE (EC 1.2.1.38) (N-ACETYL- GLUTAMATE
5 SEMIALDEHYDE DEHYDROGENASE) (NAGSA DEHYDROGENASE)
(FRAGMENT).

SEQ ID NO: __275__ ENCODED BY SEQ ID NO: __887

10

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	111	293	F	61 codons
---	-----	-----	---	-----------

15

ORF translation from 111-293, direction F

Blastp and/or MPSearch Result:

20

Description:

ESCHERICHIA COLI. PHOH PROTEIN (PHOSPHATE STARVATION-INDUCIBLE
PROTEIN PSIH).

25

SEQ ID NO: __276,277__ ENCODED BY SEQ ID NO: __888__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

30

1	196	348	R	51 codons
2	481	852	R	124 codons

ORF translation from 196-348, direction R

35

Blastp and/or MPSearch Result:

Result: UNK

40

ORF translation from 481-852, direction R

Blastp and/or MPSearch Result:

Result: UNK

5

SEQ ID NO: __278,279__ ENCODED BY SEQ ID NO: __889__

ORF #	Start	End	Direction	Codon Length
1	339	1004	F	222 codons
2	1193	1750	F	186 codons

ORF translation from 339-1004, direction F

15

Blastp and/or MPSearch Result:

Description:

S.carnosus mtlA gene for enzyme II(Mannitol).

20

ORF translation from 1193-1750, direction F

25

Blastp and/or MPSearch Result:

Result: UNK

SEQ ID NO: __280__ ENCODED BY SEQ ID NO: __890__

30

ORF #	Start	End	Direction	Codon Length
1	111	446	R	112 codons

35

ORF translation from 111-446, direction R

Blastp and/or MPSearch Result:

40

Result: UNK

SEQ ID NO: __281,282__ ENCODED BY SEQ ID NO: __891__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

5	1	305	637	R	111 codons
	2	664	1473	R	270 codons

ORF translation from 305-637, direction R

10

Blastp and/or MPSearch Result:

Result: UNK

15

ORF translation from 664-1473, direction R

Blastp and/or MPSearch Result:

20

Description:
glucoamylase-like protein

25 SEQ ID NO: __283__ ENCODED BY SEQ ID NO: __892__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

30	2	962	1159	F	66 codons
----	---	-----	------	---	-----------

ORF translation from 962-1159, direction F

Blastp and/or MPSearch Result:

35

Result: UNK

SEQ ID NO: __284__ ENCODED BY SEQ ID NO: __893__

40

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

2	1102	1683	F	194 codons
---	------	------	---	------------

ORF translation from 1102-1683, direction F

5

Blastp and/or MPSearch Result:

Description:

botulinum neurotoxin type C1 precursor - Clostridium botulinum

10

SEQ ID NO: __285 ENCODED BY SEQ ID NO: __894__

ORF #	Start	End	Direction	Codon Length
1	256	474	F	73 codons

ORF translation from 256-474, direction F

Blastp and/or MPSearch Result:

Result: UNK

SEQ ID NO: __286__ ENCODED BY SEQ ID NO: __895__

ORF #	Start	End	Direction	Codon Length
1	132	353	F	74 codons

ORF translation from 132-353, direction F

Blastp and/or MPSearch Result:

Result: UNK

40

SEQ ID NO: __287__ ENCODED BY SEQ ID NO: __896__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	82	585	F	168 codons
---	----	-----	---	------------

5

ORF translation from 82-585, direction F

10 Blastp and/or MPSearch Result:

Result: UNK

15

SEQ ID NO: __288__ ENCODED BY SEQ ID NO: __897__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	80	229	F	50 codons
---	----	-----	---	-----------

ORF translation from 80-229, direction F

25 Blastp and/or MPSearch Result:

Result: UNK

30 SEQ ID NO: __289,290__ ENCODED BY SEQ ID NO: __898__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	271	987	F	239 codons
2	1131	1436	F	102 codons

ORF translation from 271-987, direction F

40 Blastp and/or MPSearch Result:

Result: UNK

ORF translation from 1131-1436, direction F

5 Blastp and/or MPSearch Result:

Result: UNK

10

SEQ ID NO: __291__ ENCODED BY SEQ ID NO: __899__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

15	1	62	454	F	131 codons
----	---	----	-----	---	------------

ORF translation from 62-454, direction F

20 Blastp and/or MPSearch Result:

Result: UNK

SEQ ID NO: __292__ ENCODED BY SEQ ID NO: __900__

25

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	225	509	R	95 codons
---	-----	-----	---	-----------

30

ORF translation from 225-509, direction R

Blastp and/or MPSearch Result:

35

Description:

clumping factor - Staphylococcus aureus

40

SEQ ID NO: __293__ ENCODED BY SEQ ID NO: __901__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

130

 1 1183 1527 R 115 codons

- 5 ORF translation from 1183-1527, direction R

Blastp and/or MPSearch Result:

Description:

- 10 anaerobic ribonucleoside-triphosphate reductase (nrdD) homolog -

SEQ ID NO: __294__ ENCODED BY SEQ ID NO: __902__

- 15 ORF # Start End Direction Codon Length

 1 47 364 R 106 codons

- 20 ORF translation from 47-364, direction R

Blastp and/or MPSearch Result:

Result: UNK

25

SEQ ID NO: __295,296__ ENCODED BY SEQ ID NO: __903__

- 30 ORF # Start End Direction Codon Length

 1 21 308 R 96 codons
 2 417 590 R 58 codons

35

ORF translation from 21-308, direction R

Blastp and/or MPSearch Result:

- 40 Description:

BACILLUS SUBTILIS. DIPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN
 DPPB.

ORF translation from 417-590, direction R

Blastp and/or MPSearch Result:

5

Result: UNK

SEQ ID NO: __297__ ENCODED BY SEQ ID NO: __904__

10

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	96	443	F	116 codons
---	----	-----	---	------------

15

ORF translation from 96-443, direction F

Blastp and/or MPSearch Result:

20

Description:

AZOTOBACTER CHROOCOCCUM MCD 1. NIFU PROTEIN.

SEQ ID NO: __298__ ENCODED BY SEQ ID NO: __905__

25

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

2	244	381	F	46 codons
---	-----	-----	---	-----------

30

ORF translation from 244-381, direction F

Blastp and/or MPSearch Result:

35

Result: UNK

SEQ ID NO: __299__ ENCODED BY SEQ ID NO: __906__

40

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

2	565	1086	R	174 codons
---	-----	------	---	------------

ORF translation from 565-1086, direction R

Blastp and/or MPSearch Result:

5

Result: UNK

SEQ ID NO: __300__ ENCODED BY SEQ ID NO: __907

ORF #	Start	End	Direction	Codon Length
1	868	1245	R	126 codons

15 ORF translation from 868-1245, direction R

Blastp and/or MPSearch Result:

20 Result: UNK

SEQ ID NO: __301_ ENCODED BY SEQ ID NO: __908__

25

ORF #	Start	End	Direction	Codon Length
1	129	311	R	61 codons

30

ORF translation from 129-311, direction R

Blastp and/or MPSearch Result:

35

Result: UNK

SEQ ID NO: __302_ ENCODED BY SEQ ID NO: __909__

40

ORF #	Start	End	Direction	Codon Length
1	859	1233	F	125 codons

ORF translation from 859-1233, direction F

5

Blastp and/or MPSearch Result:

Result: UNK

10

SEQ ID NO: __303_ ENCODED BY SEQ ID NO: __910__

ORF #	Start	End	Direction	Codon Length
1	292	453	F	54 codons

ORF translation from 292-453, direction F

20

Blastp and/or MPSearch Result:

Result: UNK

25

SEQ ID NO: __304,305_ ENCODED BY SEQ ID NO: __911__

ORF #	Start	End	Direction	Codon Length
1	547	1056	R	170 codons
3	1289	1597	R	103 codons

ORF translation from 547-1056, direction R

35

Blastp and/or MPSearch Result:

Description:

40 deoxyuridine 5'-triphosphatase homologue

ORF translation from 1289-1597, direction R

Blastp and/or MPSearch Result:

Result: UNK

5

SEQ ID NO: __306__ ENCODED BY SEQ ID NO: __912__

ORF #	Start	End	Direction	Codon Length
1	593	946	F	118 codons

ORF translation from 593-946, direction F

15

Blastp and/or MPSearch Result:

Result: UNK

20

SEQ ID NO: __307__ ENCODED BY SEQ ID NO: __913__

ORF #	Start	End	Direction	Codon Length
1	290	550	R	87 codons

ORF translation from 290-550, direction R

30

Blastp and/or MPSearch Result:

Result: UNK

35

SEQ ID NO: __308__ ENCODED BY SEQ ID NO: __914__

ORF #	Start	End	Direction	Codon Length
1	126	374	R	83 codons

ORF translation from 126-374, direction R

Blastp and/or MPSearch Result:

Result: UNK

5

SEQ ID NO: __309__ ENCODED BY SEQ ID NO: __915__

10 ORF # Start End Direction Codon Length

2 716 1018 F 101 codons

15 ORF translation from 716-1018, direction F

Blastp and/or MPSearch Result:

20 Result: UNK

SEQ ID NO: __310__ ENCODED BY SEQ ID NO: __916__

25 ORF # Start End Direction Codon Length

1 40 546 F 169 codons

ORF translation from 40-546, direction F

30 Blastp and/or MPSearch Result:

Result: UNK

35

SEQ ID NO: __311__ ENCODED BY SEQ ID NO: __917__

ORF # Start End Direction Codon Length

40

2 716 949 R 78 codons

ORF translation from 716-949, direction R

Blastp and/or MPSearch Result:

Result: UNK

5

SEQ ID NO: __312__ ENCODED BY SEQ ID NO: __918__

ORF #	Start	End	Direction	Codon Length
1	417	839	R	141 codons

10

ORF translation from 417-839, direction R

15

Blastp and/or MPSearch Result:

Description:

20 STAPHYLOCOCCUS AUREUS. CAPD PROTEIN.

SEQ ID NO: __313__ ENCODED BY SEQ ID NO: __919__

25

ORF #	Start	End	Direction	Codon Length
1	43	231	F	63 codons

30

ORF translation from 43-231, direction F

Blastp and/or MPSearch Result:

35

Result: UNK

40 SEQ ID NO: __314,315__ ENCODED BY SEQ ID NO: __920__

ORF #	Start	End	Direction	Codon Length
_____	_____	_____	_____	_____

1 429 956 F 176 codons
2 1135 1299 F 55 codons

ORF translation from 429-956, direction F

5

Blastp and/or MPSearch Result:

Result: UNK

10

ORF translation from 1135-1299, direction F

Blastp and/or MPSearch Result:

15

Result: UNK

SEQ ID NO: __316__ ENCODED BY SEQ ID NO: __921__

20

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

2	617	862	F	82 codons
---	-----	-----	---	-----------

25

ORF translation from 617-862, direction F

Blastp and/or MPSearch Result:

30

Description:

STAPHYLOCOCCUS AUREUS. CAPB PROTEIN.

35 SEQ ID NO: __317__ ENCODED BY SEQ ID NO: __922__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	163	777	R	205 codons
---	-----	-----	---	------------

40

ORF translation from 163-777, direction R

Blastp and/or MPSearch Result:

Description:

STAPHYLOCOCCUS AUREUS. CAPB PROTEIN.

5

SEQ ID NO: __318__ ENCODED BY SEQ ID NO: __923__

ORF #	Start	End	Direction	Codon Length
1	385	813	F	143 codons

ORF translation from 385-813, direction F

15 Blastp and/or MPSearch Result:

Description:

ESCHERICHIA COLI. THREONINE DEHYDRATASE CATABOLIC (EC 4.2.1.16)
(THREONINE DEAMINASE).

20

SEQ ID NO: __319,320__ ENCODED BY SEQ ID NO: __924__

25

ORF #	Start	End	Direction	Codon Length
1	69	635	F	189 codons
4	2862	3095	F	78 codons

30

ORF translation from 69-635, direction F

Blastp and/or MPSearch Result:

35 Result: UNK

ORF translation from 2862-3095, direction F

40

Blastp and/or MPSearch Result:

Result: UNK

5

SEQ ID NO: __321,322__ ENCODED BY SEQ ID NO: __925__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

10

1	213	593	F	127 codons
2	848	1657	F	270 codons

ORF translation from 213-593, direction F

15

Blastp and/or MPSearch Result:

Description:

20

nerve growth factor (promoter) [human, Genomic, 486 nt]. ptsG protein - Staphylococcus carnosus

ORF translation from 848-1657, direction F

Blastp and/or MPSearch Result:

25

Description:

Bacillus subtilis phospho-beta-glucosidase (bglA) gene, complete

SEQ ID NO: __323__ ENCODED BY SEQ ID NO: __926__

30

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	235	342	F	36 codons
---	-----	-----	---	-----------

35

ORF translation from 235-342, direction F

Blastp and/or MPSearch Result:

40

Result: UNK

SEQ ID NO: __324__ ENCODED BY SEQ ID NO: __927__

5 ORF # Start End Direction Codon Length

1 345 743 R 133 codons

ORF translation from 345-743, direction R

10

Blastp and/or MPSearch Result:

Description:

15 ENTEROCOCCUS FAECALIS (STREPTOCOCCUS FAECALIS). AUTOLYSIN (EC
3.5.1.28) (N-ACETYLMURAMOYL-L-ALANINE AMIDASE).

SEQ ID NO: __325__ ENCODED BY SEQ ID NO: __928__

20 ORF # Start End Direction Codon Length

2 647 877 F 77 codons

25 ORF translation from 647-877, direction F

Blastp and/or MPSearch Result:

30 Result: UNK

35 SEQ ID NO: __326__ ENCODED BY SEQ ID NO: __929__

ORF # Start End Direction Codon Length

1 57 431 F 125 codons

40

ORF translation from 57-431, direction F

Blastp and/or MPSearch Result:

Result: UNK

5

SEQ ID NO: __327,328,329__ ENCODED BY SEQ ID NO: __930__

ORF #	Start	End	Direction	Codon Length
1	22	216	R	65 codons
2	231	707	R	159 codons
3	874	1119	R	82 codons

15

ORF translation from 22-216, direction R

Blastp and/or MPSearch Result:

20

Result: UNK

ORF translation from 231-707, direction R

25

Blastp and/or MPSearch Result:

Description:

aspartate carbamoyltransferase (EC 2.1.3.2) - *Bacillus caldolyticus*

30

ORF translation from 874-1119, direction R

Blastp and/or MPSearch Result:

35

Description:

aspartate carbamoyltransferase (EC 2.1.3.2) - *Bacillus caldolyticus*

40

SEQ ID NO: __330__ ENCODED BY SEQ ID NO: __931__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

142

 1 198 506 F 103 codons

5 ORF translation from 198-506, direction F

Blastp and/or MPSearch Result:

10 Description:
 BACILLUS SUBTILIS. ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1)
 (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA
 SYNTHASE).

15 SEQ ID NO: __331,332,333,334__ ENCODED BY SEQ ID NO: __932__

ORF # Start End Direction Codon Length

20 1 10 342 F 111 codons
 2 582 749 R 56 codons
 3 1262 1597 F 112 codons
 4 1634 1948 F 105 codons

25 ORF translation from 10-342, direction F

Blastp and/or MPSearch Result:

30 Description:
 bicyclomycin resistance protein (bcr) homolog - Haemophilus

ORF translation from 582-749, direction R

35 Blastp and/or MPSearch Result:

Result: UNK

40 ORF translation from 1262-1597, direction F

Blastp and/or MPSearch Result:

Description:

5 BACILLUS SUBTILIS. MEMBRANE-BOUND PROTEIN LYTR.

ORF translation from 1634-1948, direction F

Blastp and/or MPSearch Result:

10

Description:

ESCHERICHIA COLI. MULTIDRUG RESISTANCE PROTEIN A.

15

SEQ ID NO: __335,336,337__ ENCODED BY SEQ ID NO: __933__

20

ORF #	Start	End	Direction	Codon Length
1	319	696	F	126 codons
2	758	1024	F	89 codons
3	1318	1596	R	93 codons

25

ORF translation from 319-696, direction F

*

30 Blastp and/or MPSearch Result:

Result: UNK

35 ORF translation from 758-1024, direction F

Blastp and/or MPSearch Result:

Result: UNK

40

ORF translation from 1318-1596, direction R

Blastp and/or MPSearch Result:

Result: UNK

5

SEQ ID NO: __338__ ENCODED BY SEQ ID NO: __934__

10 ORF # Start End Direction Codon Length

ORF #	Start	End	Direction	Codon Length
1	72	335	F	88 codons

15 ORF translation from 72-335, direction F

Blastp and/or MPSearch Result:

Result: UNK

20

SEQ ID NO: __339,340__ ENCODED BY SEQ ID NO: __935__

25 ORF # Start End Direction Codon Length

ORF #	Start	End	Direction	Codon Length
1	108	392	R	95 codons
2	824	1660	R	279 codons

30

ORF translation from 108-392, direction R

Blastp and/or MPSearch Result:

35 Result: UNK

ORF translation from 824-1660, direction R

40 Blastp and/or MPSearch Result:

Result: UNK

5 SEQ ID NO: __341__ ENCODED BY SEQ ID NO: __936__

ORF #	Start	End	Direction	Codon Length
1	343	747	F	135 codons

10

ORF translation from 343-747, direction F

15 Blastp and/or MPSearch Result:

Description:

STREPTOCOCCUS MUTANS. MANNITOL-1-PHOSPHATE 5-DEHYDROGENASE
(EC 1.1.1.17).

20

SEQ ID NO: __342,343__ ENCODED BY SEQ ID NO: __937__

ORF #	Start	End	Direction	Codon Length
1	166	510	F	115 codons
2	511	792	F	94 codons

25

ORF translation from 166-510, direction F

30

Blastp and/or MPSearch Result:

Result: UNK

35

ORF translation from 511-792, direction F

Blastp and/or MPSearch Result:

40 Result: UNK

SEQ ID NO: __344,345__ ENCODED BY SEQ ID NO: __938__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

5	1	114	623	R	170 codons
	2	874	1248	R	125 codons

ORF translation from 114-623, direction R

10

Blastp and/or MPSearch Result:

Result: UNK

15

ORF translation from 874-1248, direction R

Blastp and/or MPSearch Result:

20 Result: UNK

SEQ ID NO: __346__ ENCODED BY SEQ ID NO: __939__

25

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	180	1130	R	317 codons
---	-----	------	---	------------

30

ORF translation from 180-1130, direction R

Blastp and/or MPSearch Result:

Result: UNK

35

SEQ ID NO: __347__ ENCODED BY SEQ ID NO: __940__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	68	271	F	68 codons
---	----	-----	---	-----------

ORF translation from 68-271, direction F

5 Blastp and/or MPSearch Result:

Description:

ESCHERICHIA COLI. SULFITE REDUCTASE (NADPH) FLAVOPROTEIN ALPHA-COMPONENT (EC 1.8.1.2) (SIR-FP).

10

SEQ ID NO: __348,349__ ENCODED BY SEQ ID NO: __941__

15 ORF # Start End Direction Codon Length

1	564	752	F	63 codons
2	1010	1549	F	180 codons

20 ORF translation from 564-752, direction F

Blastp and/or MPSearch Result:

25

Result: UNK

ORF translation from 1010-1549, direction F

30

Blastp and/or MPSearch Result:

Description:

Peptostreptococcus magnus protein L gene, complete cds.

35

SEQ ID NO: __350__ ENCODED BY SEQ ID NO: __942__

40 ORF # Start End Direction Codon Length

2	1472	1843	F	124 codons
---	------	------	---	------------

ORF translation from 1472-1843, direction F

5 Blastp and/or MPSearch Result:

Result: UNK

10

SEQ ID NO: __351_ ENCODED BY SEQ ID NO: __943__

	ORF #	Start	End	Direction	Codon Length
15	1	222	335	F	38 codons

ORF translation from 222-335, direction F

20

Blastp and/or MPSearch Result:

Result: UNK

25

SEQ ID NO: __352_ ENCODED BY SEQ ID NO: __944__

	ORF #	Start	End	Direction	Codon Length
30	1	65	511	R	149 codons

ORF translation from 65-511, direction R

35

Blastp and/or MPSearch Result:

Result: UNK

40

SEQ ID NO: __353_ ENCODED BY SEQ ID NO: __945

	ORF #	Start	End	Direction	Codon Length
5	1	259	540	R	94 codons

ORF translation from 259-540, direction R

Blastp and/or MPSearch Result:

10

Result: UNK

SEQ ID NO: __354_ ENCODED BY SEQ ID NO: __946__

	ORF #	Start	End	Direction	Codon Length
15	1	734	1033	F	100 codons

20 ORF translation from 734-1033, direction F

Blastp and/or MPSearch Result:

Description:

25 BACILLUS SUBTILIS. RIBOFLAVIN BIOSYNTHESIS PROTEIN RIBG.

SEQ ID NO: __355,356,357_ ENCODED BY SEQ ID NO: __947__

	ORF #	Start	End	Direction	Codon Length
30	1	147	362	F	72 codons
	2	510	794	F	95 codons
	3	997	1461	F	155 codons

35

ORF translation from 147-362, direction F

40 Blastp and/or MPSearch Result:

Result: UNK

ORF translation from 510-794, direction F

5 Blastp and/or MPSearch Result:

Result: UNK

10 ORF translation from 997-1461, direction F

Blastp and/or MPSearch Result:

15 Result: UNK

SEQ ID NO: __358_ ENCODED BY SEQ ID NO: __948__

20

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

2	188	811	F	208 codons
---	-----	-----	---	------------

25

ORF translation from 188-811, direction F

Blastp and/or MPSearch Result:

30

Result: UNK

SEQ ID NO: __359_ ENCODED BY SEQ ID NO: __949__

35

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	146	859	F	238 codons
---	-----	-----	---	------------

40

ORF translation from 146-859, direction F

Blastp and/or MPSearch Result:

Description:

5 BACILLUS SUBTILIS. DNA REPAIR PROTEIN REC N (RECOMBINATION
PROTEIN N).

10 SEQ ID NO: __360_ ENCODED BY SEQ ID NO: __950__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	290	592	R	101 codons
---	-----	-----	---	------------

15

ORF translation from 290-592, direction R

Blastp and/or MPSearch Result:

20

Description:

BACILLUS SUBTILIS. UTP--GLUCOSE-1-PHOSPHATE URIDYL YLTRANSFERASE
(EC 2.7.7.9) (UDP-GLUCOSE PYROPHOSPHORYLASE) (UDPGP) (ALPHA-D-
25 GLUCOSYL-1-PHOSPHATE URIDYL YLTRANSFERASE) (URIDINE
DIPHOSPHOGLUCOSE PYROPHOSPHORYLASE).

SEQ ID NO: __361_ ENCODED BY SEQ ID NO: __951

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	302	967	F	222 codons
---	-----	-----	---	------------

35 ORF translation from 302-967, direction F

Blastp and/or MPSearch Result:

Description:

40 alcohol dehydrogenase (EC 1.1.1.1) - Entamoeba histolytica

SEQ ID NO: __362_ ENCODED BY SEQ ID NO: __952__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

2	855	1202	R	116 codons
---	-----	------	---	------------

5

ORF translation from 855-1202, direction R

Blastp and/or MPSearch Result:

10 Result: UNK

SEQ ID NO: __363,364_ ENCODED BY SEQ ID NO: __953__

15

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

2	742	1053	F	104 codons
---	-----	------	---	------------

3	1267	1464	F	66 codons
---	------	------	---	-----------

20

ORF translation from 742-1053, direction F

25 Blastp and/or MPSearch Result:

Description:

E. coli priA gene.

30

ORF translation from 1267-1464, direction F

Blastp and/or MPSearch Result:

35

Result: UNK

40 SEQ ID NO: __365_ ENCODED BY SEQ ID NO: __954__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1 44 646 F 201 codons

ORF translation from 44-646, direction F

5

Blastp and/or MPSearch Result:

Description:

10 GLUCOSAMINE-6-PHOSPHATE ISOMERASE (EC 5.3.1.10) (GLUCOSAMINE-6-PHOSPHATE DEAMINASE). - ESCHERICHIA COLI.

SEQ ID NO: __366_ ENCODED BY SEQ ID NO: __955__

15

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	73	408	F	112 codons
---	----	-----	---	------------

20

ORF translation from 73-408, direction F

Blastp and/or MPSearch Result:

25 Result: UNK

SEQ ID NO: __367_ ENCODED BY SEQ ID NO: __956__

30

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	74	937	F	288 codons
---	----	-----	---	------------

35

ORF translation from 74-937, direction F

Blastp and/or MPSearch Result:

Result: UNK

40

SEQ ID NO: __368_ ENCODED BY SEQ ID NO: __957__

	ORF #	Start	End	Direction	Codon Length
5	2	797	976	R	60 codons

ORF translation from 797-976, direction R

10

Blastp and/or MPSearch Result:

Description:

15 BACILLUS SUBTILIS. QUINOL OXIDASE POLYPEPTIDE I (EC 1.9.3.-) (QUINOL
OXIDASE codons3-600, SUBUNIT QOXB).

SEQ ID NO: __369_ ENCODED BY SEQ ID NO: __958__

20

	ORF #	Start	End	Direction	Codon Length
	2	672	974	R	101 codons

25

ORF translation from 672-974, direction R

Blastp and/or MPSearch Result:

30

Description:

35 BACILLUS SUBTILIS. PTS SYSTEM, GLUCOSE-SPECIFIC IIABC COMPONENT
(EIIABC-GLC) (GLUCOSE- PERMEASE IIABC COMPONENT)
(PHOSPHOTRANSFERASE ENZYME II, ABC COMPONENT) (EC 2.7.1.69) (EII-GLC
/ EIII-GLC).

SEQ ID NO: __370_ ENCODED BY SEQ ID NO: __959__

40

	ORF #	Start	End	Direction	Codon Length
	1	195	791	R	199 codons

ORF translation from 195-791, direction R

5

Blastp and/or MPSearch Result:

Description:

10 STAPHYLOCOCCUS AUREUS. PTS SYSTEM, LACTOSE-SPECIFIC IIBC
COMPONENT (EIIBC-LAC) (LACTOSE- PERMEASE IIBC COMPONENT)
(PHOSPHOTRANSFERASE ENZYME II, BC COMPONENT) (EC 2.7.1.69) (EII-LAC).

15 SEQ ID NO: __371,372,373_ ENCODED BY SEQ ID NO: __960__

	ORF #	Start	End	Direction	Codon Length
	1	190	480	F	97 codons
20	2	536	703	F	56 codons
	3	761	1186	F	142 codons

ORF translation from 190-480, direction F

25

Blastp and/or MPSearch Result:

Result: UNK

30

ORF translation from 536-703, direction F

Blastp and/or MPSearch Result:

35

Result: UNK

ORF translation from 761-1186, direction F

40 Blastp and/or MPSearch Result:

Description:

BACILLUS SUBTILIS. DIVISION INITIATION PROTEIN (CELL DIVISION AND
SPORULATION PROTEIN).

5

SEQ ID NO: __374_ ENCODED BY SEQ ID NO: __961__

ORF #	Start	End	Direction	Codon Length
1	154	585	F	144 codons

ORF translation from 154-585, direction F

15 Blastp and/or MPSearch Result:

Result: UNK

20

SEQ ID NO: __375_ ENCODED BY SEQ ID NO: __962__

ORF #	Start	End	Direction	Codon Length
2	187	477	F	97 codons

ORF translation from 187-477, direction F

Blastp and/or MPSearch Result:

30

Result: UNK

35 SEQ ID NO: __376_ ENCODED BY SEQ ID NO: __963__

ORF #	Start	End	Direction	Codon Length
1	180	479	F	100 codons

40

ORF translation from 180-479, direction F

Blastp and/or MPSearch Result:

Description:

5 ESCHERICHIA COLI. POTASSIUM-TRANSPORTING ATPASE (EC 3.6.1.36), B
CHAIN (ATP PHOSPHOHYDROLASE (POTASSIUM-TRANSPORTING), B CHAIN).

SEQ ID NO: __377_ ENCODED BY SEQ ID NO: __964__

ORF #	Start	End	Direction	Codon Length
1	285	524	R	80 codons

ORF translation from 285-524, direction R

Blastp and/or MPSearch Result:

Result: UNK

SEQ ID NO: __378,379_ ENCODED BY SEQ ID NO: __965__

ORF #	Start	End	Direction	Codon Length
1	257	487	F	77 codons
2	551	919	F	123 codons

Blastp and/or MPSearch Result:

Description:

35 ESCHERICHIA COLI. CYTOCHROME O UBIQUINOL OXIDASE SUBUNIT I (EC
1.10.3.-).

ORF translation from 551-919, direction F

Blastp and/or MPSearch Result:

Description:

BACILLUS SUBTILIS. QUINOL OXIDASE POLYPEPTIDE III (EC 1.9.3.-) (QUINOL OXIDASE codons3-600, SUBUNIT QOXC).

5

SEQ ID NO: __380,381_ ENCODED BY SEQ ID NO: __966__

ORF #	Start	End	Direction	Codon Length
1	23	448	F	142 codons
2	525	965	F	147 codons

ORF translation from 23-448, direction F

15 Blastp and/or MPSearch Result:

Description:

BACILLUS SUBTILIS. DIPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN DPPC.

20

ORF translation from 525-965, direction F

Blastp and/or MPSearch Result:

25 Description:

BACILLUS SUBTILIS. OLIGOPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN OPPC.

30 SEQ ID NO: __382_ ENCODED BY SEQ ID NO: __967__

ORF #	Start	End	Direction	Codon Length
2	475	636	F	54 codons

35

ORF translation from 475-636, direction F

40 Blastp and/or MPSearch Result:

Result: UNK

SEQ ID NO: __383__ ENCODED BY SEQ ID NO: __968__

5 ORF # Start End Direction Codon Length

1 124 555 F 144 codons

ORF translation from 124-555, direction F

10

Blastp and/or MPSearch Result:

Result: UNK

15

SEQ ID NO: __384__ ENCODED BY SEQ ID NO: __969__

ORF # Start End Direction Codon Length

20

1 26 394 R 123 codons

ORF translation from 26-394, direction R

25

Blastp and/or MPSearch Result:

Description:

SALMONELLA TYPHIMURIUM. SULFITE REDUCTASE (NADPH)

30

FLAVOPROTEIN ALPHA-COMPONENT (EC 1.8.1.2) (SIR-FP).

35 SEQ ID NO: __385__ ENCODED BY SEQ ID NO: __970__

ORF # Start End Direction Codon Length

1 24 455 F 144 codons

40

ORF translation from 24-455, direction F

Blastp and/or MPSearch Result:

Result: UNK

5 SEQ ID NO: __386__ ENCODED BY SEQ ID NO: __971__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	347	697	F	117 codons
---	-----	-----	---	------------

10

ORF translation from 347-697, direction F

Blastp and/or MPSearch Result:

15

Description:

BACILLUS MEGATERIUM. ATP SYNTHASE ALPHA CHAIN (EC 3.6.1.34).

20

SEQ ID NO: __387__ ENCODED BY SEQ ID NO: __972__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

2	406	879	F	158 codons
---	-----	-----	---	------------

25

ORF translation from 406-879, direction F

30

Blastp and/or MPSearch Result:

Result: UNK

35

SEQ ID NO: __388__ ENCODED BY SEQ ID NO: __973__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	654	1361	F	236 codons
---	-----	------	---	------------

40

ORF translation from 654-1361, direction F

Blastp and/or MPSearch Result:

Description:

- 5 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE)
(ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE). - BACILLUS
SUBTILIS.

10

SEQ ID NO: __389,390__ ENCODED BY SEQ ID NO: __974__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

- | | | | | | |
|----|---|-----|-----|---|------------|
| 15 | 1 | 1 | 177 | F | 59 codons |
| | 2 | 197 | 568 | F | 124 codons |

ORF translation from 1-177, direction F

20

Blastp and/or MPSearch Result:

Description:

- 25 ESCHERICHIA COLI. NUCLEOSIDE PERMEASE NUPC (NUCLEOSIDE-
TRANSPORT SYSTEM PROTEIN NUPC).

ORF translation from 197-568, direction F

30 Blastp and/or MPSearch Result:

Description:

BACILLUS SUBTILIS. PYRIMIDINE NUCLEOSIDE TRANSPORT PROTEIN.

35

SEQ ID NO: __391__ ENCODED BY SEQ ID NO: __975__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

- | | | | | | |
|----|---|-----|-----|---|-----------|
| 40 | 2 | 285 | 452 | F | 56 codons |
|----|---|-----|-----|---|-----------|

ORF translation from 285-452, direction F

Blastp and/or MPSearch Result:

5 Result: UNK

SEQ ID NO: __392__ ENCODED BY SEQ ID NO: __976__

10 ORF # Start End Direction Codon Length

ORF #	Start	End	Direction	Codon Length
1	276	521	F	82 codons

ORF translation from 276-521, direction F

15 Blastp and/or MPSearch Result:

Result: UNK

20 SEQ ID NO: __393,394__ ENCODED BY SEQ ID NO: __977

ORF # Start End Direction Codon Length

ORF #	Start	End	Direction	Codon Length
1	97	444	F	116 codons
2	582	1010	F	143 codons

ORF translation from 97-444, direction F

Blastp and/or MPSearch Result:

30

Result: UNK

ORF translation from 582-1010, direction F

35

Blastp and/or MPSearch Result:

Result: UNK

40

SEQ ID NO: __395,396,397__ ENCODED BY SEQ ID NO: __978__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

5	1	71	235	F	55 codons
	2	295	477	F	61 codons
	3	546	647	F	34 codons

ORF translation from 71-235, direction F

10

Blastp and/or MPSearch Result:

Result: UNK

15

ORF translation from 295-477, direction F

20 Blastp and/or MPSearch Result:

Result: UNK

25 ORF translation from 546-647, direction F

Blastp and/or MPSearch Result:

30 Result: UNK

SEQ ID NO: __398 ENCODED BY SEQ ID NO: __979__

35

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	132	653	F	174 codons
---	-----	-----	---	------------

40

ORF translation from 132-653, direction F

Blastp and/or MPSearch Result:

Description:

CALDOCELLUM SACCHAROLYTICUM. ACETYL ESTERASE (EC 3.1.-.-).

5

SEQ ID NO: __399 ENCODED BY SEQ ID NO: __980__

ORF #	Start	End	Direction	Codon Length
1	211	381	F	57 codons

15 ORF translation from 211-381, direction F

Blastp and/or MPSearch Result:

20 Result: UNK

SEQ ID NO: __400, 401__ ENCODED BY SEQ ID NO: __981__

25

ORF #	Start	End	Direction	Codon Length
1	1	294	F	98 codons
2	753	1070	F	106 codons

30

ORF translation from 1-294, direction F

35 Blastp and/or MPSearch Result:

Description:

BACILLUS STEAROTHERMOPHILUS. PYRUVATE DEHYDROGENASE E1
COMPONENT, ALPHA SUBUNIT (EC 1.2.4.1).

40

ORF translation from 753-1070, direction F

Blastp and/or MPSearch Result:

Description:

- 5 BACILLUS STEAROTHERMOPHILUS. PYRUVATE DEHYDROGENASE E1
COMPONENT, ALPHA SUBUNIT (EC 1.2.4.1).

SEQ ID NO: __402__ ENCODED BY SEQ ID NO: __982__

10

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	173	586	F	138 codons
---	-----	-----	---	------------

15

ORF translation from 173-586, direction F

Blastp and/or MPSearch Result:

20 Description:

ESCHERICHIA COLI. PROLINE/BETAINE TRANSPORTER (PROLINE PORTER II)
(PPII).

25

SEQ ID NO: __403,404__ ENCODED BY SEQ ID NO: __983__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

30

2	259	477	R	73 codons
---	-----	-----	---	-----------

3	803	1147	R	115 codons
---	-----	------	---	------------

- 35 ORF translation from 259-477, direction R

Blastp and/or MPSearch Result:

40 Description:

BACILLUS SUBTILIS. INITIATION FACTOR IF-1.

ORF translation from 803-1147, direction R

Blastp and/or MPSearch Result:

5

Description:

BACILLUS SUBTILIS. ADENYLATE KINASE (EC 2.7.4.3) (ATP-AMP
TRANSPHOSPHORYLASE).

10

SEQ ID NO: __405__ ENCODED BY SEQ ID NO: __984

ORF #	Start	End	Direction	Codon Length
1	125	436	F	104 codons

20

ORF translation from 125-436, direction F

Blastp and/or MPSearch Result:

Result: UNK

25

SEQ ID NO: __406__ ENCODED BY SEQ ID NO: __985__

ORF #	Start	End	Direction	Codon Length
2	394	525	F	44 codons

35 ORF translation from 394-525, direction F

Blastp and/or MPSearch Result:

40 Result: UNK

SEQ ID NO: __407__ ENCODED BY SEQ ID NO: __986__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	350	709	F	120 codons
---	-----	-----	---	------------

5

ORF translation from 350-709, direction F

Blastp and/or MPSearch Result:

10

Description:

RHODOBACTER CAPSULATUS (RHODOPSEUDOMONAS CAPSULATA). PETP
PROTEIN.

15

SEQ ID NO: __408,409__ ENCODED BY SEQ ID NO: __987__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

20

1	657	770	F	38 codons
---	-----	-----	---	-----------

2	800	928	F	43 codons
---	-----	-----	---	-----------

25 ORF translation from 657-770, direction F

Blastp and/or MPSearch Result:

30 Result: UNK

ORF translation from 800-928, direction F

35

Blastp and/or MPSearch Result:

Result: UNK

40

SEQ ID NO: __410__ ENCODED BY SEQ ID NO: __988__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

168

1 98 562 F 155 codons

5 ORF translation from 98-562, direction F

Blastp and/or MPSearch Result:

10 Description:
CbrB protein - *Erwinia chrysanthemi*

15 SEQ ID NO: __411__ ENCODED BY SEQ ID NO: __989__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	125	271	F	49 codons
---	-----	-----	---	-----------

20

ORF translation from 125-271, direction F

25 Blastp and/or MPSearch Result:

Result: UNK

30

SEQ ID NO: __412__ ENCODED BY SEQ ID NO: __990__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	52	354	R	101 codons
---	----	-----	---	------------

35

ORF translation from 52-354, direction R

40 Blastp and/or MPSearch Result:

Description:

BACILLUS SUBTILIS. PHOSPHORIBOSYLGLYCINAMIDE
FORMYLTRANSFERASE (EC 2.1.2.2) (GART) (GAR TRANSFORMYLASE) (5'-
PHOSPHORIBOSYLGLYCINAMIDE TRANSFORMYLASE).

5

SEQ ID NO: __413__ ENCODED BY SEQ ID NO: __991__

ORF #	Start	End	Direction	Codon Length
2	105	527	F	141 codons

ORF translation from 105-527, direction F

15

Blastp and/or MPSearch Result:

Description:

BACILLUS SUBTILIS. ATP-DEPENDENT NUCLEASE SUBUNIT B.

20

SEQ ID NO: __414__ ENCODED BY SEQ ID NO: __992__

ORF #	Start	End	Direction	Codon Length
2	489	668	F	60 codons

ORF translation from 489-668, direction F

30 Blastp and/or MPSearch Result:

Result: UNK

35 SEQ ID NO: __415__ ENCODED BY SEQ ID NO: __993__

ORF #	Start	End	Direction	Codon Length
1	193	570	R	126 codons

40

ORF translation from 193-570, direction R

Blastp and/or MPSearch Result:

- 5 Description:
BACILLUS SUBTILIS. COMA OPERON PROTEIN 2.

SEQ ID NO: __416__ ENCODED BY SEQ ID NO: __994

10

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	302	433	F	44 codons
---	-----	-----	---	-----------

15

ORF translation from 302-433, direction F

Blastp and/or MPSearch Result:

- 20 Description:
ALCALIGENES EUTROPHUS. MEMBRANE PROTEIN.

SEQ ID NO: __417__ ENCODED BY SEQ ID NO: __995

25

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

2	569	706	F	46 codons
---	-----	-----	---	-----------

30

ORF translation from 569-706, direction F

Blastp and/or MPSearch Result:

35

Result: UNK

40

SEQ ID NO: __418__ ENCODED BY SEQ ID NO: __996__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1 248 541 F 98 codons

5 ORF translation from 248-541, direction F

Blastp and/or MPSearch Result:

10 Result: UNK

SEQ ID NO: __419__ ENCODED BY SEQ ID NO: __997__

15

ORF # Start End Direction Codon Length

2 113 481 F 123 codons

20

ORF translation from 113-481, direction F

Blastp and/or MPSearch Result:

25

Result: UNK

30

SEQ ID NO: __420__ ENCODED BY SEQ ID NO: __998__

ORF # Start End Direction Codon Length

35 1 347 586 F 80 codons

ORF translation from 347-586, direction F

40 Blastp and/or MPSearch Result:

Result: UNK

SEQ ID NO: __421__ ENCODED BY SEQ ID NO: __999__

5 ORF # Start End Direction Codon Length

1 75 521 F 149 codons

10 ORF translation from 75-521, direction F

Blastp and/or MPSearch Result:

Result: UNK

15

SEQ ID NO: __422__ ENCODED BY SEQ ID NO: __1000__

ORF # Start End Direction Codon Length

20

1 192 374 R 61 codons

ORF translation from 192-374, direction R

25

Blastp and/or MPSearch Result:

Description:

30 LEGIONELLA PNEUMOPHILA. ACONITATE HYDRATASE (EC 4.2.1.3) (CITRATE
HYDRO-LYASE) (ACONITASE) (MAJOR IRON-CONTAINING PROTEIN) (MICP)
(IP210).

35

SEQ ID NO: __423__ ENCODED BY SEQ ID NO: __1001__

ORF # Start End Direction Codon Length

40 1 149 499 F 117 codons

ORF translation from 149-499, direction F

Blastp and/or MPSearch Result:

5 Result: UNK

SEQ ID NO: __424__ ENCODED BY SEQ ID NO: __1002__

10

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	79	519	R	147 codons
---	----	-----	---	------------

15 ORF translation from 79-519, direction R

Blastp and/or MPSearch Result:

Description:

20 pyruvate synthase (EC 1.2.7.1) - Halobacterium halobium

SEQ ID NO: __425__ ENCODED BY SEQ ID NO: __1003__

25

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	168	476	F	103 codons
---	-----	-----	---	------------

30 ORF translation from 168-476, direction F

Blastp and/or MPSearch Result:

Description:

35 ATP/GTP-binding protein

SEQ ID NO: __426__ ENCODED BY SEQ ID NO: __1004__

40

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	265	843	R	193 codons
---	-----	-----	---	------------

ORF translation from 265-843, direction R

5

Blastp and/or MPSearch Result:

Description:

BACILLUS SUBTILIS. ATP SYNTHASE BETA CHAIN (EC 3.6.1.34).

10

SEQ ID NO: __427__ ENCODED BY SEQ ID NO: __1005__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

15	1	83	301	F	73 codons
----	---	----	-----	---	-----------

ORF translation from 83-301, direction F

20

Blastp and/or MPSearch Result:

Result: UNK

25

SEQ ID NO: __428__ ENCODED BY SEQ ID NO: __1006__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

30	2	1014	1160	F	49 codons
----	---	------	------	---	-----------

ORF translation from 1014-1160, direction F

35

Blastp and/or MPSearch Result:

Description:

40 scrA protein - Staphylococcus xylosus

SEQ ID NO: __429__ ENCODED BY SEQ ID NO: __1007__

ORF #	Start	End	Direction	Codon Length
5	2	718	894	R 59 codons

ORF translation from 718-894, direction R

10 Blastp and/or MPSearch Result:

Description:

ESCHERICHIA COLI. POTASSIUM-TRANSPORTING ATPASE (EC 3.6.1.36), A
CHAIN (ATP PHOSPHOHYDROLASE (POTASSIUM-TRANSPORTING), A CHAIN).

15

SEQ ID NO: __430__ ENCODED BY SEQ ID NO: __1008__

ORF #	Start	End	Direction	Codon Length
20	1	467	667	F 67 codons

ORF translation from 467-667, direction F

25

Blastp and/or MPSearch Result:

Result: UNK

30

SEQ ID NO: __431__ ENCODED BY SEQ ID NO: __1009__

ORF #	Start	End	Direction	Codon Length
35	1	102	347	F 82 codons

ORF translation from 102-347, direction F

40 Blastp and/or MPSearch Result:

Description:

ESCHERICHIA COLI. LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL.

SEQ ID NO: __432__ ENCODED BY SEQ ID NO: __1010__

5 ORF # Start End Direction Codon Length

1 411 542 F 44 codons

ORF translation from 411-542, direction F

10 Blastp and/or MPSearch Result:

Description:

ESCHERICHIA COLI. MOLYBDENUM COFACTOR BIOSYNTHESIS PROTEIN A.

15

SEQ ID NO: __433__ ENCODED BY SEQ ID NO: __1011__

20

ORF # Start End Direction Codon Length

1 109 399 F 97 codons

25

ORF translation from 109-399, direction F

Blastp and/or MPSearch Result:

30

Result: UNK

35 SEQ ID NO: __434__ ENCODED BY SEQ ID NO: __1012__

ORF # Start End Direction Codon Length

2 411 845 R 145 codons

40

ORF translation from 411-845, direction R

Blastp and/or MPSearch Result:

Description:

- 5 Aminoacyl-transfer RNA synthetase class-II

SEQ ID NO: __435__ ENCODED BY SEQ ID NO: __1013__

10	ORF #	Start	End	Direction	Codon Length
	2	333	506	R	58 codons

- 15 ORF translation from 333-506, direction R

Blastp and/or MPSearch Result:

- 20 Result: UNK

SEQ ID NO: __436__ ENCODED BY SEQ ID NO: __1014__

25

ORF #	Start	End	Direction	Codon Length
2	502	849	F	116 codons

- 30 ORF translation from 502-849, direction F

Blastp and/or MPSearch Result:

- 35 Result: UNK

SEQ ID NO: __437__ ENCODED BY SEQ ID NO: __1015__

40

ORF #	Start	End	Direction	Codon Length
1	92	391	F	100 codons

ORF translation from 92-391, direction F

5

Blastp and/or MPSearch Result:

Result: UNK

10

SEQ ID NO: __438__ ENCODED BY SEQ ID NO: __1016__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

15	1	45	305	R	87 codons
----	---	----	-----	---	-----------

ORF translation from 45-305, direction R

20

Blastp and/or MPSearch Result:

Description:

25 KLEBSIELLA AEROGENES. FORMIMINOGLUTAMASE (EC 3.5.3.8)
(FORMIMINOGLUTAMATE HYDROLASE) (HISTIDINE UTILIZATION PROTEIN G)
(FRAGMENT).

SEQ ID NO: __439__ ENCODED BY SEQ ID NO: __1017__

30

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	100	372	R	91 codons
---	-----	-----	---	-----------

35

ORF translation from 100-372, direction R

Blastp and/or MPSearch Result:

40

Description:

BACILLUS SUBTILIS. PEPTIDE SYNTHETASE 1.

SEQ ID NO: __440__ ENCODED BY SEQ ID NO: __1018__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

5	1	253	537	F	95 codons
---	---	-----	-----	---	-----------

ORF translation from 253-537, direction F

10

Blastp and/or MPSearch Result:

Result: UNK

15 SEQ ID NO: __441__ ENCODED BY SEQ ID NO: __1019__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

20	1	474	692	R	73 codons
----	---	-----	-----	---	-----------

ORF translation from 474-692, direction R

Blastp and/or MPSearch Result:

25

Description:

ABC Transporter

30 SEQ ID NO: __442__ ENCODED BY SEQ ID NO: __1020__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

35	1	234	401	R	56 codons
----	---	-----	-----	---	-----------

ORF translation from 234-401, direction R

Blastp and/or MPSearch Result:

40

Result: UNK

SEQ ID NO: __443,444__ ENCODED BY SEQ ID NO: __1021__

	ORF #	Start	End	Direction	Codon Length
5	1	20	244	R	75 codons
	2	303	584	R	94 codons

ORF translation from 20-244, direction R

10

Blastp and/or MPSearch Result:

Result: UNK

15

ORF translation from 303-584, direction R

20 Blastp and/or MPSearch Result:

Result: UNK

25 SEQ ID NO: __445__ ENCODED BY SEQ ID NO: __1022__

	ORF #	Start	End	Direction	Codon Length
30	1	98	232	R	45 codons

ORF translation from 98-232, direction R

35 Blastp and/or MPSearch Result:

Description:

ESCHERICHIA COLI. ALKYL HYDROPEROXIDE REDUCTASE F52A PROTEIN
(EC 1.6.4.-) (FRAGMENT).

40

SEQ ID NO: __446__ ENCODED BY SEQ ID NO: __1023__

ORF #	Start	End	Direction	Codon Length
2	301	756	R	152 codons

ORF translation from 301-756, direction R

Blastp and/or MPSearch Result:

Description:

BACILLUS STEAROTHERMOPHILUS. MALATE OXIDOREDUCTASE (NAD) (EC 1.1.1.38) (MALIC ENZYME).

SEQ ID NO: __447__ ENCODED BY SEQ ID NO: __1024__

ORF #	Start	End	Direction	Codon Length
2	351	578	R	76 codons

ORF translation from 351-578, direction R

Blastp and/or MPSearch Result:

Result: UNK

SEQ ID NO: __448__ ENCODED BY SEQ ID NO: __1025__

ORF #	Start	End	Direction	Codon Length
1	233	475	R	81 codons

ORF translation from 233-475, direction R

Blastp and/or MPSearch Result:

Result: UNK

5 SEQ ID NO: __449__ ENCODED BY SEQ ID NO: __1026__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	162	437	F	92 codons
---	-----	-----	---	-----------

10

ORF translation from 162-437, direction F

15 Blastp and/or MPSearch Result:

Result: UNK

20 SEQ ID NO: __450__ ENCODED BY SEQ ID NO: __1027__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	274	447	F	58 codons
---	-----	-----	---	-----------

25

ORF translation from 274-447, direction F

Blastp and/or MPSearch Result:

30

Description:

ESCHERICHIA COLI. FERRIC ENTEROBACTIN TRANSPORT PROTEIN FEPD.

35

SEQ ID NO: __451__ ENCODED BY SEQ ID NO: __1028__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

40

1	1	138	F	46 codons
---	---	-----	---	-----------

ORF translation from 1-138, direction F

Blastp and/or MPSearch Result:

5

Result: UNK

SEQ ID NO: __452__ ENCODED BY SEQ ID NO: __1029__

10 ORF # Start End Direction Codon Length

ORF #	Start	End	Direction	Codon Length
1	9	575	R	189 codons

15 ORF translation from 9-575, direction R

Blastp and/or MPSearch Result:

Description:

ASCOBOLUS IMMERSUS. HOMOSERINE O-ACETYLTRANSFERASE (EC 2.3.1.31)

20 (HOMOSERINE O-TRANS- ACETYLASE).

SEQ ID NO: __453__ ENCODED BY SEQ ID NO: __1030__

25

ORF # Start End Direction Codon Length

ORF #	Start	End	Direction	Codon Length
1	117	512	F	132 codons

30

ORF translation from 117-512, direction F

Blastp and/or MPSearch Result:

35 Result: UNK

SEQ ID NO: __454__ ENCODED BY SEQ ID NO: __1031__

40

ORF # Start End Direction Codon Length

ORF #	Start	End	Direction	Codon Length
1	115	225	F	37 codons

ORF translation from 115-225, direction F

5

Blastp and/or MPSearch Result:

Result: UNK

10

SEQ ID NO: __455__ ENCODED BY SEQ ID NO: __1032__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

15	1	101	202	F	34 codons
----	---	-----	-----	---	-----------

ORF translation from 101-202, direction F

20 Blastp and/or MPSearch Result:

Result: UNK

25 SEQ ID NO: __456__ ENCODED BY SEQ ID NO: __1033__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

30	1	79	294	R	72 codons
----	---	----	-----	---	-----------

ORF translation from 79-294, direction R

35 Blastp and/or MPSearch Result:

Description:

BACILLUS SUBTILIS. GLYCEROL-3-PHOSPHATASE TRANSPORTER (G-3-P
TRANSPORTER) (G-3-P PERMEASE).

40

SEQ ID NO: __457__ ENCODED BY SEQ ID NO: __1034__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	156	344	R	63 codons
---	-----	-----	---	-----------

ORF translation from 156-344, direction R

10 Blastp and/or MPSearch Result:

Result: UNK

15

SEQ ID NO: __458__ ENCODED BY SEQ ID NO: __1035__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

2	75	281	R	69 codons
---	----	-----	---	-----------

ORF translation from 75-281, direction R

25

Blastp and/or MPSearch Result:

Description:

30 BACILLUS SUBTILIS. GLUCONATE PERMEASE.

SEQ ID NO: __459__ ENCODED BY SEQ ID NO: __1036__

35

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	87	248	R	54 codons
---	----	-----	---	-----------

40

ORF translation from 87-248, direction R

Blastp and/or MPSearch Result:

Description:

BACILLUS SUBTILIS. GLUTAMYL-TRNA REDUCTASE (EC 1.2.1.-) (GLUTR).

5

SEQ ID NO: __460__ ENCODED BY SEQ ID NO: __1037__

10 ORF # Start End Direction Codon Length

1 35 160 R 42 codons

15 ORF translation from 35-160, direction R

Blastp and/or MPSearch Result:

Result: UNK

20

SEQ ID NO: __461__ ENCODED BY SEQ ID NO: __1038__

25 ORF # Start End Direction Codon Length

2 390 494 F 35 codons

30 ORF translation from 390-494, direction F

Blastp and/or MPSearch Result:

Result: UNK

35

SEQ ID NO: __462__ ENCODED BY SEQ ID NO: __1039__

40 ORF # Start End Direction Codon Length

1 240 374 F 45 codons

ORF translation from 240-374, direction F

5 Blastp and/or MPSearch Result:

Description:

BACILLUS SUBTILIS. ARGINASE (EC 3.5.3.1).

10

SEQ ID NO: __463__ ENCODED BY SEQ ID NO: __1040__

15 ORF # Start End Direction Codon Length

ORF #	Start	End	Direction	Codon Length
1	65	385	F	107 codons

20 ORF translation from 65-385, direction F

Blastp and/or MPSearch Result:

Description:

25 BACILLUS STEAROTHERMOPHILUS. CARBOXYLESTERASE PRECURSOR (EC 3.1.1.1).

SEQ ID NO: __464__ ENCODED BY SEQ ID NO: __1041__

30 ORF # Start End Direction Codon Length

ORF #	Start	End	Direction	Codon Length
2	309	557	F	83 codons

35 ORF translation from 309-557, direction F

Blastp and/or MPSearch Result:

40 Description:

ABC transporter

SEQ ID NO: __465__ ENCODED BY SEQ ID NO: __1042__

	ORF #	Start	End	Direction	Codon Length
5	1	487	660	F	58 codons

ORF translation from 487-660, direction F

10

Blastp and/or MPSearch Result:

Description:

15 THERMOTOGA MARITIMA. ANTHRANILATE SYNTHASE COMPONENT II (EC 4.1.3.27) (CONTAINS: GLUTAMINE AMIDOTRANSFERASE; ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.18)).

20 SEQ ID NO: __466__ ENCODED BY SEQ ID NO: __1043__

	ORF #	Start	End	Direction	Codon Length
25	1	79	303	R	75 codons

ORF translation from 79-303, direction R

30 Blastp and/or MPSearch Result:

Description:

35 BACILLUS SUBTILIS. DNA TOPOISOMERASE I (EC 5.99.1.2) (OMEGA-PROTEIN) (RELAXING ENZYME) (UNTWISTING ENZYME) (SWIVELASE).

SEQ ID NO: __467__ ENCODED BY SEQ ID NO: __1044__

	ORF #	Start	End	Direction	Codon Length
40	1	87	311	F	75 codons

ORF translation from 87-311, direction F

Blastp and/or MPSearch Result:

Description:

ESCHERICHIA COLI. FERRIC ENTEROBACTIN TRANSPORT ATP-BINDING
PROTEIN FEPC.

SEQ ID NO: __468__ ENCODED BY SEQ ID NO: __1045__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

2	190	435	F	82 codons
---	-----	-----	---	-----------

ORF translation from 190-435, direction F

Blastp and/or MPSearch Result:

Result: UNK

SEQ ID NO: __469__ ENCODED BY SEQ ID NO: __1046__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	65	664	F	200 codons
---	----	-----	---	------------

ORF translation from 65-664, direction F

Blastp and/or MPSearch Result:

Result: UNK

SEQ ID NO: __470__ ENCODED BY SEQ ID NO: __1047__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	287	484	F	66 codons
---	-----	-----	---	-----------

5

ORF translation from 287-484, direction F

Blastp and/or MPSearch Result:

10

Result: UNK

15 SEQ ID NO: __471__ ENCODED BY SEQ ID NO: __1048__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	36	416	R	127 codons
---	----	-----	---	------------

20

ORF translation from 36-416, direction R

25 Blastp and/or MPSearch Result:

Result: UNK

30

SEQ ID NO: __472,473__ ENCODED BY SEQ ID NO: __1049__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	178	312	F	45 codons
---	-----	-----	---	-----------

2	359	619	F	87 codons
---	-----	-----	---	-----------

40

ORF translation from 178-312, direction F

Blastp and/or MPSearch Result:

Result: UNK

ORF translation from 359-619, direction F

5

Blastp and/or MPSearch Result:

Result: UNK

10

SEQ ID NO: __474__ ENCODED BY SEQ ID NO: __1050__

ORF #	Start	End	Direction	Codon Length
1	211	486	R	92 codons

ORF translation from 211-486, direction R
Blastp and/or MPSearch Result:

Result: UNK

25

SEQ ID NO: __475,476__ ENCODED BY SEQ ID NO: __1051__

ORF #	Start	End	Direction	Codon Length
2	131	340	F	70 codons
3	525	626	F	34 codons

ORF translation from 131-340, direction F

35

Blastp and/or MPSearch Result:

Result: UNK

40

ORF translation from 525-626, direction F

Blastp and/or MPSearch Result:

Result: UNK

5

SEQ ID NO: __477__ ENCODED BY SEQ ID NO: __1052__

ORF #	Start	End	Direction	Codon Length
1	187	474	F	96 codons

15 ORF translation from 187-474, direction F

Blastp and/or MPSearch Result:

20 Description:

ESCHERICHIA COLI. OSMOTICALLY INDUCIBLE PROTEIN C.

SEQ ID NO: __478__ ENCODED BY SEQ ID NO: __1053__

25

ORF #	Start	End	Direction	Codon Length
1	107	520	F	138 codons

30

ORF translation from 107-520, direction F

Blastp and/or MPSearch Result:

35

Result: UNK

SEQ ID NO: __479__ ENCODED BY SEQ ID NO: __1054__

40

ORF #	Start	End	Direction	Codon Length
1	90	377	F	96 codons

ORF translation from 90-377, direction F

5

Blastp and/or MPSearch Result:

Description:

Helix-Turn-Helix containing protein

10

SEQ ID NO: __480__ ENCODED BY SEQ ID NO: __1055__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

15	1	167	475	R	103 codons
----	---	-----	-----	---	------------

ORF translation from 167-475, direction R

20

Blastp and/or MPSearch Result:

Description:

25 BACILLUS SUBTILIS. 2,3-BISPHOSPHOGLYCERATE-INDEPENDENT
PHOSPHOGLYCERATE MUTASE (EC 5.4.2.1) (PHOSPHOGLYCEROMUTASE)
(BPG-INDEPENDENT PGAM).

SEQ ID NO: _481_____ ENCODED BY SEQ ID NO: _1056_____

30	ORF #	Start	End	Direction	Codon Length
----	-------	-------	-----	-----------	--------------

	1	50	268	F	73 codons
--	---	----	-----	---	-----------

35 ORF translation from 50-268, direction F

Blastp and/or MPSearch Result:

40 Result: UNK

SEQ ID NO: _482_____ ENCODED BY SEQ ID NO: _1057_____

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

5	2	260	418	R	53 codons
---	---	-----	-----	---	-----------

ORF translation from 260-418, direction R

10 Blastp and/or MPSearch Result:

Result: UNK

15

SEQ ID NO: _483_____ ENCODED BY SEQ ID NO: _1058_____

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

20	2	214	441	R	76 codons
----	---	-----	-----	---	-----------

ORF translation from 214-441, direction R

25 Blastp and/or MPSearch Result:

Result: UNK

30

SEQ ID NO: _484_____ ENCODED BY SEQ ID NO: _1059_____

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

35	1	40	273	R	78 codons
----	---	----	-----	---	-----------

ORF translation from 40-273, direction R

40

Blastp and/or MPSearch Result:

Result: UNK

SEQ ID NO: _485_____ ENCODED BY SEQ ID NO: _1060_____

5

ORF #	Start	End	Direction	Codon Length
2	676	1125	R	150 codons

10 ORF translation from 676-1125, direction R

Blastp and/or MPSearch Result:

Description:

15 HAEMOPHILUS INFLUENZAE. LIPOPROTEIN E PRECURSOR (OUTER MEMBRANE PROTEIN P4) (OMP P4).

SEQ ID NO: _486,487_____ ENCODED BY SEQ ID NO: _1061_____

ORF #	Start	End	Direction	Codon Length
2	1018	1344	F	109 codons
3	1498	1647	R	50 codons

25 ORF translation from 1018-1344, direction F

Blastp and/or MPSearch Result:

Description:

30 BACILLUS SUBTILIS. TRYPTOPHANYL-TRNA SYNTHETASE (EC 6.1.1.2) (TRYPTOPHAN--TRNA LIGASE) (TRPRS).

ORF translation from 1498-1647, direction R

35

Blastp and/or MPSearch Result:

Description:

40 LACTOCOCCUS LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS). OLIGOPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN OPPC.

SEQ ID NO: _488,489,490_____ ENCODED BY SEQ ID NO: _1062_____

5

ORF #	Start	End	Direction	Codon Length
1	415	552	F	46 codons
2	964	1116	F	51 codons
3	1132	1401	F	90 codons

10

ORF translation from 415-552, direction F

Blastp and/or MPSearch Result:

15

Result: UNK

ORF translation from 964-1116, direction F

20

Blastp and/or MPSearch Result:

Result: UNK

25

ORF translation from 1132-1401, direction F

30

Blastp and/or MPSearch Result:

Description:

BACILLUS SUBTILIS. D-ALANINE-ACTIVATING ENZYME (EC 6.3.2.-) (DAE) (D-ALANINE-D-ALANYL CARRIER PROTEIN LIGASE) (DCL).

35

SEQ ID NO: _491_____ ENCODED BY SEQ ID NO: _1063_____

40

ORF #	Start	End	Direction	Codon Length
2	393	1070	F	226 codons

ORF translation from 393-1070, direction F

Blastp and/or MPSearch Result:

- 5 Description:
ESCHERICHIA COLI. VACB PROTEIN.

SEQ ID NO: _492_____ ENCODED BY SEQ ID NO: _1064_____

10

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

2	283	846	R	188 codons
---	-----	-----	---	------------

15

ORF translation from 283-846, direction R

Blastp and/or MPSearch Result:

- 20 Description:
BACILLUS SUBTILIS. PEPTIDE SYNTHETASE 1.

SEQ ID NO: _493,494,495_____ ENCODED BY SEQ ID NO: _1065_____

25

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	1	321	F	107 codons
2	698	814	F	39 codons
30	3	1690	2166	F 159 codons

ORF translation from 1-321, direction F

- 35 Blastp and/or MPSearch Result:

Result: UNK

- 40 ORF translation from 698-814, direction F

Blastp and/or MPSearch Result:

Result: UNK

- 5 ORF translation from 1690-2166, direction F

Blastp and/or MPSearch Result:

- 10 Description:
BACILLUS SUBTILIS. BMRU PROTEIN.

SEQ ID NO: _496_____ ENCODED BY SEQ ID NO: _1066_____

- 15 ORF # Start End Direction Codon Length

 2 785 1003 R 73 codons

- 20 ORF translation from 785-1003, direction R

Blastp and/or MPSearch Result:

Result: UNK

- 25 SEQ ID NO: _497_____ ENCODED BY SEQ ID NO: _1067_____

- 30 ORF # Start End Direction Codon Length

 1 459 755 F 99 codons

ORF translation from 459-755, direction F

- 35 Blastp and/or MPSearch Result:

Result: UNK

- 40 SEQ ID NO: _498,499_____ ENCODED BY SEQ ID NO: _1068_____

ORF # Start End Direction Codon Length
199

1	186	320	F	45 codons
3	1135	1251	F	39 codons

5

ORF translation from 186-320, direction F

Blastp and/or MPSearch Result:

10

Result: UNK

ORF translation from 1135-1251, direction F

15

Blastp and/or MPSearch Result:

Description:

20

peptidase-like protein

SEQ ID NO: _500_____ ENCODED BY SEQ ID NO: _1069_____

25

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	437	646	R	70 codons
---	-----	-----	---	-----------

30

ORF translation from 437-646, direction R

Blastp and/or MPSearch Result:

35

Description:

ENTEROCOCCUS FAECALIS (STREPTOCOCCUS FAECALIS). CELL WALL
ENZYME EBSB.

40

SEQ ID NO: _501_____ ENCODED BY SEQ ID NO: _1070_____

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

200

1 68 259 F 64 codons

5 ORF translation from 68-259, direction F

Blastp and/or MPSearch Result:

Description:

10 BACILLUS SUBTILIS. AMPS PROTEIN (FRAGMENT).

SEQ ID NO: _502_____ ENCODED BY SEQ ID NO: _1071_____

15

ORF # Start End Direction Codon Length

1 1199 1648 R 150 codons

20

ORF translation from 1199-1648, direction R

Blastp and/or MPSearch Result:

25

Description:

BACILLUS SUBTILIS. BMRU PROTEIN.

30 SEQ ID NO: _503,504_____ ENCODED BY SEQ ID NO: _1072_____

ORF # Start End Direction Codon Length

2 701 970 F 90 codons

35 3 1941 2075 R 45 codons

ORF translation from 701-970, direction F

40 Blastp and/or MPSearch Result:

Result: UNK

ORF translation from 1941-2075, direction R

5 Blastp and/or MPSearch Result:

Description:

ATP/GTP-binding protein

10

SEQ ID NO: _505_____ ENCODED BY SEQ ID NO: _1073_____

15 ORF # Start End Direction Codon Length

ORF #	Start	End	Direction	Codon Length
1	185	928	R	248 codons

20 ORF translation from 185-928, direction R

Blastp and/or MPSearch Result:

Description:

nerve growth factor { promoter } [human, Genomic, 486 nt]. ptsG protein - Staphylococcus

25 carnosus

SEQ ID NO: _506_____ ENCODED BY SEQ ID NO: _1074_____

30 ORF # Start End Direction Codon Length

ORF #	Start	End	Direction	Codon Length
2	323	1648	R	442 codons

35 ORF translation from 323-1648, direction R

Blastp and/or MPSearch Result:

Description:

40 STAPHYLOCOCCUS AUREUS. MERCURIC REDUCTASE (EC 1.16.1.1) (HG(II) REDUCTASE).

SEQ ID NO: _507_____ ENCODED BY SEQ ID NO: _1075_____

5 ORF # Start End Direction Codon Length

 1 627 1061 F 145 codons

ORF translation from 627-1061, direction F

10

Blastp and/or MPSearch Result:

Result: UNK

15

SEQ ID NO: _508,509,510,511_____ ENCODED BY SEQ ID NO: _1076_____

20 ORF # Start End Direction Codon Length

 1 204 344 F 47 codons
 2 491 808 F 106 codons
 3 961 1227 F 89 codons
 5 2808 3092 F 95 codons

25

ORF translation from 204-344, direction F

30 Blastp and/or MPSearch Result:

Description:

BACILLUS SUBTILIS. SUCCINATE DEHYDROGENASE FLAVOPROTEIN
SUBUNIT (EC 1.3.99.1).

35

ORF translation from 491-808, direction F

40 Blastp and/or MPSearch Result:

Description:

BACILLUS SUBTILIS. SUCCINATE DEHYDROGENASE FLAVOPROTEIN
SUBUNIT (EC 1.3.99.1).

- 5 ORF translation from 961-1227, direction F

Blastp and/or MPSearch Result:

- 10 Description:
BACILLUS SUBTILIS. SUCCINATE DEHYDROGENASE FLAVOPROTEIN
SUBUNIT (EC 1.3.99.1).

- 15 ORF translation from 2808-3092, direction F

Blastp and/or MPSearch Result:

Description:

- 20 hydroxyneurosporene dehydrogenase - Myxococcus xanthus

SEQ ID NO: _512,513,514,515,516_ ENCODED BY SEQ ID NO: _1077_

25	ORF #	Start	End	Direction	Codon Length
	1	257	934	F	226 codons
	2	945	1280	F	112 codons
	3	1610	2362	F	251 codons
30	5	3173	3364	F	64 codons
	6	3380	3559	F	60 codons

ORF translation from 257-934, direction F

35

Blastp and/or MPSearch Result:

Description:

BACILLUS SP. (STRAIN C-125). PREPROTEIN TRANSLOCASE SECY SUBUNIT.

40

ORF translation from 945-1280, direction F

Blastp and/or MPSearch Result:

Result: UNK

5

ORF translation from 1610-2362, direction F

Blastp and/or MPSearch Result:

Result: UNK

10

ORF translation from 3173-3364, direction F

15 Blastp and/or MPSearch Result:

Result: UNK

20 ORF translation from 3380-3559, direction F

Blastp and/or MPSearch Result:

25 Result: UNK

SEQ ID NO: _517,518_____ ENCODED BY SEQ ID NO: _1078_____

30

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

3	1310	2068	F	253 codons
---	------	------	---	------------

4	2110	2355	F	82 codons
---	------	------	---	-----------

35

ORF translation from 1310-2068, direction F

Blastp and/or MPSearch Result:

Description:

40 STAPHYLOCOCCUS AUREUS. CAPM PROTEIN.

ORF translation from 2110-2355, direction F

Blastp and/or MPSearch Result:

Result: UNK

5

SEQ ID NO: _519___ ENCODED BY SEQ ID NO: _1079___

ORF #	Start	End	Direction	Codon Length
1	92	484	F	131 codons

ORF translation from 92-484, direction F

15

Blastp and/or MPSearch Result:

Description:

Rhizobium leguminosarum pss4 gene encoding a protein involved in

20

SEQ ID NO: _520___ ENCODED BY SEQ ID NO: _1080___

ORF #	Start	End	Direction	Codon Length
2	866	1414	F	183 codons

ORF translation from 866-1414, direction F

Blastp and/or MPSearch Result:

Description:

ESCHERICHIA COLI. GALACTITOL-1-PHOSPHATE DEHYDROGENASE (EC 1.1.1.-).

40

SEQ ID NO: _521___ ENCODED BY SEQ ID NO: _1081___

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1 642 1322 R 227 codons

- 5 ORF translation from 642-1322, direction R

Blastp and/or MPSearch Result:

- 10 Description:
BACILLUS SUBTILIS. EXCINUCLEASE ABC SUBUNIT C.

- 15 SEQ ID NO: _522,523,524,525____ ENCODED BY SEQ ID NO: _1082____

	ORF #	Start	End	Direction	Codon Length
20	1	144	866	R	241 codons
	2	1267	1857	R	197 codons
	3	1978	2250	R	91 codons
	5	2561	2794	R	78 codons

- 25 ORF translation from 144-866, direction R

Blastp and/or MPSearch Result:

- 30 Description:
ESCHERICHIA COLI. RESPIRATORY NITRATE REDUCTASE 2 ALPHA CHAIN
(EC 1.7.99.4).

- 35 ORF translation from 1267-1857, direction R

Blastp and/or MPSearch Result:

- 40 Description:
BACILLUS MEGATERIUM. UROPORPHYRIN-III C-METHYLTRANSFERASE (EC
2.1.1.107) (UROGEN III METHYLASE) (SUMT) (UROPORPHYRINOGEN III
METHYLASE) (UROM).

ORF translation from 1978-2250, direction R

Blastp and/or MPSearch Result:

5

Description:

BACILLUS MEGATERIUM. UROPORPHYRIN-III C-METHYLTRANSFERASE (EC 2.1.1.107) (UROGEN III METHYLASE) (SUMT) (UROPORPHYRINOGEN III METHYLASE) (UROM).

10

ORF translation from 2561-2794, direction R

15 Blastp and/or MPSearch Result:

Description:

BACTRPC2 NCBI gi: 710 - Bacillus subtilis (strain 168TrpC2,) DNA.

20

SEQ ID NO: _526,527___ ENCODED BY SEQ ID NO: _1083___

25	ORF #	Start	End	Direction	Codon Length
	1	384	596	R	71 codons
	2	626	970	R	115 codons

30 ORF translation from 384-596, direction R

Blastp and/or MPSearch Result:

35 Result: UNK

ORF translation from 626-970, direction R

40 Blastp and/or MPSearch Result:

Description:

BACILLUS SUBTILIS. OROTATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.10) (OPRT).

SEQ ID NO: _528_ ENCODED BY SEQ ID NO: _1084_

5

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	24	893	R	290 codons
---	----	-----	---	------------

10

ORF translation from 24-893, direction R

Blastp and/or MPSearch Result:

15

Description:

ESCHERICHIA COLI. ALCOHOL DEHYDROGENASE (EC 1.1.1.1) (ADH) /
ACETALDEHYDE DEHYDROGENASE (ACETYLATING) (EC 1.2.1.10) (ACDH) /
PYRUVATE-FORMATE-LYASE DEACTIVASE (PFL DEACTIVASE).

20

SEQ ID NO: _529_ ENCODED BY SEQ ID NO: _1085_

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

25

5	2558	3331	R	258 codons
---	------	------	---	------------

ORF translation from 2558-3331, direction R

Blastp and/or MPSearch Result:

30

Description:

STAPHYLOCOCCUS STAPHYLOLYTICUS. LYSOSTAPHIN PRECURSOR (EC
3.5.1.-).

35

SEQ ID NO: _530_ ENCODED BY SEQ ID NO: _1086_

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

40

2	280	1095	F	272 codons
---	-----	------	---	------------

ORF translation from 280-1095, direction F
Blastp and/or MPSearch Result:

Description:

- 5 ESCHERICHIA COLI. RESPIRATORY NITRATE REDUCTASE 1 ALPHA CHAIN
(EC 1.7.99.4).

SEQ ID NO: _531___ ENCODED BY SEQ ID NO: _1087___

10

ORF #	Start	End	Direction	Codon Length
3	701	1195	R	165 codons

15

ORF translation from 701-1195, direction R

Blastp and/or MPSearch Result:

20 Description:

LACTOCOCCUS LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS). 3-
ISOPROPYLMALATE DEHYDRATASE (EC 4.2.1.33) (ISOPROPYLMALATE
ISOMERASE) (ALPHA-IPM ISOMERASE).

25

SEQ ID NO: _532___ ENCODED BY SEQ ID NO: _1088___

ORF #	Start	End	Direction	Codon Length
1	16	288	F	91 codons

30

ORF translation from 16-288, direction F

35

Blastp and/or MPSearch Result:

Result: UNK

40

SEQ ID NO: _533_ ENCODED BY SEQ ID NO: _1089_

5 ORF # Start End Direction Codon Length

 1 302 508 R 69 codons

10 ORF translation from 302-508, direction R

Blastp and/or MPSearch Result:

15 Result: UNK

SEQ ID NO: _534_ ENCODED BY SEQ ID NO: _1090_

20 ORF # Start End Direction Codon Length

 1 182 505 F 108 codons

25 ORF translation from 182-505, direction F

Blastp and/or MPSearch Result:

30 Description:
BACILLUS SUBTILIS. PHENYLALANYL-TRNA SYNTHETASE BETA CHAIN (EC
6.1.1.20) (PHENYLALANINE-- TRNA LIGASE BETA CHAIN) (PHERS).

35 SEQ ID NO: _535,536_ ENCODED BY SEQ ID NO: _1091_

40 ORF # Start End Direction Codon Length

 2 618 1097 F 160 codons
 3 1150 1542 F 131 codons

ORF translation from 618-1097, direction F

Blastp and/or MPSearch Result:

5

Description:

ANACYSTIS NIDULANS. ELONGATION FACTOR G (EF-G).

10 ORF translation from 1150-1542, direction F

Blastp and/or MPSearch Result:

15

Description:

MYCOBACTERIUM LEPRAE. ELONGATION FACTOR G (EF-G).

20 SEQ ID NO: _537___ ENCODED BY SEQ ID NO: _1092___

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	637	1287	R	217 codons
---	-----	------	---	------------

25

ORF translation from 637-1287, direction R

Blastp and/or MPSearch Result:

30

Result: UNK

SEQ ID NO: _538___ ENCODED BY SEQ ID NO: _1093___

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

2	513	1124	F	204 codons
---	-----	------	---	------------

40 ORF translation from 513-1124, direction F

Blastp and/or MPSearch Result:

Description:

Human KIP2 gene for p57KIP2. high-affinity choline transport protein (betT) homolog -

5 SEQ ID NO: _539,540___ ENCODED BY SEQ ID NO: _1094___

	ORF #	Start	End	Direction	Codon Length
	1	66	368	F	101 codons
10	2	580	1011	F	144 codons

ORF translation from 66-368, direction F

15 Blastp and/or MPSearch Result:

Description:

secA protein - Staphylococcus carnosus

20

ORF translation from 580-1011, direction F

Blastp and/or MPSearch Result:

25

Description:

BACILLUS SUBTILIS. PREPROTEIN TRANSLOCASE SECA SUBUNIT.

30 SEQ ID NO: _541,542___ ENCODED BY SEQ ID NO: _1095___

	ORF #	Start	End	Direction	Codon Length
	1	747	926	F	60 codons
35	2	998	1285	F	96 codons

ORF translation from 747-926, direction F

40

Blastp and/or MPSearch Result:

Description:

LACTOCOCCUS LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS). DI-
TRYPEPTIDE TRANSPORTER.

- 5 ORF translation from 998-1285, direction F

Blastp and/or MPSearch Result:

Description:

- 10 LACTOCOCCUS LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS). DI-
TRYPEPTIDE TRANSPORTER.

SEQ ID NO: _543_ ENCODED BY SEQ ID NO: _1096_

- | 15 | ORF # | Start | End | Direction | Codon Length |
|----|-------|-------|------|-----------|--------------|
| | 3 | 914 | 1297 | R | 128 codons |

- 20 ORF translation from 914-1297, direction R

Blastp and/or MPSearch Result:

Result: UNK

25

SEQ ID NO: _544_ ENCODED BY SEQ ID NO: _1097_

- | 30 | ORF # | Start | End | Direction | Codon Length |
|----|-------|-------|-----|-----------|--------------|
| | 1 | 89 | 763 | R | 225 codons |

- 35 ORF translation from 89-763, direction R

Blastp and/or MPSearch Result:

Description:

- 40 ESCHERICHIA COLI. BETAINE ALDEHYDE DEHYDROGENASE (EC 1.2.1.8)
(BADH).

SEQ ID NO: _545___ ENCODED BY SEQ ID NO: _1098___

5 ORF # Start End Direction Codon Length

 1 126 236 F 37 codons

10 ORF translation from 126-236, direction F

Blastp and/or MPSearch Result:

15 Description:
STAPHYLOCOCCUS AUREUS. PROBABLE CADMIUM-TRANSPORTING ATPASE
(EC 3.6.1.-) (CADMIUM EFFLUX ATPASE).

20 SEQ ID NO: _546___ ENCODED BY SEQ ID NO: _1099___

25 ORF # Start End Direction Codon Length

 2 2412 2747 F 112 codons

ORF translation from 2412-2747, direction F

30 Blastp and/or MPSearch Result:

Description:
mercuric reductase-like protein

35 SEQ ID NO: _547___ ENCODED BY SEQ ID NO: _1100___

40 ORF # Start End Direction Codon Length

 2 843 1154 R 104 codons

ORF translation from 843-1154, direction R
Blastp and/or MPSearch Result:

Description:

thiolase (EC 2.3.1.9) - Clostridium acetobutylicum

5

SEQ ID NO: _548___ ENCODED BY SEQ ID NO: _1101___

ORF #	Start	End	Direction	Codon Length
1	420	938	F	173 codons

15 ORF translation from 420-938, direction F
Blastp and/or MPSearch Result:

Description:

ALCALIGENES EUTROPHUS. ACETYL-COA ACETYLTRANSFERASE (EC 2.3.1.9)
(ACETOACETYL-COA THIOLASE).

20

SEQ ID NO: _549,550___ ENCODED BY SEQ ID NO: _1102___

ORF #	Start	End	Direction	Codon Length
1	386	562	F	59 codons
2	845	1195	F	117 codons

25

30 ORF translation from 386-562, direction F

Blastp and/or MPSearch Result:

35 Result: UNK

ORF translation from 845-1195, direction F

40

Blastp and/or MPSearch Result:

Result: UNK

5 SEQ ID NO: _551___ ENCODED BY SEQ ID NO: _1103___

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

2	357	647	R	97 codons
---	-----	-----	---	-----------

10

ORF translation from 357-647, direction R

15 Blastp and/or MPSearch Result:

Result: UNK

20

SEQ ID NO: _552,553___ ENCODED BY SEQ ID NO: _1104___

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	173	397	R	75 codons
2	443	697	R	85 codons

25

ORF translation from 173-397, direction R

30

Blastp and/or MPSearch Result:

Description:

35 fructose-permease IIBC component (fruA) homolog - Haemophilus

ORF translation from 443-697, direction R

40 Blastp and/or MPSearch Result:

Description:

XANTHOMONAS CAMPESTRIS (PV. CAMPESTRIS). PTS SYSTEM, FRUCTOSE-
SPECIFIC IIBC COMPONENT (EIIBC-FRU) (FRUCTOSE- PERMEASE IIBC
COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, BC COMPONENT) (EC
2.7.1.69) (EII-FRU).

5

SEQ ID NO: _554___ ENCODED BY SEQ ID NO: _1105___

ORF #	Start	End	Direction	Codon Length
1	277	531	F	85 codons

ORF translation from 277-531, direction F

15 Blastp and/or MPSearch Result:

Result: UNK

20 SEQ ID NO: _555___ ENCODED BY SEQ ID NO: _1106___

ORF #	Start	End	Direction	Codon Length
1	43	861	R	273 codons

25

ORF translation from 43-861, direction R

30 Blastp and/or MPSearch Result:

Description:

STREPTOCOCCUS PNEUMONIAE. MALTODEXTRIN TRANSPORT SYSTEM
PERMEASE PROTEIN MALC.

35

SEQ ID NO: _556___ ENCODED BY SEQ ID NO: _1107___

ORF #	Start	End	Direction	Codon Length
1	253	618	R	122 codons

40

ORF translation from 253-618, direction R
Blastp and/or MPSearch Result:

Description:

- 5 ESCHERICHIA COLI. GLUTAMATE SYNTHASE (NADPH) LARGE CHAIN
PRECURSOR (EC 1.4.1.13) (GLUTAMATE SYNTHASE ALPHA SUBUNIT) (NADPH-
GOGAT) (GLTS ALPHA CHAIN).

10

SEQ ID NO: _557___ ENCODED BY SEQ ID NO: _1108___

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

15	1	210	398	R	63 codons
----	---	-----	-----	---	-----------

ORF translation from 210-398, direction R

20

Blastp and/or MPSearch Result:

Result: UNK

25

SEQ ID NO: _558___ ENCODED BY SEQ ID NO: _1109___

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

30	1	246	806	F	187 codons
----	---	-----	-----	---	------------

ORF translation from 246-806, direction F

35 Blastp and/or MPSearch Result:

Description:

ABC transporter

40

SEQ ID NO: _559___ ENCODED BY SEQ ID NO: _1110___

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

219

1 576 1160 F 195 codons

5 ORF translation from 576-1160, direction F

Blastp and/or MPSearch Result:

10 Description:

2 622 38.7 262 1 FABI_ECOLI ENOYL-[ACYL-CARRIER-PR 1.40e-110

SEQ ID NO: _560,561____ ENCODED BY SEQ ID NO: _1111__

15

ORF # Start End Direction Codon Length

1 527 811 F 95 codons

2 849 950 F 34 codons

20

ORF translation from 527-811, direction F

Blastp and/or MPSearch Result:

25 Result: UNK

ORF translation from 849-950, direction F

30

Blastp and/or MPSearch Result:

Result: UNK

35

SEQ ID NO: _562____ ENCODED BY SEQ ID NO: _1112__

ORF # Start End Direction Codon Length

40 1 292 513 R 74 codons

ORF translation from 292-513, direction R

Blastp and/or MPSearch Result:

Description:

- 5 BACILLUS SUBTILIS. PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE
(EC 4.1.2.15) (PHOSPHO-2- KETO-3-DEOXYHEPTONATE ALDOLASE) (DAHP
SYNTHETASE) (3-DEOXY-D-ARABINO- HEPTULOSONATE 7-PHOSPHATE
SYNTHASE) / CHORISMATE MUTASE (EC 5.4.99.5).

10

SEQ ID NO: _563___ ENCODED BY SEQ ID NO: _1113__

ORF #	Start	End	Direction	Codon Length
1	977	1207	F	77 codons

ORF translation from 977-1207, direction F

Blastp and/or MPSearch Result:

Result: UNK

30 SEQ ID NO: _564___ ENCODED BY SEQ ID NO: _1114__

ORF #	Start	End	Direction	Codon Length
2	448	678	R	77 codons

ORF translation from 448-678, direction R

Blastp and/or MPSearch Result:

Result: UNK

SEQ ID NO: _565___ ENCODED BY SEQ ID NO: _1115___

ORF #	Start	End	Direction	Codon Length
2	121	267	R	49 codons

ORF translation from 121-267, direction R

Blastp and/or MPSearch Result:

Result: UNK

SEQ ID NO: _566___ ENCODED BY SEQ ID NO: _1116___

ORF #	Start	End	Direction	Codon Length
2	440	736	F	99 codons

ORF translation from 440-736, direction F

Blastp and/or MPSearch Result:

Description:

ESCHERICHIA COLI. FERRIC ENTEROBACTIN TRANSPORT ATP-BINDING
PROTEIN FEPC.

SEQ ID NO: _567___ ENCODED BY SEQ ID NO: _1117___

ORF #	Start	End	Direction	Codon Length
1	355	735	F	127 codons

ORF translation from 355-735, direction F

Blastp and/or MPSearch Result:

5 Result: UNK

SEQ ID NO: _568__ ENCODED BY SEQ ID NO: _1118__

10 ORF # Start End Direction Codon Length

1 199 555 R 119 codons

ORF translation from 199-555, direction R

15

Blastp and/or MPSearch Result:

Result: UNK

20

SEQ ID NO: _569__ ENCODED BY SEQ ID NO: _1119__

25

ORF # Start End Direction Codon Length

2 914 1282 F 123 codons

30

ORF translation from 914-1282, direction F

Blastp and/or MPSearch Result:

35 Description:

beta-ketothiolase=poly(3-hydroxyalkanoate) synthase - Thiocystis

SEQ ID NO: _570__ ENCODED BY SEQ ID NO: _1120__

40

ORF # Start End Direction Codon Length

2 570 974 F 135 codons

223

ORF translation from 570-974, direction F

5

Blastp and/or MPSearch Result:

Description:

10 ESCHERICHIA COLI. UDP-N-ACETYL-D-MANNOSAMINURONIC ACID
DEHYDROGENASE (EC 1.1.1.-) (UDP-MANNACA DEHYDROGENASE).

SEQ ID NO: _571__ ENCODED BY SEQ ID NO: _1121__

15 ORF # Start End Direction Codon Length

1 258 521 F 88 codons

20 ORF translation from 258-521, direction F

Blastp and/or MPSearch Result:

Description:

25 ABC transporter

SEQ ID NO: _572__ ENCODED BY SEQ ID NO: _1122__

30

ORF # Start End Direction Codon Length

1 316 867 R 184 codons

35

ORF translation from 316-867, direction R

Blastp and/or MPSearch Result:

40 Description:

Potentially prenylated protein

SEQ ID NO: _573__ ENCODED BY SEQ ID NO: _1123__

5 ORF # Start End Direction Codon Length

 2 334 576 R 81 codons

10 ORF translation from 334-576, direction R

Blastp and/or MPSearch Result:

15 Result: UNK

SEQ ID NO: _574__ ENCODED BY SEQ ID NO: _1124__

20 ORF # Start End Direction Codon Length

 1 85 372 R 96 codons

25 ORF translation from 85-372, direction R

Blastp and/or MPSearch Result:

Description:

30 BACILLUS SUBTILIS. OLIGOPEPTIDE TRANSPORT ATP-BINDING PROTEIN
 OPPD.

35 SEQ ID NO: _575__ ENCODED BY SEQ ID NO: _1125__

 ORF # Start End Direction Codon Length

 1 319 774 F 152 codons

40 ORF translation from 319-774, direction F

Blastp and/or MPSearch Result:

Description:

5 D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95) (PGDH). - BACILLUS
SUBTILIS.

SEQ ID NO: _576__ ENCODED BY SEQ ID NO: _1126__

10	ORF #	Start	End	Direction	Codon Length
	1	375	734	F	120 codons

15 ORF translation from 375-734, direction F

Blastp and/or MPSearch Result:

Description:

20 >GLTB_ECOLI GLUTAMATE SYNTHASE (NADPH) LARGE CHAIN PRECURSOR
(EC 1.4.1.13) (GLUTAMATE SYNTHASE ALPHA SUBUNIT) (NADPH-GOGAT).-
ESCHERICHIA COLI. Length = 1514

SEQ ID NO: _577__ ENCODED BY SEQ ID NO: _1127__

25	ORF #	Start	End	Direction	Codon Length
	1	12	533	R	174 codons

30 ORF translation from 12-533, direction R

Blastp and/or MPSearch Result:

35 Result: UNK

SEQ ID NO: _578__ ENCODED BY SEQ ID NO: _1128__

40	ORF #	Start	End	Direction	Codon Length
	1	216	524	R	103 codons

ORF translation from 216-524, direction R

5

Blastp and/or MPSearch Result:

Description:

gluconate permease - *Bacillus licheniformis*

10

SEQ ID NO: _579_ ENCODED BY SEQ ID NO: _1129_

ORF #	Start	End	Direction	Codon Length
1	332	430	F	33 codons

15

ORF translation from 332-430, direction F

20

Blastp and/or MPSearch Result:

Description:

Putative transaldolase

25

SEQ ID NO: _580_ ENCODED BY SEQ ID NO: _1130_ ORF # Start End
Direction Codon Length

30

1	186	311	F	42 codons
---	-----	-----	---	-----------

ORF translation from 186-311, direction F

35

Blastp and/or MPSearch Result:

Result: UNK

40

SEQ ID NO: _581_ ENCODED BY SEQ ID NO: _1131_

ORF #	Start	End	Direction	Codon Length
2	130	363	R	78 codons

5

ORF translation from 130-363, direction R

Blastp and/or MPSearch Result:

10 Result: UNK

15 SEQ ID NO: _582__ ENCODED BY SEQ ID NO: _1132__

ORF #	Start	End	Direction	Codon Length
2	371	469	F	33 codons

20

ORF translation from 371-469, direction F

25 Blastp and/or MPSearch Result:

Result: UNK

30

SEQ ID NO: _583__ ENCODED BY SEQ ID NO: _1133__

ORF #	Start	End	Direction	Codon Length
1	170	565	F	132 codons

35

ORF translation from 170-565, direction F

40

Blastp and/or MPSearch Result:

Description:

lipoate biosynthesis protein A (lipA) homolog - Haemophilus

5 SEQ ID NO: _584__ ENCODED BY SEQ ID NO: _1134__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	233	457	F	75 codons
---	-----	-----	---	-----------

10

ORF translation from 233-457, direction F

Blastp and/or MPSearch Result:

15

Result: UNK

20 SEQ ID NO: _585__ ENCODED BY SEQ ID NO: _1135__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	173	454	R	94 codons
---	-----	-----	---	-----------

25

ORF translation from 173-454, direction R

30 Blastp and/or MPSearch Result:

Result: UNK

35

SEQ ID NO: _586__ ENCODED BY SEQ ID NO: _1136__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

40

1	58	261	R	68 codons
---	----	-----	---	-----------

ORF translation from 58-261, direction R

Blastp and/or MPSearch Result:

Result: UNK

SEQ ID NO: _587_ ENCODED BY SEQ ID NO: _1137_

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	143	745	F	201 codons
---	-----	-----	---	------------

ORF translation from 143-745, direction F

Blastp and/or MPSearch Result:

Description:

ESCHERICHIA COLI. BACTRACIN RESISTANCE PROTEIN (PUTATIVE UNDECAPRENOL KINASE) (EC 2.7.1.66).

SEQ ID NO: _588_ ENCODED BY SEQ ID NO: _1138_

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	124	411	R	96 codons
---	-----	-----	---	-----------

ORF translation from 124-411, direction R

Blastp and/or MPSearch Result:

Description:

STREPTOMYCES HYGROSCOPICUS. ACETYL-HYDROLASE (EC 3.1.-.-).

SEQ ID NO: _589_ ENCODED BY SEQ ID NO: _1139_

5 ORF # Start End Direction Codon Length

ORF #	Start	End	Direction	Codon Length
1	288	494	F	69 codons

10 ORF translation from 288-494, direction F

Blastp and/or MPSearch Result:

15 Result: UNK

SEQ ID NO: _590_ ENCODED BY SEQ ID NO: _1140_

20

ORF # Start End Direction Codon Length

ORF #	Start	End	Direction	Codon Length
1	37	396	R	120 codons

25

ORF translation from 37-396, direction R

Blastp and/or MPSearch Result:

30

Description:

BACTEROIDES NODOSUS (DICHELOBACTER NODOSUS). PEPTIDE CHAIN
RELEASE FACTOR 3 (RF-3).

35

SEQ ID NO: _591_ ENCODED BY SEQ ID NO: _1141_

ORF # Start End Direction Codon Length

ORF #	Start	End	Direction	Codon Length
2	140	283	R	48 codons

40

ORF translation from 140-283, direction R

Blastp and/or MPSearch Result:

5

Result: UNK

10 SEQ ID NO: _592,593__ ENCODED BY SEQ ID NO: _1142__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	1	150	R	50 codons
15	2	164	400	R 79 codons

ORF translation from 1-150, direction R

20

Blastp and/or MPSearch Result:

Result: UNK

25

ORF translation from 164-400, direction R

Blastp and/or MPSearch Result:

30

Description:

ligoendopeptidase F - *Lactococcus lactis*

35

SEQ ID NO: _594,595__ ENCODED BY SEQ ID NO: _1143__

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

40	1	365	808	R 148 codons
	2	860	1075	R 72 codons

ORF translation from 365-808, direction R

Blastp and/or MPSearch Result:

5

Result: UNK

ORF translation from 860-1075, direction R

10

Blastp and/or MPSearch Result:

Result: UNK

15

SEQ ID NO: _596__ ENCODED BY SEQ ID NO: _1144__

20 ORF # Start End Direction Codon Length

ORF #	Start	End	Direction	Codon Length
1	37	360	F	108 codons

25 ORF translation from 37-360, direction F

Blastp and/or MPSearch Result:

30 Description:

2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase - Escherichia coli

SEQ ID NO: _597__ ENCODED BY SEQ ID NO: _1145__

35

ORF # Start End Direction Codon Length

ORF #	Start	End	Direction	Codon Length
2	367	504	R	46 codons

40

ORF translation from 367-504, direction R

Blastp and/or MPSearch Result:

Result: UNK

5

SEQ ID NO: _598,599_ ENCODED BY SEQ ID NO: _1146_

ORF #	Start	End	Direction	Codon Length
3	1375	1902	F	176 codons
4	1963	2421	F	153 codons

15 ORF translation from 1375-1902, direction F

Blastp and/or MPSearch Result:

20 Description:
glucose-fructose oxidoreductase (EC 1.1.--) precursor - Zymomonas

ORF translation from 1963-2421, direction F

25 Blastp and/or MPSearch Result:

Result: UNK

30 SEQ ID NO: _600_ ENCODED BY SEQ ID NO: _1147_

ORF #	Start	End	Direction	Codon Length
1	195	317	F	41 codons

35

ORF translation from 195-317, direction F

Blastp and/or MPSearch Result:

40

Result: UNK

SEQ ID NO: _601 ENCODED BY SEQ ID NO: _1148__

5 ORF # Start End Direction Codon Length

 1 1 372 F 124 codons

ORF translation from 1-372, direction F

10

Blastp and/or MPSearch Result:

Result: UNK

15

SEQ ID NO: _602_ ENCODED BY SEQ ID NO: _1149__

20 ORF # Start End Direction Codon Length

 1 166 711 R 182 codons

ORF translation from 166-711, direction R

25

Blastp and/or MPSearch Result:

Result: UNK

30

SEQ ID NO: _603_ ENCODED BY SEQ ID NO: _1150__

35 ORF # Start End Direction Codon Length

 1 390 917 R 176 codons

ORF translation from 390-917, direction R

40

Blastp and/or MPSearch Result:

Result: UNK

SEQ ID NO: _604_ ENCODED BY SEQ ID NO: _1151_

5

ORF #	Start	End	Direction	Codon Length
1	20	433	F	138 codons

ORF translation from 20-433, direction F

10

Blastp and/or MPSearch Result:

Description:

15 BACILLUS SUBTILIS. CITRATE SYNTHASE I REPRESSOR.

SEQ ID NO: _605_ ENCODED BY SEQ ID NO: _1152_

20

ORF #	Start	End	Direction	Codon Length
1	52	585	R	178 codons

25

ORF translation from 52-585, direction R

Blastp and/or MPSearch Result:

30

Description:

STAATL NCBI gi: 765069 NCBI gi: 4737 - Staphylococcus aureus (strain 8325/4) DNA

35 SEQ ID NO: _606_ ENCODED BY SEQ ID NO: _1153_

ORF #	Start	End	Direction	Codon Length
1	85	315	R	77 codons

40

ORF translation from 85-315, direction R

Blastp and/or MPSearch Result:

Description:

BACILLUS SUBTILIS. ARGININE HYDROXIMATE RESISTANCE PROTEIN.

5

SEQ ID NO: _607_ ENCODED BY SEQ ID NO: _1154__

ORF #	Start	End	Direction	Codon Length
10	1	256	594	F 113 codons

ORF translation from 256-594, direction F

15

Blastp and/or MPSearch Result:

Result: UNK

20

SEQ ID NO: _608_ ENCODED BY SEQ ID NO: _1155__

25

ORF #	Start	End	Direction	Codon Length
2	603	1148	R	182 codons

30

ORF translation from 603-1148, direction R

Blastp and/or MPSearch Result:

35

Result: UNK

40

SEQ ID NO: _609_ ENCODED BY SEQ ID NO: _1156__

ORF #	Start	End	Direction	Codon Length
				237

1 223 354 R 44 codons

- 5 ORF translation from 223-354, direction R
MTQARPGNHMYLSRLKPNGQFIDRLLVKNNGGHGTHNAYRYIVQ*

Blastp and/or MPSearch Result:

- 10 Result: UNK

SEQ ID NO: _610,611,612,613_ ENCODED BY SEQ ID NO: _1157_

15

ORF #	Start	End	Direction	Codon Length
-------	-------	-----	-----------	--------------

1	679	1272	F	198 codons
3	1668	1844	F	59 codons
20 4	1885	2064	F	60 codons
5	2326	2832	F	169 codons

- 25 ORF translation from 679-1272, direction F

Blastp and/or MPSearch Result:

- 30 Result: UNK

ORF translation from 1668-1844, direction F

- 35 Blastp and/or MPSearch Result:

Result: UNK

- 40 ORF translation from 1885-2064, direction F

Blastp and/or MPSearch Result:

Result: UNK

- 5 ORF translation from 2326-2832, direction F

Blastp and/or MPSearch Result:

- 10 Description:
STAPHYLOCOCCUS AUREUS. AUTOLYSIN (EC 3.5.1.28) (N-
ACETYLMURAMOYL-L-ALANINE AMIDASE).

15

SEQ ID NO: _614,615_ ENCODED BY SEQ ID NO: _1158_

	ORF #	Start	End	Direction	Codon Length
20	1	95	925	R	277 codons
	2	945	1538	R	198 codons

ORF translation from 95-925, direction R

25

Blastp and/or MPSearch Result:

- Description:
30 MORAXELLA SP. HALOACETATE DEHALOGENASE H-1 (EC 3.8.1.3).

ORF translation from 945-1538, direction R

- 35 Blastp and/or MPSearch Result:

Result: UNK

SEQ ID NO: _616__ ENCODED BY SEQ ID NO: _1159__

ORF #	Start	End	Direction	Codon Length
2	189	518	F	110 codons

ORF translation from 189-518, direction F

10 Blastp and/or MPSearch Result:

Description:

BACILLUS SUBTILIS. SUCCINATE DEHYDROGENASE IRON-SULFUR PROTEIN
(EC 1.3.99.1).

15

SEQ ID NO: _617__ ENCODED BY SEQ ID NO: _1160__

20

ORF #	Start	End	Direction	Codon Length
1	1	138	R	46 codons

25

ORF translation from 1-138, direction R

Blastp and/or MPSearch Result:

30

Result: UNK

SEQ ID NO: _618__ ENCODED BY SEQ ID NO: _1161__

35

ORF #	Start	End	Direction	Codon Length
1	303	455	F	51 codons

40

ORF translation from 303-455, direction F

Blastp and/or MPSearch Result:

Result: UNK

5

SEQ ID NO: _619,620_ ENCODED BY SEQ ID NO: _1162_

	ORF #	Start	End	Direction	Codon Length
10	1	80	457	F	126 codons
	2	586	891	F	102 codons

ORF translation from 80-457, direction F

15

Blastp and/or MPSearch Result:

Description:

20 ESCHERICHIA COLI. TYPE I RESTRICTION ENZYME ECOR124/3 I M PROTEIN
(EC 2.1.1.72).

ORF translation from 586-891, direction F

Blastp and/or MPSearch Result:

25

Description:

TYPE I RESTRICTION ENZYME ECOKI SPECIFICITY PROTEIN (S PROTEIN). -
ESCHERICHIA COLI.

30

SEQ ID NO: _621_ ENCODED BY SEQ ID NO: _1163_

	ORF #	Start	End	Direction	Codon Length
35	1	114	635	R	174 codons

40 ORF translation from 114-635, direction R

Blastp and/or MPSearch Result:

Result: UNK

5

SEQ ID NO: _622_ ENCODED BY SEQ ID NO: _1164_

ORF #	Start	End	Direction	Codon Length
1	178	492	F	105 codons

ORF translation from 178-492, direction F

15 Blastp and/or MPSearch Result:

Description:

ESCHERICHIA COLI. PHOSPHOPENTOMUTASE (EC 5.4.2.7)
(PHOSPHODEOXYRIBOMUTASE).

20

SEQ ID NO: _623_ ENCODED BY SEQ ID NO: _1165_

ORF #	Start	End	Direction	Codon Length
1	101	238	R	46 codons

ORF translation from 101-238, direction R

30

Blastp and/or MPSearch Result:

Description:

STAPHYLOCOCCUS AUREUS. 6-PHOSPHO-BETA-GALACTOSIDASE (EC 3.2.1.85)
35 (BETA-D-PHOSPHOGALACTOSIDE GALACTOHYDROLASE).

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Black, Michael
Burnham, Martin
Hodgson, John
Knowles, David
Nicholas, Richard
Pratt, Julie
Reichard, Raymond
Rosenberg, Martin
Ward, Judith
- (ii) TITLE OF THE INVENTION: Novel Compounds
- (iii) NUMBER OF SEQUENCES: 1166
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: SmithKline Beecham Corporation
(B) STREET: 709 Swedeland Road
(C) CITY: King of Prussia
(D) STATE: PA
(E) COUNTRY: USA
(F) ZIP: 19406-0939
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE: 19-FEB-1997
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 60/011,888
(B) FILING DATE: 20-FEB-1996

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Gimmi, Edward R
- (B) REGISTRATION NUMBER: 38,891
- (C) REFERENCE/DOCKET NUMBER: GM50006

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 610-270-4478
- (B) TELEFAX: 610-270-5090
- (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```

Met Gln Phe Ser Leu Leu Ile Tyr Ile Val Val Ile Cys Ala Val Met
 1             5             10             15
Tyr Phe Leu Met Ile Arg Pro Gln Gln Lys Arg Ala Lys Gln His Arg
 20             25             30
Glu Leu Ile Asn Asn Ile Gln Ser Gly Gln Arg Ile Thr Thr Ile Gly
 35             40             45
Gly Ile Lys Gly Thr Val Lys Ala Val Asp Glu Thr Thr Val Val Ile
 50             55             60
Thr Val Asn Gly His Gly Thr Glu Leu Thr Phe Glu Lys Pro Ala Ile
 65             70             75             80
Lys Gln Val Gly Pro Xaa Ile Thr Arg Ser Gly Ile Lys Lys Asp Glu
 85             90             95
Thr Asn Ser Val Ser Ser Leu Leu Lys Leu Xaa Val Xaa Leu
 100            105            110

```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

Met Leu Ser His Ile Thr Ala Tyr Glu Ile Leu Ser Glu Ile Arg Lys
 1             5             10             15
Lys Leu Ala Gln Lys Leu Met Arg Leu Pro Leu Gly Val Val Glu Ser
          20             25             30
Lys Lys Ile Gly Glu Leu Lys Asn Ile Phe Xaa Asp Lys Val Glu Thr
          35             40             45
Ile Glu Leu Pro Leu Ala His Met Ile Pro Glu Val Xaa Gly Asn Leu
          50             55             60
Leu Val Ala Ala Ala Ile Phe Leu Tyr Ile Met Xaa Xaa Asp Trp Arg
65             70             75             80
Ile Gly

```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```

Met Ala Thr Leu Gly Phe Thr Thr Leu Val Met Gln Asp Gly Phe Met
 1             5             10             15
Xaa Gly Leu Ile Gly Xaa Ala Thr Xaa Gly Pro Xaa Leu Xaa Xaa Phe
          20             25             30
Pro Val Tyr Tyr His Arg Tyr Leu Ile Trp Ile Asn Asp Gly Leu
          35             40             45

```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

Met Leu Phe Met Val Ile Lys Thr Leu Gly Gly Ile Trp Thr Leu Lys
 1             5             10             15
Leu Phe Ile Leu Pro Asn His Pro Ile Ile Lys Ser Gly Leu Tyr Lys
          20             25             30
Ile Thr Lys Thr Pro Lys Leu Leu Leu Lys His His Ser
      35             40             45

```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```

Met Gly Glu Asn Lys Asn Asn Leu Ser Ile Asn Asp Asp His Ser Asn
 1             5             10             15
Ala Ala Met Thr His Thr Ser Asp Ala Ile Ala Ser Ser Asp Phe Ile
          20             25             30
Ile Arg Glu Leu Asp Leu Asn Gln Glu Pro Glu Met Gln Arg Glu Ser
      35             40             45
Thr Xaa Ser Arg Gln Asp Ala Trp Xaa Gln Leu Lys Arg Xaa Lys Leu
      50             55             60
Ala Val Val Gly Met Ile Gly Gly Xaa Xaa His Xaa Pro Ile Xaa Phe
      65             70             75             80
Tyr Arg Ser Ser Xaa
          85

```

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```

Met Lys Ser Asp Ser Leu Lys Glu Asn Ile Ile Tyr Gln Gly Leu Tyr
 1             5             10             15
Gln Leu Ile Arg Thr Met Thr Pro Leu Ile Thr Ile Pro Ile Ile Ser
      20             25             30
Arg Ala Phe Gly Pro Ser Gly Val Gly Ile Val Ser Phe Ser Phe Asn
      35             40             45
Ile Val Gln Tyr Phe Leu Met Ile Ala Ser Val Gly Val Gln Leu Tyr
      50             55             60
Phe Asn Arg Val Ile Ala Lys Ser Val Asn Asp Lys Arg Gln Leu Ser
      65             70             75             80
Gln Gln Phe Trp Asp Ile Phe Val Ser Lys Leu Phe Leu Ala Leu Thr
      85             90             95
Val Phe Ala Val Tyr Met Val Val Ile Thr Ile Phe Ile Asp Asp Tyr
      100            105            110
Tyr Leu Ile Phe Leu Leu Gln Gly Ile Tyr Ile Ile Gly Ala Ala Leu
      115            120            125
Asp Ile Ser Trp Phe Tyr Ala Gly Xaa Glu Lys Phe Lys Ile Pro Ser
      130            135            140
Leu Ser Asn Ile Val Ala Ser Gly Ile Val Leu Ser Val Val Val Ile
      145            150            155            160
Phe Val Lys Asp Gln Ser Asp Leu Ser Leu
      165            170

```

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```

Met Gly Glu Ser Asp Glu Leu Leu Leu Lys Asn Ile Leu His Phe Lys
 1             5             10             15
Asn Leu Lys Gln Val Ile Asn Glu Leu Asp Ile Glu Gln Glu Lys Leu
      20             25             30
Ile Phe Leu Asn Val Glu Asn His Lys Leu Leu Asn Asn Lys Glu Arg
      35             40             45
Asp Leu Ser Asn Ser Ala Pro Leu Ile Tyr Lys Thr Leu Ser Ala Leu
      50             55             60
Tyr His Asn Phe Asp Gly Phe Gly Leu Asn Asn Phe
65             70             75

```

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```

Met Thr Lys Glu Tyr Ala Thr Leu Ala Gly Gly Cys Xaa Trp Cys Met
 1             5             10             15
Val Lys Pro Phe Thr Ser Tyr Pro Gly Ile Lys Ser Val Val Ser Gly
      20             25             30
Tyr Ser Gly Gly His Val Asp Asn Pro Thr Tyr Glu Gln Val Cys Thr
      35             40             45
Asn Lys Thr Gly His Val Glu Ala Xaa Gln Ile Thr Cys Asp Pro Glu
      50             55             60
Val Thr Ser Xaa Glu Asn Ile Leu Asp Ile Tyr Phe Lys Thr Cys Xaa
65             70             75             80
Pro Xaa

```

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```

Met Ser Asp Thr Ile Asn Asn Lys Glu Asp Leu Arg Glu Ile Ala Glu
 1             5             10             15
Phe Gln Glu Glu Asp Ala Val Phe Asn Lys Val Leu Xaa Asn Val Ser
          20             25             30
Ile Lys Ile Met His Thr Asp Ile Ala Asn Asn Arg Asp Arg Ile Asp
      35             40             45
Ile Val Ser Asp Ile Pro Asp Asn Leu Ile Phe Tyr Ile Tyr Asp Ser
      50             55             60
Leu Ser Val Gly Phe Ile His Trp Ile Lys Asp Val Lys Ile Xaa Cys
65             70             75             80
Pro Val Xaa Asp Ile Asp Asn Ile Phe His Arg Leu Ile Asn Ile Asn
          85             90             95
Ile Xaa

```

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```

Met Lys Tyr Ala Leu His Met Tyr Leu Tyr Val Gly Ile Trp Asp Asn
 1             5             10             15
Gln Leu Leu Glu Met Ile Cys Phe Asp Gly Tyr Asn Gln Asn Arg Ser
          20             25             30
Ala Pro Pro Glu Glu Leu Ile Pro Gln Phe Asp Tyr Val Lys Glu Ile
      35             40             45
Ser Glu Gln Phe Gly Phe Val Asn Ile Gly Val Lys Asn Tyr Glu Ala
      50             55             60

```

```

Asp Asp Val Ile Gly Thr Leu Ala Gln Gln Tyr Ser Thr Asp Xaa Asp
65              70              75              80
Val Tyr Ile Ile Thr Gly Asp Lys Asp Leu Leu Gln Cys Ile Asn Asp
              85              90              95
Asn Val Glu Val Trp Leu Ile Lys Lys Gly Phe Asn Ile Tyr Asn Arg
              100             105             110
Tyr Thr Leu His Arg Phe Asn Glu Tyr Ala Leu Glu Pro Gln Gln
              115             120             125
Leu Ile Asp Ile Lys Ala Phe Met Gly Asp Thr Ala Asp Gly Tyr Ala
              130             135             140
Gly Val Lys Gly Ile Gly
145              150

```

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```

Met Val Thr Xaa Leu Val Ile Pro Ile Tyr Xaa Gln Xaa Asp Tyr Val
1              5              10              15
Xaa Thr Thr Tyr Asp Arg Trp Val Val Ser Glu Ile Asp Asn His Gln
              20              25              30
Ile Ile Trp Val Ile Leu Asn Tyr Glu Phe Asn Glu Ala Arg Pro Thr
              35              40              45
Ile Gly Gln Ser Asp Glu Asp Glu Lys Ser Glu
50              55

```

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

250

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```

Met Ile Asp Xaa Phe Met Gln Val Leu Lys Leu Ile Lys Glu Lys Arg
 1             5             10             15
Thr Asn Asn Val Val Lys Lys Ser Asp Trp Asp Lys Gly Asp Leu Tyr
          20             25             30
Lys Thr Leu Xaa His Asp Lys Leu Pro Lys Gln Leu Lys Val His Ile
      35             40             45
Lys Glu Asp Lys Tyr Ser Xaa Val Gly Lys Val Ala Thr Gly Asn Tyr
      50             55             60
Ser Lys Xaa Pro Trp Ile Xaa Ile Tyr Pro Pro Arg
65             70             75

```

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```

Met Xaa Pro Arg Asp Lys Asn Ala Ala Lys Gln Arg Ala Leu Thr Leu
 1             5             10             15
Ser Ser Glu Leu Asn Lys Tyr Ile Thr Ser Asn Glu Phe Asn Thr Gly
          20             25             30
Arg Phe Tyr Tyr Ala Glu Asn Lys Asp Ser Ser Tyr Asp Leu Lys Asn
      35             40             45
Asp Tyr Pro Ser Gly Tyr Ser His Gly Ser Ile Arg Xaa Lys Tyr Tyr
      50             55             60
Asp Xaa Asn Glu Gly Xaa Thr Glu Glu Asp Met Leu Glu Asp Leu Xaa
65             70             75             80
Lys Xaa Xaa Xaa Glu Leu Ile Xaa
          85

```

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```

Met Phe Asp Phe Gly Val Leu Lys Arg Pro His Ile Phe Tyr Ala Tyr
 1             5             10             15
Asp Leu Asp Lys Tyr Gly Asp Glu Leu Arg Gly Phe Tyr Met Asp Tyr
          20             25             30
Lys Lys Glu Leu Pro Gly Pro Ile Val Val Asn His Thr Ala Leu Ile
          35             40             45
Asp Ala Leu Lys Xaa Ile Asp Glu Thr Xaa Xaa Glu Tyr Ile Glu Ala
          50             55             60
Arg Ala Val Phe Tyr His Lys Phe Cys Ser Leu Glu Asp Gly Gln Ala
65             70             75             80
Ser Gln Arg Ile Cys Gln Pro Ile Phe Lys
          85             90

```

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```

Met Phe Gly Phe Ile Gly Met Leu Ile Val Gly Gly Leu Ile Gly Trp
 1             5             10             15
Ala Ala Gly Ala Ile Met Gly Lys Asp Ile Pro Gly Gly Ile Leu Gly
          20             25             30
Asn Ile Ile Ala Gly Ile Ile Gly Ser Xaa Gly
          35             40

```

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```

Met Asn Asn Gly Phe Phe Asn Ser Asp Phe Asp Ser Ile Phe Arg Arg
 1           5           10           15
Met Met Gln Asp Met Gln Gly Ser Asn Gln Val Gly Asn Lys Lys Tyr
          20           25           30
Tyr Ile Asn Gly Lys Glu Val Ser Pro Glu Glu Leu Ala Gln Leu Thr
          35           40           45
Gln Gln Gly Ser Asn Gln Ser Ala Glu Gln Ser Ala Gln Ala Phe Ser
          50           55           60
Thr Lys Gln His Lys Asp Asn Lys Gly Asn Lys Val Ala Thr Ala Ile
65           70           75           80
Ile

```

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```

Met Ile Arg Phe Lys Met Arg Ala Val Ile Lys Gln Gln Ala Leu Lys
 1           5           10           15
Ala Ile Gln Gln Glu His His Pro Val Lys Val Phe Val Ala Pro Thr
          20           25           30
Ile Lys Phe Met Glu Trp Arg Val Ala Ile Gln Thr Asp Ala His Asp
          35           40           45
Tyr Val Gly Lys Ala Tyr Gly Arg Asn Val Xaa Phe Ser Asp Xaa Val
          50           55           60
Glu Arg Ser Asn Ile Ile Asn Arg Leu His Phe Met Glu Ser Gln Arg
          253

```

65

70

75

80

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```

Met Tyr Ile His Lys Trp Lys Asp Asp Ile Met Thr Ser Ile Lys Thr
 1             5             10             15
Ile Thr Pro Lys Asp Phe Ile Phe Arg Val Leu Ser Gly Val Ala Ile
      20             25             30
Gly Ile Val Ala Gly Leu Xaa Pro Asn Ala Ile Leu Gly Glu Ile Phe
      35             40             45
Lys Tyr Phe Met Asp Tyr His Pro Ile Phe Lys Thr Leu Leu Gly Val
      50             55             60
Val Gly Ala Ile Gln Phe Thr Val Pro Ala Leu Ile Gly Ala Leu Gly
65             70             75             80
Cys His Glu Ile

```

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```

Met Lys Ala Thr Thr Ile Ile Gly Ile Ala Gly Gly Ser Gly Ser Gly
 1             5             10             15
Lys Thr Thr Val Thr Asn Glu Ile Met Lys Asn Leu Glu Gly His Ser
      20             25             30
                        254

```

Val Ala Leu Leu Ala Gln Asp Tyr Tyr Tyr Lys Xaa Ser Lys Ser Thr
 35 40 45

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Xaa Ile Xaa Pro Xaa Leu Asp Ala Val Leu Ser Ser Asp Thr Thr
 1 5 10 15
 Thr Leu Arg Ile Ile Lys Gln Tyr Glu Gln Ala Val Xaa Ala Tyr Ala
 20 25 30
 Asp Asp Gln Ser Asp Lys Leu Phe Lys Arg Met Ile Asp Ala Gln Asp
 35 40 45
 Ala Met Asp Gln His Asp Ala Trp Asp Tyr Asn Ala Glu Ile Lys Thr
 50 55 60
 Ile Leu Ser Lys Leu Gly Ile His Asp Thr Thr Lys Tyr Ile Lys Glu
 65 70 75 80
 Leu Ser Gly Gly Gln Lys Arg Val Val Leu Ala
 85 90

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Met Ser Gln Phe Tyr Leu Asn Lys Met Ala Ser Ile Asp His His
 1 5 10 15
 Pro Ile Pro Phe Arg Asn Leu Phe Ile Glu Asp Ser Glu Gln Leu Asn
 255


```

                20                25                30
Ser Xaa Asp Asn Trp Leu Xaa Ser Thr Lys Phe Met Leu Pro Lys Trp
    35                40                45
Leu Tyr Lys Ile Ala Lys Gln Arg Ala Asp Asn Lys Gln Leu Gln Asn
    50                55                60
Phe Gly Leu Tyr Thr Lys Gln Pro Asn Val Leu Lys Asp His Ile Val
    65                70                75                80
Phe Ile Gly Asp His His Gln Tyr Ile Gly Asn Ser Lys Tyr Leu Phe
                85                90                95
Thr Tyr Phe Xaa Lys His Asn Pro Met Thr Ala Cys Tyr Leu Val Thr
    100                105                110
Asp Asp Arg Arg Gly Thr Thr Phe His Xaa Thr
    115                120

```

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```

Met Xaa Xaa Ser Ala Cys Met Pro Gly Ile Xaa Xaa Ile Asp Asp Xaa
  1                5                10                15
Xaa Pro Ser Gln Ala Leu Ile Gly Asn Xaa Asp Glu His Leu Lys Ala
    20                25                30
Ile Xaa Glu Ser Phe Asp Val Val Ile His Xaa Arg Gly Gln Glu Val
    35                40                45
Ala Val Lys Gly Xaa Thr Asn Arg Lys Arg Arg Glu Ser Gly Ile Ser
    50                55                60
Ile Asn Gln Phe Ala Xaa Gly Tyr
    65                70

```

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met	Ala	Gly	Leu	Leu	Lys	Gly	Thr	Ala	Ser	Ile	Asn	Glu	Leu	Leu	Gln
1				5					10					15	
His	Gly	Asp	Leu	Gly	Ile	Ala	Thr	Leu	Thr	Gly	Xaa	Lys	Arg	Val	Arg
			20					25						30	

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met	Leu	Leu	Ile	Val	Thr	Ala	Cys	Gly	Pro	Asn	Arg	Ser	Xaa	Glu	Asp
1				5					10					15	
Ile	Xaa	Xaa	Ala	Leu	Xaa	Xaa	Asp	Asn	Xaa	Xaa	Asp	Lys	Xaa	Asn	Gln
			20					25						30	
Leu	Thr	Met	Trp	Xaa	Gly	Trp	Arg	Gln	Ser	Lys	Trp	Arg	Phe	Xaa	Xaa
		35					40						45		
Lys	Ile	Thr	Ala	Ser	Ile	Ile	Leu	Lys	Lys	Leu	Ala	Ser	Xaa		
		50					55						60		

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```

Met Ala Lys Lys Ile Val Ser Asp Leu Asp Leu Lys Gly Lys Thr Val
 1           5           10           15
Leu Val Arg Ala Asp Phe Asn Val Pro Leu Lys Asp Gly Glu Ile Thr
          20           25           30
Asn Asp Asn Arg Ile Xaa Gln Ala Leu Pro Thr Ile Gln Tyr Ile Ile
          35           40           45
Glu Gln Gly Gly Lys Ile Val Leu Phe Xaa His Leu Gly Lys Val Lys
          50           55           60
Glu Glu Ser Asp Lys Ala Lys Leu Thr Leu Arg Pro Val Ala
65           70           75

```

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```

Met Leu Gly Xaa Leu Leu Ile Phe Ser Ile Leu Gly Met Leu Val Val
 1           5           10           15
Gln Tyr Ala Tyr Met Ala Ser Ile Asn Thr Gly Asn Ala Ala Ile Ala
          20           25           30
Thr Leu Leu Gln Tyr Xaa Ala Pro Val Tyr Xaa Ile Ile Xaa Xaa Xaa
          35           40           45
His Lys Arg Arg Xaa Glu Asn
          50           55

```

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```

Met Lys Lys Arg Arg Lys Cys Met Leu Gln Val Thr Asp Val Ser Leu
 1           5           10           15
Arg Xaa Gly Asp Arg Lys Leu Phe Glu Asp Val Asn Ile Lys Phe Thr
          20           25           30
Glu Gly Asn Cys Tyr Gly Leu Ile Gly Ala Asn Gly Ala Gly Lys Ser
          35           40           45
Thr Phe Leu Xaa Ile Leu Ser Gly Glu Leu Asp Ser Gln Thr Gly Gln
          50           55           60
Xaa Phe Xaa Arg Val Lys Met Asn Xaa
65           70

```

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```

Met Glu Gln Ile Asn Ile Gln Phe Pro Asp Gly Asn Lys Lys Ala Phe
 1           5           10           15
Asp Lys Gly Thr Thr Thr Glu Asp Ile Ala Gln Ser Ile Ser Pro Gly
          20           25           30
Leu Arg Lys Lys Ala Val Xaa Gly Lys Ile
          35           40

```

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

```

Met Ile Asp Lys Asp Asp Val His Xaa Glu Thr Lys Asp Val Gly Trp
 1               5               10               15
Gln His Ile Xaa Trp Xaa Met Xaa Xaa Xaa Gln Xaa Xaa Asn Xaa Asn
          20               25               30
Phe Arg Glu Thr Phe Lys
      35

```

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

[illegible]

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

```

Met Asn Leu Lys Gln Ser Ile Glu Glu Ile Ile Asn Gln Pro Glu Tyr
 1             5             10             15
Glu Pro Met Ser Val Ser Asp Phe Gln Asp Ala Leu Gly Leu Ser Ser
          20             25             30
Ala Asp Ser Phe Arg Asp Leu Ile Xaa Val Xaa Val Glu Leu Glu Xaa
      35             40             45
Ser Gly Leu Ile Glu Arg Thr Lys Xaa Xaa Arg Tyr Gln Xaa Lys His
      50             55             60
Ser Xaa Xaa Gly Xaa Ser Xaa Leu Ile Lys Gly Thr Leu Xaa Gln Asp
65             70             75             80
Lys Lys Gly Phe Xaa Ile Leu Lys Thr
          85

```

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```

Met Ala Met Tyr Leu Ile Arg Asn Asn Phe Lys Ala Xaa Xaa Pro Phe
 1             5             10             15
Leu Xaa Glu Glu Ile Gly Leu Ser Thr Leu Glu Leu Gly Tyr Ile Gly
          20             25             30
Leu Ala Val Ser Ile Thr Tyr Gly Leu Gly Lys Thr Leu Leu Gly Tyr
      35             40             45
Xaa Val Asp Gly Arg Asn Thr Lys Arg Ile Ile Ser Xaa Leu Leu Ile
      50             55             60
Leu Ser Ala Ile Thr Val Leu Ile Met Gly Phe Gly Phe Lys Leu Leu
65             70             75             80
Trp Phe Leu

```

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

```

Met Asp Met Lys Ile Xaa Xaa Leu Phe Pro Glu Xaa Gly Glu Gly Gln
 1             5             10             15
Glu Asn Gln Leu Xaa Asn Thr Xaa Lys Xaa Ile Gly Leu Lys Thr Phe
          20             25             30
Xaa Glu Glu Arg Gly Thr
          35

```

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

```

Met Lys Asn Ala Arg Pro Glu Ile Gln Ala Leu Thr Ser Asp Val Thr
 1             5             10             15
Ala Tyr Thr Asn Glu Glu Asp Gly Ala Pro Lys Tyr Leu Ala Lys His
          20             25             30
Phe Leu Ala Asp
          35

```

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

```

Met Tyr Gln Asp Leu Ile Val Asn Asn Arg Lys Thr Glu Ile Asp Tyr
 1           5           10           15
Ile Asn Gly Ala Val Ala Thr Leu Gly Lys Gln Arg His Ile Glu Ala
      20           25           30
Pro Val Asn Arg Phe Ile Thr Asp Leu Ile His Thr Lys Glu Ser Gln
      35           40           45
Arg His Ala Gln Asp
      50

```

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

```

Met Glu Gly Ile Ser His Glu Pro Xaa Ser Phe Ala Gly His Asn Lys
 1           5           10           15
Leu Ser Lys Leu Val Val Leu Tyr Asp Ser Xaa Asp Ile Ser Leu Asp
      20           25           30
Gly Glu Leu Asn Lys Ala Phe Ser Glu Asn Thr Xaa Ala Arg Phe Glu
      35           40           45
Ala Tyr Gly Trp Asn Tyr Leu Leu Val Lys Arg Trp
      50           55           60

```

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

```

Met Thr Lys Glu Met His Xaa Ser Gly Asn Val Thr Leu Phe Lys Gln
 1           5           10           15
Ile Gly Met Ile Met Xaa Thr Ile Ala Ser Val Lys His Val Ile Glu
          20           25           30
Gln Trp Phe Glu Asp Asn Arg Asn Lys Ser Phe Xaa Thr Tyr Glu Ala
          35           40           45
Ala Leu Lys Leu Xaa Asp Ser Leu Glu Asn Thr Pro Ala Ala Arg Ala
          50           55           60
Thr Ile Val Met Xaa Leu Tyr Gln Met Phe His Val Leu Xaa Ser Phe
          65           70           75           80
Xaa Ser Ser Ile Trp Xaa Asp Ser Glu Ala Gly Leu Ser Asn
          85           90

```

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

```

Met Asp Ile Ser Pro Gly Gly Val Ile Val Xaa Leu Leu Val Ile Leu
 1           5           10           15
Leu Met Ile Thr Met Xaa Tyr Gln Lys Met Arg Met Lys Phe Lys Lys
          20           25           30
Gly Ala Asn Ile Asn Glu Tyr Lys
          35           40

```

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

```

Met Pro Thr Lys Gly Asp Val Tyr Leu Asn Ser Glu Ser Ile Phe Glu
 1             5             10             15
Asn Ser Thr Leu Lys Lys Arg Asp Phe Ser His Thr Xaa Lys Ser Leu
      20             25             30
Phe Xaa

```

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

```

Met Thr Lys Gly Lys Glu Val Glu Arg Asp Gly Phe Gln Ile Arg Arg
 1             5             10             15
Thr Thr Val Glu Asn Gly Ile Pro Cys Leu Thr Ser Leu Asp Thr Ala
      20             25             30
Asn Ala Leu Thr Asn Val Ile Glu Ser Met Thr Phe Thr Met Arg Gln
      35             40             45
Met

```

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

265

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

```

Met Lys Thr Ile Glu Val Asp Asp Glu Leu Tyr Ser Tyr Ile Ala Ser
 1             5             10             15
His Thr Lys His Ile Gly Glu Ser Ala Ser Asp Ile Leu Arg Arg Met
      20             25             30
Leu Lys Phe Ser Ala Ala Ser Gln Pro Ala Ala Pro Val Thr Lys Glu
      35             40             45
Val Arg Val Ala Ser Pro Ala Ile Val Glu Ala Lys Pro Val Lys Thr
      50             55             60
Ile Lys Asp Lys Val Arg Ala Met Arg Glu Leu Leu Leu Ser Asp Glu
65             70             75             80
Tyr Ala Glu Gln Lys Arg Ala Gly Asn Arg Phe Met Leu Leu Leu Ser
      85             90             95
Ser Leu Tyr Phe Ser
      100

```

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

```

Met Phe Val Phe Pro His Gly Ala Gln Asp Arg His Thr Gln Ala Tyr
 1             5             10             15
Asp Tyr Leu Val Asp Glu Ala Glu Phe Lys Phe Ile Ala Gly Val Gly
      20             25             30
Pro His Asn Phe Thr Asp Ile Ser Ala Xaa Asn Val Tyr Gln Asp Arg
      35             40             45
Val Ala Ile Asp Gly Leu Asn Leu Phe Glu Phe Lys Tyr Lys Leu Gln
      50             55             60
Thr Val Phe
65

```

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

```

Met Val Ser Ile Arg His Arg Ala Thr Ser Ile Gln Leu His Asp Xaa
 1             5             10             15
Asn Lys Leu Asp Arg Tyr Gln Phe Leu Glu Arg Leu Leu Gln Glu Ile
      20             25             30
Xaa Lys Arg Tyr Asn Gln Phe Leu Thr Leu Pro Phe Ser Glu Ile Arg
      35             40             45
Glu Glu Tyr Ile Ala Ala Ser Asn Ile Trp Asn Arg Thr Leu Leu Phe
      50             55             60
Thr Glu Asn Asp Lys Gln Phe Lys Gly Gln Ala Ile Asp Leu Asp Tyr
65             70             75             80
Asp Gly Tyr Leu Ile Val Arg Asp Glu Ala Gly Glu Ser His Arg Leu
      85             90             95
Ile Ser Ala Asp Ile Asp Phe
      100

```

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

```

Met Gly Ile Ala Ala Leu Phe Thr Glu Ala Leu Val Gly Ala Asn Tyr
 1             5             10             15
Ala Ile Ala Val Val Phe Ile Thr Ile Gln Val Ile Leu Met Asn Gly
      20             25             30
Leu Ala Ser Gln Asn Leu Thr Ile Asn Ile Ala Xaa Pro Arg Val Ile
      35             40             45

```

Asp Val Ala Ile Gly Ile Val Ile Ala Ile Ile Gly Leu Phe Gly Pro
 50 55 60
 Trp Thr Thr Tyr Arg Ile Pro Tyr Leu Val Pro
 65 70 75

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Met Ile His Val Ala Leu Val Ser Asp Gly Phe Phe Pro Met Gly Asp
 1 5 10 15
 Thr Val Glu Leu Ala Ala Gln His Gly Ile Lys Ala Ile Ile Gln Pro
 20 25 30
 Gly Gly Ser Ile Lys Asp Gln Asp Ser Ile Asp Met Ala Asn Lys His
 35 40 45
 Gly Ile Ala Met Val Val Thr Gly Thr Arg His Phe Lys His
 50 55 60

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Met Leu Ser Tyr Gly Gly Leu Leu Lys Glu Lys His Lys Xaa Leu Asn
 1 5 10 15
 Leu Asp Asp Ala Glu Asp Gly Asn Leu Ile Asn Thr Xaa Asp Glu Asp
 20 25 30
 Lys Thr Thr Asp Glu Glu Glu Lys Ala His Ser Xaa Thr Xaa Xaa Trp
 268

35 40 45
 Xaa Xaa Glu Xaa Gln Asn Tyr Tyr Leu Gln Asn Leu Arg Ser Xaa Lys
 50 55 60
 Tyr Glu His
 65

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Met Gln Ala Leu Lys Thr Lys Ser Asn Ile Gly Glu Met Phe Asn Ile
 1 5 10 15
 Gln Glu Lys Glu Asn Gly Xaa Ile Ala Ile Ser Gly Arg Glu Leu His
 20 25 30
 Gln Ala Leu Glu Val Xaa Thr Arg Tyr Asp Lys Trp Ser Glu Arg Met
 35 40 45
 Thr Glu Tyr Gly Leu Glu Xaa Gly Ile Gly Phe Tyr Phe Ala Ser Trp
 50 55 60
 Xaa Xaa Tyr Thr Gly Gln Xaa Lys Gly Ala Val Leu Ile Glu Gln Ser
 65 70 75 80

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Met Val Gln Tyr Ser Met Ser Ile Leu Thr Phe Gly Asp Val Asn Met
 1 5 10 15

```

Asn Lys Pro Phe Ile Ala Ile Glu Gly Pro Ile Gly Val Gly Lys Ser
      20              25              30
Ser Leu Ala His Lys Leu Ser Gln Thr Leu Asp Phe Tyr Glu Glu Lys
      35              40              45
Glu Ile Ile Thr Glu Asn Pro Phe Leu Ser Asp Phe Leu
      50              55              60

```

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

```

Met Arg Ile Leu Val Glu Ile Ala Tyr Xaa Gly Asn Asn Phe Leu Gly
 1              5              10              15
Phe Xaa Ile Gln Gln Asn Gly Arg Thr Val Gln Gln Gln Phe Glu Lys
      20              25              30
Leu Leu Gln Arg Met His Lys Arg His Val Arg Ile His Pro Ser Ser
      35              40              45
Arg Thr Asp Arg Gly Val His Ala Ile Gln Gln Tyr Phe His Phe Asp
      50              55              60
Thr Glu Leu Asn Ile Pro Met Ser Gln Trp Gln Tyr Ala Met Asn Arg
      65              70              75              80
Thr Leu Pro Asp Asp Ile Tyr Val Asn Asn Val Val Thr Val Asp Asp
      85              90              95
Asp Phe His Cys Arg Tyr Asp Cys Val Gly Lys Arg Tyr Arg
      100              105              110

```

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

```

Met Ser Arg Lys Glu Ser Arg Val Gln Ala Phe Gln Thr Leu Phe Gln
 1           5           10           15
Leu Glu Met Lys Asp Ser Asp Leu Thr Ile Asn Glu Ala Ile Ser Phe
           20           25           30
Ile Lys Asp Asp Asn Pro Asp Leu Asp Phe Glu Phe Ile His Trp Leu
           35           40           45
Val Ser Gly Val Lys Asp His Glu Pro Val Leu Asp Glu Thr Ile Ser
           50           55           60
Pro Tyr Leu Lys Asp Trp Thr Ile Gly Arg Leu Leu Lys Thr Gly Arg
65           70           75           80
Ile Phe

```

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

```

Met Met Lys Arg Asn Ile Leu Ala Val Ile Val Pro Ala Leu Leu Val
 1           5           10           15
Ala Gly Thr Ala Asn Ala Ala Glu Ile Tyr Asn Lys Asp Gly Asn Lys
           20           25           30
Val Asp Leu Tyr Gly Lys Ala Val Gly Leu His Xaa Phe Ser Lys Gly
           35           40           45
Asn Gly Glu Asn Ser Tyr Gly Gly Asn Gly Asp Met Thr Tyr Ala Arg
           50           55           60
Leu Gly Phe Lys Gly Glu Thr Gln Xaa Asn Ser Xaa Leu Asp Arg Leu
65           70           75           80
Trp Ser Val Gly Ile Xaa Leu Pro Gly
           85

```

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

```

Met His Val Ala Glu Phe Lys Arg Met Asn Ala Asn Ile Asn Val Glu
 1             5             10             15
Gly Arg Ser Ala Lys Leu Glu Gly Lys Ser Gln Leu Gln Gly Ala Gln
          20             25             30
Val Xaa Ser Asp
          35

```

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

```

Met Asp Lys Ile Val Leu Lys Gly Gly Asn Lys Leu Thr Gly Glu Val
 1             5             10             15
Lys Val Glu Gly Ala Lys Asn Ala Ser Ile Thr Asn Ile Asp Lys His
          20             25             30
Leu Leu Leu Ala Ser Asp Asn Pro Ser Lys Leu Gly
          35             40

```

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

```

Met Pro Lys Ile Xaa Lys Gln Ala Ile Xaa Thr Ile Leu Ala Thr Arg
 1             5             10             15
Ile Glu Arg His Xaa Ala Gln Leu Leu Ala Asp Leu Ile Thr Lys Ile
      20             25             30
Glu Thr Asp His Asn Lys Ile Phe Asn Leu Val Lys Ser Ala Leu Xaa
      35             40             45
Gly Lys Ala Asp Asp Leu Leu Asn Leu Xaa Lys Arg Leu Asn Gln Thr
      50             55             60
Lys Lys Asp Ile Asp
65

```

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

```

Met Gly Phe Ala Arg Thr Val Ala Asp Arg Val Ile Phe Met Asp Arg
 1             5             10             15
Gly Glu Ile Val Glu Gln Ala Ala Pro Asp Glu Phe Phe Ala His Pro
      20             25             30
Lys Ser Glu Arg Thr Arg Ala Phe Leu Ser Gln Val Ile His
      35             40             45

```

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

```

Met Ile Xaa Xaa Ala Ser Leu Ala Ile Leu Asp Asp Ile Asp Xaa Leu
 1             5             10             15
Ala Asp Met Ile Val Ala Ser Asp Xaa Tyr Ala Ser Phe Glu Gln Ala
      20             25             30
Lys Gln Ala Leu Xaa Asn Asn Xaa Glu Ala His Leu Leu Tyr Gln Ser
      35             40             45
Xaa Xaa Gln Ser Lys Glu Lys Xaa Asp Glu Val Val Arg Phe Gly Lys
      50             55             60
Tyr His Pro Gly Leu
65

```

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

```

Met Phe Val Glu Arg Val Asn Xaa Asp Gly Xaa Ile Leu Val Ser Glu
 1             5             10             15
Xaa Xaa Tyr Ser Xaa Ala Pro Gly Ile Leu Thr Tyr Arg Ser Val Pro
      20             25             30
Ala Tyr Gln Val Asn Asn Tyr Arg Tyr Ile His
      35             40

```

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

```

Met Val Glu Gly Ala Ser Ile Asp Lys Ser Ala His Ser Asn Asp Ile
 1             5             10             15
Thr Gly Val Met Ser Glu Met Glu Gly Phe Glu Lys Ala Phe Asp Asp
      20             25             30
Ala Ile Gln Tyr Ala Lys Lys His Lys Asp Thr Leu Val Val Ala Thr
      35             40             45
Ala Asp His Ser Thr Gly Gly Leu Thr Ile Gly Lys Asp Lys Gly Tyr
      50             55             60
Glu Trp Asn Pro Gln Pro Ile Lys Ser Met Lys His Ser Gly Ser
65             70             75

```

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

```

Met Lys His Tyr Xaa Xaa Xaa Xaa Ile Asn Asn Arg Lys Met Ser Lys
 1             5             10             15
Asp Ile Gln Arg Ala Leu Leu Ser Ser Glu Asp Val Leu Lys Ile Met
      20             25             30
Asn Lys Leu Asp Ser Met Leu Val Asn Lys Ile Asn Ile Leu Tyr Ser
      35             40             45
Asp Asn Glu Gly Asp Gly Thr Met Thr Phe Val Thr Gly Thr Glu Tyr
      50             55             60
Phe Lys Trp Tyr Phe Pro Glu Tyr Pro Asp Xaa Ile Xaa Thr Leu Lys
65             70             75             80
Ile Val Asp Val Asn Lys His Thr Phe Thr Asp Lys
      85             90

```

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

```

Met Phe Val Arg Thr Ala Gly Cys Asp Tyr Arg Cys Ser Trp Cys Asp
 1             5             10             15
Ser Ala Phe Thr Trp Asp Gly Ser Ala Lys Gly Asp Ile Lys Thr His
             20             25             30
Asp Arg

```

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

```

Met Cys Lys Val Leu Lys Ile Pro Arg Ser Thr Tyr Tyr Asp Ser Ile
 1             5             10             15
Lys Arg Xaa Asp Asn Lys Ile Thr Lys Asp Asp Ser His Val Glu Arg
             20             25             30
Ala Ala Ile Asn Ile Phe Asn Ser Asn Arg Lys Val Phe Ser Thr Arg
             35             40             45
Arg Ile Lys Asn His Leu Asn Asp Lys Gly Leu Thr Val Ser Gly Gln
             50             55             60
Lys Ile Gly Arg Leu
65

```

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

```

Met Ser His Arg His Thr Leu Ile Ser His Ser Phe Lys Phe Ser Arg
 1             5             10             15
Leu Pro Gln Asp Ile Asn Phe Phe Ser Trp Xaa Gln His Val Lys Asp
          20             25             30
Ser Asp Lys Thr Asp Glu Leu Thr Tyr Ser Glu Ser Leu Xaa Pro Glu
          35             40             45
Gly His Pro Thr His Pro Leu Thr Pro Thr Lys Leu Pro Xaa Thr Met
          50             55             60
Glu Glu Val Arg Ala Tyr Ala Pro Glu Phe Asp Xaa Arg Asn Pro Phe
65             70             75             80
Ala Thr Leu

```

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 129 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

```

Met Gly Ile Leu Ser Xaa Gln Pro Tyr Ile Phe Ser Ala Ser Xaa Lys
 1             5             10             15
Glu Asn Xaa Xaa Met Phe Xaa Asp Ile Glu Asn Asn Xaa Ile Glu Glu
          20             25             30
Val Leu Xaa Glu Val Gly Leu Leu Asp Lys Val Gln Ser Phe Thr Lys
          35             40             45
Gly Ile Asn Thr Ile Ile Gly Glu Gly Gly Glu Met Leu Ser Gly Gly
          50             55             60
Gln Met Arg Arg Ile Glu Leu Cys Arg Leu Leu Val Met Lys Pro Asp
65             70             75             80
Leu Val Ile Phe Asp Glu Pro Ala Thr Gly Leu Asp Ile Gln Thr Glu

```

[illegible]

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Met Ile Ala Ala Phe Lys Val Ser Lys Asp Ser Lys Leu Ala Ser Leu
1 5 10 15
Leu Ile Ile Thr Ser Xaa Gln Ala Val Xaa Ile Trp Asn Xaa Gly Ile
20 25 30
Lys Thr Ala Ala Ala Gln Asn Ile Xaa Ala Asn
35 40

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Met Ser Glu Thr Ile Phe Gly Lys Ile Leu Thr Gly Glu Ile Pro Ser
1 5 10 15
Phe Lys Val Tyr Glu Asp Asp Tyr Val Tyr Ala Phe Leu Asp Ile Ser
20 25 30
278

```

Gln Val Thr Lys Gly His Thr Leu Leu Ile Pro Lys Lys Ala Ser Ala
  35              40              45
Asn Ile Phe Glu Thr Asp Glu Glu Thr Met Lys His Ile Gly Ala Ala
  50              55              60
Leu Pro Lys Val Ala Asn Ala Ile Lys Arg Ala Phe Xaa Pro Xaa Gly
  65              70              75              80
Leu Asn Ile Ile Gln Asn Asn Gly Glu Phe Gly Asp Gln Ser Cys Ile
              85              90              95
Ser Tyr Ser Xaa Xaa Thr
              100

```

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

```

Met Leu Ile Leu Ala Val Ile Leu Ala Gly Ser Ala Ile Ser Val Val
  1              5              10              15
Gly Gly Ile Ser Phe Leu Gly Leu Ile Ala Pro His Ile Ala Ser Gln
              20              25              30
Leu Ile Gly Asn Lys Thr Leu His Val Ile Ile Met Ser Gly Leu Ile
              35              40              45
Gly Ala Ile Leu Leu Thr Phe Gly Asp Gly Leu Ala Arg Gly Ile His
              50              55              60
Pro Pro Leu Asp Ile Pro Val Gly Val Ile Ile Ala Ile Ile Gly Ala
  65              70              75              80
Pro Tyr Phe Leu Ile Leu Leu Arg Arg Met Lys
              85              90

```

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

```

Met Leu Ser Pro Leu Leu Ile Ile Phe Phe Ile Val Leu Ser Ile Leu
 1             5             10             15
Glu Glu Arg Lys Arg Thr Lys Lys Lys Gln Leu Glu Lys Glu Lys Ala
      20             25             30
Asn Thr Leu Asn Gln Asn Thr Asn Asp Thr Glu Ser Ser Asn Gln Glu
      35             40             45
Pro Ser Leu Gln Gln Thr Lys Glu Gln Lys Asp Asn Lys Gly
      50             55             60

```

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

```

Met Asp Arg Met Tyr Glu Gln Asn Gln Xaa Pro His Asn Asn Glu Ala
 1             5             10             15
Glu Gln Ser Val Leu Gly Ser Xaa Ile Ile Asp Pro Glu Leu Ile Asn
      20             25             30
Thr Thr Gln Glu Val Xaa Leu Pro Glu Ser Phe Tyr Arg Gly Ala His
      35             40             45
Gln His Ile Phe Arg Ala Met Met His Leu Asn Glu Asp Asn Lys Glu
      50             55             60
Ile Asp Val Val Thr Leu Met Asp Gln Leu Ser Thr Glu Gly Thr Leu
      65             70             75             80
Asn Glu Ala Gly Gly Pro Gln Tyr Leu Ala Glu Leu Ser Thr Asn Val
      85             90             95
Pro Thr Thr Arg Asn Val Gln Tyr Tyr Thr Asp Ile Xaa Ser Xaa Ala
      100             105             110
Cys Ile Lys Xaa Val Gly Leu Ile Gln Thr Ala Asp Ser Ile Ala Asn
      115             120             125
Asp Gly Tyr Xaa Asp Glu Leu Gly Leu Asp Ala Ile
                        280

```

130

135

140

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

```

Met Asn Lys Pro Tyr Ile Lys Met Ala Gln Leu Phe His Val Pro Thr
 1             5             10             15
Xaa Thr Ile Leu Ile Arg His Leu Thr Pro Lys Ile Ile Pro Ala Ile
      20             25             30
Ile Val Leu Met Val Val Asp Phe Gly Lys Ile Ile Leu Tyr Ile Ser
      35             40             45
Ser Leu Ser Phe Ile Gly Leu Gly Ala Gln Pro Pro Thr Pro Glu Trp
      50             55             60
Gly Ala Met Xaa Gln Gln Gly Arg Asp Phe Ile Ser Ser His Pro Ile
65             70             75             80
Met Leu Ile Ala Pro Ala Ser Val Ile Ala Ile Thr Ile Leu Ile Phe
      85             90             95
Asn Leu Thr Gly Asp Ala Leu Arg Asp Arg Leu Leu Lys Xaa Arg Gly
      100            105            110
Gly Tyr Asp Glu Ser His
      115

```

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Met Thr Xaa Gly Lys Arg Leu Tyr Ser Asn Gln Tyr Lys Asn Ser Pro
 1 5 10 15
 Ser Xaa Ser Leu Thr Xaa Xaa His Lys Ile Lys Ile Asn Glu Gly Asp
 20 25 30
 Glu Xaa Phe
 35

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Met Asn Gln Ser Val Xaa Leu Leu Lys His Leu Thr Asp Val Asn Gly
 1 5 10 15
 Ile Ala Gly Tyr Glu Met Gln Val Xaa Glu Ala Met Arg Xaa Tyr Ile
 20 25 30
 Glu Leu Ser Gly Xaa Asn Ile Gly Asp Asn Leu Gly Gly Asn Leu Gly
 35 40 45
 Xaa Glu Lys Cys
 50

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Met Arg Phe Val Gly Met Asn Leu Xaa Ile Xaa Ile Asn Asn Thr Thr
 1 5 10 15
 Val Ile Ala Thr Gly Tyr Thr Met Leu Asn Thr Gly Ile Asp Ile Glu
 282

```

                20                25                30
Ile Thr Ala Phe Lys Pro Trp Leu Ala Ile Ile Lys Leu Ile Lys Met
    35                40                45
Lys Thr Asn Thr Asn Ala Leu Tyr Asp Thr Leu Gly Thr Ile Leu Trp
    50                55                60
Lys Tyr Ser Glu Thr Ala Thr Ile Ser Pro His Ala Val Val Arg His
    65                70                75                80
Ala Ser Ala Thr Met Met Pro Asn Lys Tyr Phe Pro Asn Glu Pro Asn
                85                90                95
Pro Val Glu Ala Ile Val Val Asn Lys Tyr Val Pro Met Phe Arg Ser
    100                105                110
Leu Asp Phe Asn
    115

```

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

```

Met Ile Phe Ala Leu Gly Val Xaa Ile Gly Leu Ala Gly Gly Asp Gly
  1                5                10                15
Val Ala Ala Ile Ala Ala Phe Val Gly Tyr Ile Ile Met Asn Lys Thr
                20                25                30
Met Gly Asp Phe Leu Gln Val Thr Pro Lys Asn Val Xaa Glu Pro Thr
    35                40                45
Ser Gly Xaa Xaa
    50

```

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

```

Met Arg Leu Ser Thr Phe Thr Phe Met Thr Lys Arg Met Asn Leu Pro
 1           5           10           15
Glu Val Asp Leu Glu Lys Val Ile Ala Pro Trp Lys Glu Ile Leu Ala
          20           25           30
Thr Asn Arg Glu Ile Pro Asn Leu Asp Asn Gln Met Cys Ile Gly Gly
          35           40           45
Leu Asp Phe Ala Asn Ile Arg Asp Phe Xaa Ser Val Gly Leu Leu Phe
          50           55           60
Arg Lys Asn Asp Asp Tyr Ile Trp Leu Gly His Ser Xaa Val Arg Gln
        65           70           75           80
Gly Phe Leu Asp Asp Val Lys Leu Glu Pro Pro Ile Lys Glu Trp Gly
          85           90           95
Lys Met Gly Leu Leu Thr Xaa Val Asp Asp Asp Val Ile Glu Ile Glu
          100          105          110
Tyr Ile Val Gly Xaa Gly Phe Xaa Xaa Gln Lys Ala Arg Glu Lys Tyr
          115          120          125
Gly Ile Glu Lys Val Ile Gly
          130          135

```

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

```

Met Asp Lys Asp Phe Gln Glu Lys Leu Lys Lys Ala Phe Ile Asp Ile
 1           5           10           15
Ala Lys Ser Lys Glu Gly His Lys Ile Ile Ser Glu Val Tyr Ser His
          20           25           30
Glu Gly Tyr Thr Glu Thr Lys Asp Ser Asn Phe Asp Ile Val Arg Glu
          35           40           45
Tyr Glu Lys Leu Val Lys Asp Met Lys
          50           55

```

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

```

Met Ser Gln Ile Glu Phe Lys Asn Val Ser Lys Val Tyr Pro Asn Gly
 1           5           10           15
His Val Gly Leu Lys Asn Ile Asn Leu Asn Ile Glu Lys Gly Glu Phe
          20           25           30
Ala Val Ile Val Gly Leu Ser Gly Ala Gly Lys Ser Thr Leu Leu Arg
          35           40           45
Ser Cys Lys Ser Xaa Ala
 50

```

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

```

Met Tyr Gly Trp Lys Pro Pro Pro Gly Tyr Asp Ser Asp Gln Phe Asp
 1           5           10           15
Gln Phe Leu Val Gln Glu Lys Ser Ile Leu Val Ala Pro Gly Lys Pro
          20           25           30
Phe Gly Glu Asn Gly Asn Arg Tyr Val Arg Ile Ser Leu Ala Leu Asp
          35           40           45
Asp Gln Lys Leu Asp Glu Ala Ala Ile Arg Leu Thr Glu Leu Ala Tyr
          50           55           60
Leu Tyr Glu

```

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Met	Asn	Val	Lys	Gly	Ser	Tyr	Ile	Val	Tyr	Glu	Pro	Phe	Val	His	Pro
1				5					10					15	
Glu	Thr	Asp	Lys	Tyr	Arg	Leu	Val	Tyr	Gln	Gly	Gly	Asn	Tyr	Asn	Tyr
			20					25					30		

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Met	Gln	Leu	Leu	Gln	Lys	Asn	Pro	Met	Ala	Ile	Gly	Val	Trp	Ala	Gly
1				5					10					15	
Leu	Cys	Gln	Met	Ile	Lys	Pro	Thr	Val	Ile	Asp	Trp	Asp	Ile	Ser	Glu
			20					25					30		
Tyr	Thr	Pro	Lys	Pro	Ala	Trp	Met	Gln	Ala	Thr	Lys	Ala	Arg	Ala	Tyr
		35				40						45			
Val	Pro	Arg	Ile	Leu	Val	Glu	Lys	Leu	Leu	Ile	Xaa	Ile	Asp	Asp	Met
	50					55				60					
Leu	Glu	Gly	Ile	Glu	Ile	Tyr	Asp	Xaa	Xaa	Glu	Ser	Arg			
65					70					75					

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

```

Met Thr Gln His Glu Pro Asp Leu Pro Glu Ala Glu Lys Leu Tyr Leu
 1             5             10             15
Thr Leu His Leu Leu Ser Thr Ser Val Gln Trp Thr Asp Leu Gln Glu
      20             25             30
Ser Asp Asn Ile Ser Asn Leu Thr Met Ala Ile Ala Gln Met Ile His
      35             40             45
His Cys Glu Gln Ile Thr Phe Ile Asn Ile Glu Asp Lys Glu Lys Leu
      50             55             60
Ser Gln Gln Leu Leu Leu His Leu Thr Pro Ala Phe Tyr Arg Ile Lys
      65             70             75             80
Tyr Asn Leu Thr Asp Pro
              85

```

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

```

Met Thr Lys Lys Met Gly Leu Leu Val Met Ala Tyr Gly Thr Pro Tyr
 1             5             10             15
Lys Glu Ser Asp Ile Glu Pro Tyr Tyr Thr Asp Ile Arg His Gly Lys
      20             25             30
Arg Pro Ser Glu Glu Glu Leu Gln Asp Xaa Xaa Asp Arg Tyr Xaa Phe
      35             40             45
Ile Gly Gly Lys Leu Ile Asp Thr Val Asp Leu Glu Gly Gly Ser Gly
              287

```


50
Thr Gln Phe Ala Leu
65

55

60

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

```

Met Thr Leu Asp Lys Leu Asp Leu Pro Ile Val Gly Lys Pro Thr Ser
 1              5              10              15
Tyr Lys Thr Leu Pro Asn Arg Tyr Lys Asp Val Pro Glu Ile Gly Gln
      20              25              30
Pro Met Glu Pro Asn Val Glu Ala Val Lys Lys Leu Lys Pro Thr His
      35              40              45
Val Leu Ser Val Ser Thr Ile Lys Asp Glu Met Gln Pro Phe Tyr Lys
      50              55              60
Gln Leu Asn Met Lys Gly Tyr Phe Tyr Asp Phe Asp Ser Leu Lys Gly
65              70              75              80
Met Gln Lys Ser Ile Thr Gln Leu Gly Asp Gln Phe Asn Arg Lys Ala
      85              90              95
Gln Ala Lys Glu Leu Xaa Asp His Leu Xaa Ser Val Lys Gln Lys Ile
      100              105              110
Xaa Asn Lys Ala Gly Lys Gln Lys Lys His Pro Xaa Val Leu Ile Leu
      115              120              125
Met Gly Val Pro Gly Arg Tyr Leu Val Ala Thr Asp Lys Ser Tyr Ile
      130              135              140
Gly
145

```

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

```

Met Met Met Lys Phe Xaa His Asn Leu Asp Met Xaa Leu Glu Leu Phe
 1             5             10             15
Asn Lys Ala Xaa Xaa Asn Gln Lys Asn Lys Xaa Trp Asn Gly Leu Ala
      20             25             30
Asn Ala Cys Arg Asn Pro Tyr Val Arg His Ile Ala His Pro Thr Gly
      35             40             45
Arg Ile Ile Gly Arg Arg Asp Gly Tyr Lys Pro Asn Ile Glu Gln Leu
      50             55             60
Met Ala Leu Ala Glu Glu Thr Asn Thr Val Leu Glu Ile Asn Ala Asn
65             70             75             80
Pro His Arg Leu Asp Leu Glu Arg
      85

```

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

```

Met Ser Lys Thr Ala Ile Ile Phe Pro Gly Gln Gly Ala Gln Lys Val
 1             5             10             15
Gly Met Ala Gln Asp Leu Phe Asn Asn Asn Asp Gln Ala Thr Glu Ile
      20             25             30
Leu Thr Ser Ala Ala Lys Thr Leu Asp Phe Asp Ile Leu Glu Thr Met
      35             40             45
Phe Thr Asp Glu Glu Gly Lys Leu Gly Glu Thr Glu Asn Thr Gln Pro
      50             55             60
Ala Leu Leu Thr His Trp Ser Gly Ile Ile Ser Ser Ala Lys Asn Leu
65             70             75             80
Gly Ser Leu Ile Leu Leu Trp Gly Ile Ser Leu Gly Trp Asn Phe Gln
      85             90             95

```

Ser Leu Val Gly Gly Xaa Arg Xaa Xaa Ser Ile Xaa Arg Met Gln Xaa
 100 105 110
 Xaa Leu Val Glu Thr Xaa Xaa Xaa
 115 120

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Met Ala Arg Gly Leu Lys Phe Lys Ile Met Phe Asn Phe Gly Leu Pro
 1 5 10 15
 Leu Val Ile Ala Leu Ser His Ala Tyr Phe Thr Ser Leu Ala Tyr Met
 20 25 30
 Lys Leu Met Gly Thr Xaa Asn Gln Ile Pro Val Phe Ile Val Met Gly
 35 40 45
 Leu Tyr Ile Cys Met Tyr Ala Val Phe Ala Val Thr Ala Tyr Asn His
 50 55 60
 Ser Lys Arg Thr Ile Arg His Ser Ile
 65 70

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Met Leu Lys Ser Lys Met Lys Leu Asn Tyr Arg Gly Asp Asn Met Asn
 1 5 10 15
 Phe Glu Glu Lys Leu Ser Gln Met Tyr Asn Glu Ile Ala Asn Glu Ile
 290

	20	25	30
Ser Gly Met Ile Pro Val Glu Trp Glu Gln Val Phe Thr Ile Ala Tyr			
35	40	45	
Val Thr Asp Gln Ala Gly Glu Val Ile Phe Asn Tyr Thr Lys Pro Gly			
50	55	60	
Ser Asp Glu Leu Asn Tyr Tyr Thr Tyr Ile Pro Arg Glu Tyr Tyr Val			
65	70	75	80
Ser Glu Lys Val Phe Tyr Asp Leu Trp Thr Asp Leu Tyr Arg Leu Xaa			
85	90	95	

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Met Ile Pro Val Xaa Trp Xaa Lys Val Tyr Ala Met Ala Tyr Val Asn			
1	5	10	15
Glu Xaa Ser Gly Glu Val Phe Tyr Asn Tyr Thr Glu Pro Arg Ser Asp			
20	25	30	
Glu Leu Phe Tyr Tyr Thr Ser Val Leu Asn Lys Tyr Asn Ile Ser Arg			
35	40	45	
Ser Glu Phe Met Asp Ser Val Tyr Glu Leu Tyr Lys Xaa Phe Asp Lys			
50	55	60	
Leu Arg Asp Leu Phe Lys Glu Glu Gly Leu Glu Pro Trp Thr Ser Cys			
65	70	75	80
Glu Phe Asp Phe Thr Arg Asp Gly Lys Leu Asn			
85	90		

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

```

Met Val Gln His Leu Leu Asn Glu Gly Leu Ser Arg Phe Glu Asp Lys
 1             5             10             15
Phe Val Gly Val Tyr Leu Glu Val Asp Asn Xaa Asn Xaa Glu Ala Val
      20             25             30
Ala Tyr Tyr Lys Glu Gln Gly Phe Thr Ile Leu Arg Ser Tyr Gln Pro
      35             40             45
Glu Met Tyr Gly Glu Lys Leu Asp Leu Ala Leu Met Tyr Lys Ala Phe
 50             55             60

```

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

```

Met Asp Gln His Ile Asn Ile Leu Gly Ala Ser Ser Asp His Leu Met
 1             5             10             15
Leu Asp Leu Asn Gly Gln Gly His Tyr Gln Val Gly Asp His Ile Ser
      20             25             30
Phe Ser Leu Asn Tyr Glu Ala Leu Ser His Ser Met Tyr Met Lys Asn
      35             40             45
Leu His Lys Val Tyr Ile Asp Asp Ser Lys Ile Asp Thr Leu Leu Gln
      50             55             60
Asn Phe Asp Val Lys Ser Pro Ala Met Val Asn Gln Tyr
 65             70             75

```

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

```

Met Leu Tyr Gln Asp Ala Ile Thr Leu Glu Ala Glu Ile Leu Glu Ile
 1             5             10             15
Lys Pro Arg Val Asn Thr His Thr His Glu Ser Phe Leu Gln Ala Ile
             20             25             30
Val Asp Ile Gly Tyr Xaa Arg Tyr Thr Ser Arg
             35             40

```

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

```

Met Ser Ile His Thr Glu Leu Ser Thr Ile His Xaa Ile Asn Glu Val
 1             5             10             15
Ala Glu Val Leu Gly Lys Lys His Lys Ile Leu Leu Met Val Asp Trp
             20             25             30
Lys Asp Val Arg Glu Gly Val Leu Thr Tyr Asp Val Leu Asp Tyr Xaa
             35             40             45
Lys Glu Ile Ile His Leu Xaa Asn Ile His Phe Val Gly Leu Ala Phe
             50             55             60
Asn Phe Met Cys Phe Lys Ser Asp Ala Pro Ser Gly Xaa Asp Ile Phe
             65             70             75             80
Met Ile Asn Arg Phe Val Ser Ala Val Xaa Arg Glu Ile Gly Tyr Arg
             85             90             95
Xaa Xaa Ile Ile Ser Gly Trp
             100

```

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

```

Met Gly Gly Ile Gln Ile Ile Pro Glu Thr Asn Gln Val Ile Ser Pro
 1             5             10             15
Arg Phe Gly Thr Leu Thr Asn Met Ile Ala Ile Gly Gln Met Thr Asn
          20             25             30
Gly Val Asn Lys Leu Arg Asn Gly Val Lys Met Ile Val Glu Gln Val
      35             40             45
Ala His Thr Val Ser Gln Leu Tyr Asp Ala Leu Glu Ser Asn Glu Gln
      50             55             60
Gln Gln Arg Ser Tyr Asn Gln
65             70

```

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

```

Met Asp Asp Asn Asp Ile Xaa Arg Leu Lys Asn Ile Ser Asn Arg Leu
 1             5             10             15
Arg Ser Lys Ile Ile Val Lys Asp Gln Pro Glu Xaa Met Val Ser Thr
          20             25             30
Leu Gln Phe Xaa Val Ile Ala Pro Gly Val
      35             40

```

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

```

Met Lys Asp Val Met Ala Ile Gly Asp Asn Leu Asn Asp Leu Ser Met
 1             5             10             15
Leu Glu Lys Val Gly Tyr Pro Val Ala Met Glu Asn Gly Ala Glu Glu
      20             25             30
Val Lys Lys Ile Ala Lys Tyr Val Thr Asp Thr Asn Glu Asn Ser Gly
      35             40             45
Val Gly Lys Ala Ile Met Lys Leu Leu Arg Glu Gln Gln Val
 50             55             60

```

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

```

Met Lys Asp Val Met Pro Ile Gly Asp Asn Leu Asn Asp Leu Ser Met
 1             5             10             15
Leu Glu Lys Val Gly Tyr Pro Val Ala Met Glu Asn Gly Ala Glu Glu
      20             25             30
Val Lys Lys Ile Ala Lys Tyr Val Thr Asp Thr Asn Glu Asn Ser Gly
      35             40             45
Val Gly Lys Ala Ile Met Lys Leu Leu Arg Glu Gln Gln Val
 50             55             60

```

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

```

Met Gly Arg Gln Asp Ile Ala Val Ala Lys Gly Ala Asp Arg Pro Leu
 1             5             10             15
Ile Lys Pro Ala Ala Phe Ala Ser Glu Ile His Gly Glu Ser Gly Leu
          20             25             30
Asp Gly Pro Lys Leu Pro Ser Thr Pro Ser Arg Gln Ala Val Ala Met
      35             40             45
Pro Ala
      50

```

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

```

Met Ser Glu Val Ser Ala Ile Ile Ala Glu His Cys Leu Phe Asp Leu
 1             5             10             15
Asp Ala Pro Ile Met Arg Leu Ala Ala Pro Asp Val Pro Ser Met Pro
          20             25             30
Phe Ser Pro Val
      35

```

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

```

Met Leu Gly Ile Asp Ile Asn Thr Gln Thr Arg Ala Lys Leu Ile Gln
 1             5             10             15
Asn Ile Leu Asn Gln Phe Asn Leu Lys Leu Val Asp Xaa Glu Ile Thr
      20             25             30
Ala Asp Val Lys Asn Glu Ser Phe Ala Gln Ser Lys His Asn Leu Ile
      35             40             45
Gln Gly Ile Leu
      50

```

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

```

Met Gly Phe Gly Ile Pro Ser Ser Ile Gly Ala Lys Leu Ala Asn Pro
 1             5             10             15
Asp Lys Thr Val Val Cys Phe Val Gly Asp Gly Gly Phe Gln Met Pro
      20             25             30
Asn Gln Glu Met Ala Leu Leu Pro Glu Tyr Gly Leu Asp Val Lys Ile
      35             40             45
Val Leu Ile Asn Asn Gly Thr Leu Gly Met Val Lys Gln Trp Gln Asp
      50             55             60
Lys Phe Phe Asn Gln Arg Phe Ser His Ser Val Phe Asn Gly Gln Pro
      65             70             75             80
Asp Phe Met Lys Met Ala Glu Ala Tyr Gly Val Lys Gly Phe Leu Ile
      85             90             95
Asp Lys Pro Glu Gln Leu Glu Glu Gln Leu Asp Ala Ala Phe Ala Tyr
      100            105            110
Gln Gly Pro Val Leu Ile Glu Val Arg Ile Ser Pro Thr Glu Ala Val
      115            120            125
Thr Pro Met Val Pro Ser Gly Lys Ser Asn His Glu Met Glu Gly Leu
      130            135            140

```

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

```

Met Lys Ala Ile Ser Glu Ser Asp Thr Val Ile Leu Ala Tyr Gly Ala
 1             5             10             15
Tyr Ala Lys Arg Pro Val Val Ile Asp Arg Val Glu Gln Val Met Glu
      20             25             30
Met Leu Lys Pro His Lys Lys Lys Val Lys Lys Leu Ile Asn Pro Val
      35             40             45
Thr Asn Glu Ile Met His Pro Leu Asn Pro Lys Ala Arg Gln Lys Trp
      50             55             60
Ile Leu Lys Ser
65

```

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

```

Met Asn Ile Asn Ser Ala Gln Thr Glu Glu Met Gly Glu Thr Tyr Leu
 1             5             10             15
Glu Val Gln Arg Ile Tyr Phe Leu Lys Asp Phe Gln Gly Gly Gly Arg
      20             25             30
Gly Ser Gln Leu Ile Glu Leu Ala Glu Lys Ile Ala Pro Arg Thr
      35             40             45

```

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

```

Met Ser Leu Ile Met Gly Leu Leu Ser Glu Lys Arg Leu Ile Phe Lys
 1             5             10             15
Phe Ser Ile Gly Val Leu Val Trp Gly Ile Gly Leu Ser Ile Ile Asn
          20             25             30
Val Phe Pro Ser Val Ala Ile Leu Tyr Ile Gly Ala Thr Leu Val Gly
          35             40             45
Leu Gly Gln Ser Ile Glu Gly Leu Thr Arg Ser Val Xaa Xaa Gln Ile
          50             55             60
Lys Asn Ala Lys Xaa Phe Gly Trp Gly Lys Gly Ile
65             70             75

```

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

```

Met Tyr Leu Leu Lys His Xaa Pro Glu Thr Lys Ala Xaa Pro Ile Lys
 1             5             10             15
Gly Met Lys Ala Glu Ala Lys Lys Cys Asp Val Ile Gly Leu Asp Ile
          20             25             30
Xaa Val Gly Thr Met Leu Ser Leu Asn Val Ile Ile Thr Gln Thr Ser
          35             40             45
His Val Gly Leu Val Ser Gln Arg
          50             55

```

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

```

Met Ser Phe Asp Pro Glu Met Val Lys Glu Ala Ile Gln Glu Tyr Tyr
 1             5             10             15
Pro Asn Phe Thr Leu Asp Tyr Asp Val Asp Pro Ile Arg Gln Gly Ile
      20             25             30
Ala Asn Ser Trp Pro Asp Ser Ile Asp Thr Ser Cys Ser Arg Gly Glu
      35             40             45
Trp Gly Phe Asp Pro Lys Tyr Asp Leu Ala Ser Met Thr Lys Leu Met
      50             55             60
Leu Glu Ala Ile Glu Gln Lys Asp Thr Val Lys Asn Asn Asn
65             70             75

```

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

```

Met Ala Val Lys Val Ala Ile Asn Gly Phe Gly Arg Ile Gly Arg Leu
 1             5             10             15
Ala Phe Arg Arg Ile Gln Glu Val Glu Gly Leu Glu Val Val Ala Val
      20             25             30
Asn Asp Leu Thr Asp Asp Asp Met Leu Ala His Leu Leu Lys Tyr Asp
      35             40             45
Thr Met Gln Gly Arg Phe Thr Gly Glu Val Glu Val Val Asp Gly Gly
      50             55             60

```

Phe Arg Val Asn Gly Lys Glu Val Lys Ser Phe Ser Glu Pro Asp Ala
 65 70 75 80
 Ser Lys Leu Pro Trp Lys Asp Leu Asn Ile Asp Val Val Leu Glu Cys
 85 90 95
 Thr Gly Phe Tyr Thr Asp Lys Asp Lys Ala Gln Ala His Ile Glu Ala
 100 105 110
 Gly Ala Lys Lys Val Leu Ile Ser Ala Xaa Ala Thr Gly Asp Leu Lys
 115 120 125
 Thr Ile Arg Ile Gln His Tyr Thr Thr Lys Ser
 130 135

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Met Arg Thr Ile Ser Ile Asn Val Phe Leu Met Leu Val Gln Phe Leu
 1 5 10 15
 Xaa Asn Ile Gln Val Thr Tyr Thr His Ala Gln Leu Lys Gly Gly Asn
 20 25 30
 Lys Glu Pro Tyr Arg Ile Gly Leu Lys Leu Ser Asn Gly Gly Trp Val
 35 40 45
 Tyr Val Gln Gly Leu Thr His Xaa Glu Val Asn Glu His Asp Glu Phe
 50 55 60
 Leu Ile Ala Gly Phe Xaa Tyr Xaa Gly Xaa Leu Ala Ala Ala Leu Xaa
 65 70 75 80
 Ile Ser Gly Ala Thr Xaa Xaa Phe Ile Glu Glu Ala Ser Thr Leu Thr
 85 90 95
 Gly Arg Lys Asp Met Phe Phe Ser Thr Ile Ser Thr Ser
 100 105

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

```

Met Ile Lys Glu Val Ala Val Lys Arg Tyr Asn Arg Ile Gly Ala Glu
 1             5             10             15
Gly Met Thr Ser Glu Ala Val Asp Gly Arg Ser Asn Ala Tyr Glu Leu
             20             25             30
Asn Asp Phe Lys Glu Tyr Glu Ala Ile Ile Asp Asn Tyr Phe Asn Ala
             35             40             45
Arg Thr Arg Thr Lys Lys Gly Arg Ala Val Phe Phe
             50             55             60

```

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 298 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

```

Met Arg Val Xaa Ile Ile Xaa Met Gly Pro Ala Gly Val Ser Val Leu
 1             5             10             15
Arg Glu Leu Val Lys Xaa Pro Lys Phe Asn Gln Leu Asp Ile Asp Leu
             20             25             30
Tyr Asp Asp Lys Val Xaa Met Gly Gln Gly Val Pro Phe Gln Asn Asp
             35             40             45
Ser Ser Glu Leu Leu Ile Asn Met Pro Ser Xaa Xaa Met Ser Leu Asn
             50             55             60
Leu Asp Asp Glu Thr Glu Phe Trp Lys Trp Tyr Xaa Gln Gln Xaa Asp
             65             70             75             80
Phe Asn Phe Asp Glu Pro Ala Tyr Leu Pro Arg Phe Val Phe Gly His
             85             90             95
Tyr Met Lys Ser Tyr Leu Ser Met Phe Thr Lys Lys Tyr Pro Asn Ile
             100            105            110
Ser Thr Asn Tyr Asn Lys Val Gln Glu Ile Tyr Thr Asn Ser Asn Ile
                        302

```

```

      115              120              125
Asp Glu Xaa Asn Leu Thr Tyr Tyr Ile Cys Thr Thr Asn Ser Glu Gln
      130              135              140
Ser Trp Gln Ala Tyr Asp Tyr Val Phe Leu Thr Cys Gly Thr Phe Ala
      145              150              155              160
Tyr His Asp Pro Tyr Asn Leu Lys Gly Lys Lys Gly Tyr Ile Ala Thr
      165              170              175
Pro Tyr Pro Thr Tyr Asn Thr Leu Asp Glu Val Asn Glu Leu Asp Asp
      180              185              190
Ile Ala Ile Ile Gly Thr Gly Leu Ala Ser Leu Asp Val Val Arg Tyr
      195              200              205
Val Ala Ala His His Pro Lys Leu Pro Ile Thr Met Thr Ser Arg Ser
      210              215              220
Ala His Leu Pro Ser Val Arg Gly Thr Met Ile Asp Val Thr Phe Lys
      225              230              235              240
Tyr Leu Thr Lys Asp Lys Leu Asn Asp Ile Lys Lys His His Phe Gly
      245              250              255
Asn Ala Pro Leu Asp Thr Ile Xaa Ser Phe Ile Phe Lys Arg Met Cys
      260              265              270
Leu Asn Met Thr Leu Ile Phe Lys Lys Leu Val His Arg Arg Thr Arg
      275              280              285
Lys Ser Tyr Cys Arg Phe Glu Val Leu Ile
      290              295

```

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

```

Met Ile Glu His Leu Xaa Glu Asn Leu Asn Trp Ile Trp Asn Ser Leu
 1              5              10              15
Ser Ile Glu Asp Gln His Gln Phe Asn Pro Lys Ile Xaa Lys Asp Asp
      20              25              30
Ser Ile Lys Ser Lys Ser Asn Xaa Ser Lys Xaa Cys
      35              40

```


(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Met	Ser	Tyr	Ser	His	Lys	Glu	Leu	Ile	Glu	Ala	His	Phe	Gly	Leu	Gln
1				5				10					15		
Asn	His	Val	Phe	Thr	Leu	His	Glu	Tyr	Val	Lys	Glu	Ala	Gly	Glu	Val
			20				25					30			
Ile	Asp	Pro	Tyr	Gly	Gly	Thr	Lys	Glu	Met	Tyr	Val	His	Thr	Tyr	Glu
		35				40					45				
Glu	Leu	Val	Ser	Leu	Ile	Leu	Lys	Leu	Lys	Asp	Ile	Ile	Cys		
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Met	Pro	Asn	His	Gln	Phe	Glu	Ser	Arg	Gly	Ile	Phe	Ala	Val	Asn	Asn
1				5				10					15		
Gln	Gly	Val	Ser	Asn	Tyr	Val	Glu	Asp	Leu	Val	Glu	Glu	His	His	Leu
			20				25				30				
Ala	Glu	Xaa	Asp	Leu	Ile	Ala	Thr	Ile	Tyr						
		35				40									

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

```

Met Tyr Met Arg Lys Ile Ile Gly Leu Leu Leu Val Ser Thr Leu Ala
 1           5           10           15
Leu Thr Ala Cys Gly Glu Lys Glu Asn Pro Xaa Lys Glu Glu Asn Lys
          20           25           30
Xaa Ser His Thr His Gln His Xaa Xaa Xaa Xaa His Gln Xaa Arg Asn
        35           40           45
Lys Glu Asn Xaa Lys Lys Ala Asp Asp Lys Ile His Leu Ile Ile Ala
        50           55           60
Tyr Lys Ile Ile Gln Thr Ile Lys Thr Ser Gln Asn Ile Asn Leu Ile
65           70           75           80
Ile Ser Asp Pro Ser Tyr Asn Thr Pro Gly Asn Tyr
          85           90

```

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

```

Met Asn Glu His Tyr Val Val Glu Lys Ile Thr Tyr Asp Arg Ala Asn
 1           5           10           15
Ala Phe Lys Leu Asn Gln Glu Leu Lys Asn Tyr Gly Phe Glu Thr Glu
          20           25           30
Glu Thr Arg Gln Gly Ala Leu Thr Leu Ser Pro Ala Leu Lys Asp Leu
        35           40           45
Lys Glu Met Phe Leu Asp Gly Lys Ile Ile Phe Asn Asn Asn Pro Leu
        50           55           60
Met Lys Trp Tyr Ile Asn Asn Val Gln Leu Lys Leu Asp Arg Asn Gly
          65           70           75           80
          85           90
          95          100          105          110          115
          120          125          130          135          140
          145          150          155          160          165
          170          175          180          185          190
          195          200          205          210          215
          220          225          230          235          240
          245          250          255          260          265
          270          275          280          285          290
          295          300          305

```

65		70		75		80
Asn Trp Leu Pro Ser Lys Gln Ser Arg Tyr Arg Xaa Ile Asp Gly Phe						
	85		90		95	
Ala Ala Phe Ser Asn Thr Tyr Thr Asp Ile Met Xaa Lys Xaa Val Ser						
	100		105		110	
Asp Lys Gly Glu Gly Xaa Xaa Xaa Phe Ile Ser Xaa Lys Asp Xaa Met						
	115		120		125	
Arg						

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Met Ser Ile Met Ile Cys Lys Glu Gly Leu Phe Met Ile Met Gly Asn			
1	5	10	15
Leu Arg Phe Gln Gln Glu Tyr Phe Arg Ile Tyr Lys Asn Asn Thr Glu			
	20	25	30
Ser Thr Thr His Arg Asn Ala Tyr Trp Val Lys Leu Ala Lys Asn Val			
	35	40	45
Glu Ala Thr Lys Met Met Tyr Ala Leu Ser Thr Ile Val Gln Gln His			
50	55	60	
Ala Ser Ile Arg His Phe Phe Asp Val Thr Thr Asp Asp Asn Leu Thr			
65	70	75	80
Met Ile Leu His Glu Phe Leu Pro Phe Ile Glu Ile Lys Gln Val Pro			
	85	90	95
Ser Ser Ser Ala Asn Tyr Asp Leu Glu Ala Phe Phe Lys Gln Glu Leu			
	100	105	110
Ser Thr Tyr His Phe Asn Asp Ser Pro Leu Phe Lys Val Lys Leu Phe			
	115	120	125
Gln Phe Ala Asp Ala Ala Tyr Ile Leu Leu Asp Phe His Val Ser Ile			
	130	135	140
Phe Asp Asp Ser Gln Ile Asp Ile Phe Leu Asp Asp Leu Cys Asn Ala			
145	150	155	160
Tyr Arg Gly Asn Thr Val Ile Asn Tyr Thr Arg His His Ala His Ile			

165

170

175

Lys

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

```

Met Glu Ala Thr Ile Glu Val Val Thr Asp His Lys Val Ile Asp Trp
 1             5             10             15
Leu Trp Glu Thr Gln Asp Lys Ser Phe Phe Ser Ser Xaa Glu Asp Pro
          20             25             30
Glu Leu Cys Val Leu Lys Val Thr Pro Gln Ser Val Lys Leu Met Asn
          35             40             45
Asp Lys Ser Leu Asp Thr Pro Ile Lys Ile Asp Leu
          50             55             60

```

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

```

Met Asp Leu Tyr Thr Ala Lys Gln Phe Ala Tyr Gly Lys Ala Lys Asp
 1             5             10             15
Asn Lys Val Ala Ala Val Trp Lys Leu Asp Leu Lys Gly His Lys Pro
          20             25             30
Ala Leu Glu Gly Pro Glu Glu Thr Leu
          35             40

```

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

```

Met Ser Phe Tyr Val Val Leu Ile Ile Ile Ile Val Ala Leu Ile Gly
 1             5             10             15
Ile Leu Val Leu Asn Gln Arg Tyr Ser Asn Ser Lys Ile Asp Thr Glu
          20             25             30
Val Tyr Ala Arg Lys Gln Leu Ile Lys Lys Asn Lys Ala Leu Ser Ala
          35             40             45
Glu Asn Ala Glu Leu Arg Ser Gln Met Leu Ser Xaa Asn Asn Asp Val
          50             55             60
Gly Thr Pro Met Gln Tyr Lys Lys Cys
65             70

```

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

```

Met Ala Leu Thr Ala Gly Ile Val Gly Leu Pro Asn Val Gly Lys Ser
 1             5             10             15
Thr Leu Phe Asn Ala Ile Thr Lys Ala Gly Ala Leu Gly Xaa Asn Tyr
          20             25             30
Pro Xaa Ala Thr Xaa Asp Pro Asn Val Gly Ile Val Glu Val Xaa Asp
          35             40             45
Ala Arg Leu Leu Lys Leu Glu Glu Met Val Gln Pro Lys Lys Thr Leu
                                308

```

50 55 60
 Pro Thr Thr Phe Xaa Phe Thr Asp Phe Gly Gly Ile Gly Lys Gly Ala
 65 70 75 80
 Ser

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Met Ala Val Phe Lys Val Phe Tyr Gln His Asn Arg Asp Glu Val Ile
 1 5 10 15
 Val Arg Glu Asn Thr Gln Ser Leu Tyr Val Glu Ala Gln Thr Glu Glu
 20 25 30
 Gln Val Arg Arg Tyr Leu Lys Asp Arg Asn Phe Asn Ile Glu Phe Ile
 35 40 45
 Thr Lys Leu Glu Gly Ala His Leu Asp Tyr Glu Lys Glu Asn Ser Glu
 50 55 60
 His Phe Asn Val Glu Ile Ala Lys
 65 70

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Met Gly Leu Leu Asp Ala Val Ser Lys Gly Ile Ile Ser Met Glu Asp
 1 5 10 15

Ile Ala Met Ile Ala Leu Leu Ile Gly Gly Leu Val Gly Ile Ile Gln
 20 25 30
 His Asn Gly Gly Ile Glu Trp Leu Leu Gln Phe Val Arg Ser Lys Val
 35 40 45
 Lys Ser Lys Arg Gly Ala Glu Leu Gly Ile Ala Ser Leu Val Ser Val
 50 55 60
 Ala Asp Ile Ala Thr Ala Asn Asn Thr Ile Ser Ile Ser Met Ser Gly
 65 70 75 80
 Pro Leu Ala Lys His Ile Ala Asp Glu Tyr Asp Val Asp Ser Arg Lys
 85 90 95
 Ser Ala Ser Ile Leu Asp Ile Phe Gly Arg Leu Leu Pro Arg Xaa Xaa
 100 105 110
 Thr Ile

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Met Leu Ile Asn Tyr His Leu Asp Leu Gly Asn Gly Leu Tyr Leu Phe
 1 5 10 15
 Ile Asp Arg Lys Asn Lys Val Gly Glu Ala Ile Lys Asn Ala Lys Asn
 20 25 30
 Tyr Leu Asp Arg Trp Lys Pro Lys Tyr Glu Lys Lys Ile Ile Ala Gln
 35 40 45
 Ile Asp Ile Lys Val Lys Glu Asn Arg Leu Met Asp Leu Asp Asp His
 50 55 60
 Asp Asn Gln Tyr Glu Phe Asn Ser Phe Xaa Xaa Glu Asn Glu Glu Thr
 65 70 75 80
 Ile Tyr Asn Glu Leu Asp Lys Xaa Ile Asn Asn Asn Thr Lys Ser Arg
 85 90 95
 Gly Asn Ile Asp Gly Leu Ile Ile Glu Ile Met Ile Arg Glu Tyr Tyr
 100 105 110
 Leu Gly Asn
 115

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

```

Met Thr Met Ile Glu Tyr Asn His Gln Arg Ile Asp Lys Ile Ile Tyr
 1             5             10             15
Phe His Ser Pro Gln Ala Glu Asn Lys Lys Ser Ser Val Ala Ile Ile
      20             25             30
Met Asn Pro Thr Thr Gly Asn His Phe Gln Ala Phe Tyr Ile Met Ile
      35             40             45
Asn Ala Ile Lys Tyr Pro Tyr Pro Asp Ser Asn Lys Lys Phe Gln Met
      50             55             60
Ile Asn Asp Cys Ala Glu Lys Phe Asp Ile Pro Ile Leu Gly Ile Asp
65             70             75             80
Val Gln Pro Pro Gln Ala Phe His Asp Leu Ser Val Ile Leu
      85             90

```

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

```

Met Leu Ile Ile Asp Thr Xaa Gln Gln Xaa Ser Val Arg Lys Leu Trp
 1             5             10             15
Lys Gly Val Lys His Val Ile Leu Xaa Ser Pro Thr Phe Gly Ser Gln
      20             25             30
Met Ile Val Glu Gln Phe Met Ser Lys Phe Ser Gln Asp Ile Glu Val
                        311

```



```

          35          40          45
Ile Ser Phe Ser Thr Tyr Leu Gly Asp Thr Arg Ile Val Asp Lys Glu
    50          55          60
Ala Pro Asn His Val Leu Thr Thr Gly Val Lys Lys Lys Leu Tyr Met
    65          70          75          80
Gly Ser Thr His Ser Xaa Ser Thr Met Cys Gln Arg Ile Ser Ala Leu
          85          90          95
Ala Glu Gln Leu Lys Ile His Ile Arg Ile Arg Trp Val Ala Thr Ala
          100          105          110
Cys

```

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

```

Met Ser Lys Leu Leu Met Ile Gly Thr Gly Pro Val Ala Ile Gln Leu
  1          5          10          15
Ala Asn Ile Cys Tyr Leu Lys Ser Asp Tyr Glu Ile Asp Met Val Gly
          20          25          30
Arg Ala Ser Thr Ser Glu Lys Ser Lys Arg Leu Tyr Gln Ala Tyr Lys
          35          40          45
Lys Glu Lys Gln Phe Glu Val Lys Ile Gln Asn Glu Ala His Gln His
          50          55          60
Leu Glu Gly Lys Phe Gly Asn
    65          70

```

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

```

Met Phe Trp Glu Gln Leu Asn Phe Arg His Ile Asp Val Pro Tyr Asn
 1             5             10             15
Gln Ile Asn Glu Ile Xaa Thr Ile Ile Asp Arg Phe Ile Asn Xaa Lys
      20             25             30
Asn Lys Ala Xaa Tyr Ile Glu Pro Arg Phe Asn Asn Pro Thr Gly Arg
      35             40             45
Ser Leu Thr Asn Glu Gln Lys Lys Asn Xaa Ile Thr Tyr Xaa Glu Arg
      50             55             60
His Asn Ile Pro Ile Ile Xaa Asp Asp Ile Phe Arg Asp Ile Xaa Phe
65             70             75             80
Ser Asp Pro Thr Pro Ala Ile Lys Thr Tyr Asp Lys Leu Gly Lys Val
      85             90             95
Ile His Ile Ser Ser Phe Ser Lys Thr Ile Ala Pro Ala Ile Arg Ile
      100            105            110
Gly Gly Leu Xaa Leu Leu Lys Lys
      115            120

```

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

```

Met Thr Arg Ser Ala Leu Lys Pro Phe Lys Asn Lys Arg Val Met Val
 1             5             10             15
Thr Gly Arg Ile Gln Arg Val Xaa Phe Lys Asn Tyr Leu Asp Arg His
      20             25             30
Ser Thr Phe Xaa Pro Asn Val Arg Ile Leu Leu Lys Asp Val Phe Val
      35             40             45
Ser Gly Val Ser Ile Asp His Leu Trp Leu Tyr Glu Thr Asn Lys Tyr
      50             55             60
Tyr Ala Leu Ala Met Glu Leu Ile His Gln Arg Val Lys Phe Ser Ala
65             70             75             80

```

Asn Val Gly Thr Ile Phe Thr Lys Leu Asn Arg Asn
85 90

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Met Gly Ala Glu Asn Ile Ile Met Ala Phe Ile Leu Thr Arg Trp Ala
1 5 10 15
Trp Phe Cys Arg Val Ile Arg Thr Ser Val Met Gln Tyr Thr Ala Ser
20 25 30
Asp His Val Arg Phe Ala Lys Thr Ile Gly Met Asn Asp Met Lys Ile
35 40 45
Ile His Lys His Ile Met Pro Leu Thr Leu Ala Asp Ile Ala Ile Ile
50 55 60
Ser Ser Ser Ser Met Cys Ser Met Ile Leu Gln Ile Ser Gly Phe Ser
65 70 75 80
Phe Leu Gly Leu Gly Val Lys Ala Pro Thr Ala Glu Trp Gly Met Met
85 90 95
Leu Asn Glu Ala Arg Lys Val Met Phe Thr His Pro Glu Met Met Phe
100 105 110
Xaa Pro Gly Ile Ala Ile Gly Ile Ile Val Met Ala Phe Asn Phe Leu
115 120 125
Ser Asp Ala Leu Gln Asn Xaa Tyr Trp Ile Pro Arg Ile Ser Phe Leu
130 135 140
Lys Ile Asn Phe Arg Xaa Leu
145 150

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

```

Met Ile Glu Ser Asp Ser Xaa Xaa Asn Ala Xaa Leu Leu Ala Glu Ser
 1             5             10             15
Xaa His Ala Gly Val Glu Thr Ala Tyr Lys Ala Val Met Lys Pro Xaa
      20             25             30
Glu Gly Thr Ile Leu Thr Gly Gly Lys Asp Ala Ala Gln Ala Ala Ile
      35             40             45
Glu Lys Ala Asn Asn Thr Glu Asp Cys Ile Arg Ile Asn Gly Xaa His
      50             55             60
Tyr Trp
65

```

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

```

Met Leu Arg Ile Ala Ile Ala Lys Gly Arg Leu Met Asp Ser Leu Ile
 1             5             10             15
Asn Tyr Leu Asp Val Ile Glu Tyr Thr Thr Leu Ser Glu Thr Leu Lys
      20             25             30
Asn Arg Glu Arg Gln Leu Leu Leu Ser Val Asp Asn Ile Glu Cys Ile
      35             40             45
Leu Xaa Lys Gly Ser Asp Val Pro Ile Tyr Val Glu Gln Gly Met Ala
      50             55             60
Asp Ile Gly Ile Val Gly Ser Asp Ile Leu Asp Glu Arg Gln Tyr Asn
65             70             75             80
Val Asn Asn Leu Leu Asn Met Pro Phe Gly Ala Cys His Xaa Ala Val
      85             90             95
Ala Ala Lys Pro Glu Thr Thr Asn Tyr Arg Lys Ile Ala Thr Ser Tyr
      100             105             110
Val His Thr Ala Glu Thr Tyr Phe Lys Ser Lys Gly Ile Asp Val Glu
315

```

```

      115              120              125
Leu Ile Lys Leu Asn Gly Ser Val Glu Leu Ala Cys Val Val Asp Met
      130              135              140
Val Asp Gly Ile Val Asp Ile Ala Gln Thr Gly Thr Thr Leu Lys Ala
      145              150              155              160
Asn Gly Leu Val Glu Lys Gln His Ile Ser Asp Ile Asn Ala Arg Leu
      165              170              175
Ile Thr Asn Lys Ala Ala Tyr Phe
      180

```

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

```

Met Asn Asn Met Pro Thr Val Leu Ile Asp Ala Ile Ala Ile Gly Gln
 1              5              10              15
Ser Asn Val His Gly Met Leu Lys Glu Gly Leu Ile Tyr Ala Xaa Val
      20              25              30
Ile Gly Ser Asp Leu Gly Pro Xaa Asn Tyr Thr Asp Xaa Leu Phe Ser
      35              40              45
Tyr Ile Xaa Val Val Thr Arg Leu Asn Thr Lys Arg Cys
      50              55              60

```

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

```

Met Met Arg Val Ala Leu Ser Ile Gln Gln Ser Arg Ile Glu Ala Gln
 1             5             10             15
Arg Ser Asn Xaa Lys Ala Val Ile Ser Gln Ser Asp Val Leu Ala Arg
      20             25             30
Met Thr Ile Glu Glu His Glu Gln Asp Gly Glu Lys Ala Tyr Gln Tyr
      35             40             45
Val Leu Asn Ala Glu Pro Ser Asn Leu Phe Glu Thr Lys Ile Arg His
      50             55             60
Ser Ser Asn Ile Lys Ile Asn Asn Xaa Arg Phe Ile Asn Pro Ser Ile
65             70             75             80
Asn Asp Val Val Gln Ala Ile Arg Asn Gly Asn
      85             90

```

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

```

Met Met Ala Gln Gly Ile Gly Arg Leu Thr Gly Lys Pro Gly Val Val
 1             5             10             15
Leu Val Thr Ser Xaa Pro Gly Val Ser Asn Leu Thr Thr Gly Leu Leu
      20             25             30
Thr Ala Thr Ser Glu Gly Asp Pro Val Leu Ala Leu Gly Gly Gln Val
      35             40             45
Lys Arg Asn Asp Leu Leu Arg Leu Ala His Gln Ser Ile Asp Asn Ala
      50             55             60
Ala Leu Leu Lys Tyr Ser Ser Lys Tyr Ser Glu Glu Val Gln Asp Pro
65             70             75             80
Glu Ser Leu Ser Glu Val Met Thr Thr Cys Asn Ser Asn Cys Tyr Xaa
      85             90             95
Arg Xaa Xaa Trp Arg Lys Xaa His
      100

```

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

317

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

```

Met Met Ile Gly Glu Asp Phe Ser His Tyr Leu Xaa Val Arg Pro Gly
 1             5             10             15
Ala Phe Phe Leu Thr Gly Cys Gly Asn Glu Ser Lys Gly Ile Thr Ala
      20             25             30
Pro His His Asn Pro Lys Phe Asp Ile Asp Xaa Lys Ser Leu Lys Tyr
      35             40             45
Ala Val Ala Val Phe Leu Lys Ile Ile Glu Leu Glu Gln Val Phe Lys
      50             55             60
Xaa Xaa
65

```

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

```

Met Val Leu Gly Val Ser Xaa Phe Leu Glu Thr Xaa Ile Asn Asn Leu
 1             5             10             15
Ser Glu Glu Leu Ser Val Ile Asn Thr Ser Lys Leu Glu Ser Ile Thr
      20             25             30
His Tyr His Phe Asp Xaa Val Asp Leu Leu Ile Thr Xaa His Asp Ile
      35             40             45
Pro Lys Gln Thr Leu Asn Ile Leu Pro Lys His Leu Thr Thr Ile Lys
      50             55             60
Val Ala Pro Leu Phe Ser Glu Asp Asp Arg His Lys Ile Arg His Val
65             70             75             80
Val Lys Gln Lys Gln Asn Pro Val Gln Ala His His His Met Asp Thr

```

	85	90	95
Val Asn Phe Leu Val Gly Asn Thr Glu Gln Lys Ser Arg His Thr Val			
100	105	110	
Gln Ile Leu Glu Glu Ala Gln Lys Ile Leu Gln Ala His His Ala Ile			
115	120	125	
Gly Arg Arg Ile Xaa Arg Ile Ser Phe Arg Ala			
130	135		

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Met Leu Ile Asp Trp Arg Met Ala Ser Ala Leu Leu Val Thr Ile Pro			
1	5	10	15
Ile Ser Ile Phe Ala Phe Lys Lys Val Met Ser Gly Phe Asn Glu Thr			
20	25	30	
Tyr Ala Glu Gln Met Lys Ser Asn Asn Tyr Met Asn Ser Ala Ile Val			
35	40	45	
Glu Phe Ile Glu Gly Ile Glu Val Ile Lys Thr Phe Asn Gln Ser Gln			
50	55	60	
Ser Ser Tyr			
65			

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Met Ala Ile Ile Arg Gln Arg Tyr Gln Glu Gln Leu Asp Asp Leu Ile
 1 5 10 15
 Lys Glu Leu Arg Arg Leu Gly Ala Asn Val Tyr Val Ser Ile Glu Asn
 20 25 30
 Gly Ile Lys Ser Leu Ser Ile Asp Asp Arg Gly Phe Xaa Arg Gln Thr
 35 40 45
 Val Lys Asn Asp Lys His Ile Asn Gln Leu Asn Tyr Asp Ile Asn Glu
 50 55 60
 Arg Val Ile Met Leu Ile Thr Lys Gln Gln Xaa Ile Ala Ser Asp Leu
 65 70 75 80
 Arg Met Met Ile Ser Ser Xaa Lys Asn Arg Leu Arg Phe Arg Lys Asn
 85 90 95
 Arg Arg

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

Met Lys Glu Arg Gly His Ile Glu Gln Leu Trp Arg Glu Glu Lys Tyr
 1 5 10 15
 His Val Leu Leu His Ser Gln Gln Ser Tyr Gln Met Ile Arg Asn Ala
 20 25 30
 Leu Lys Thr Asp Leu Ser Leu His Gln Val Gln Gln Met Ile Asp Asp
 35 40 45
 Ala Leu Leu Xaa Xaa Pro Ser Ile Gly Ser Val Cys Asn Ala Phe Ala
 50 55 60
 His Met Trp Gly Tyr Phe Lys Lys Cys Ala Asn Glu Glu Glu Arg Lys
 65 70 75 80
 His Ser Xaa Leu Leu Thr Ala Asp Phe Ile Asn Gly Lys Ile Asp Thr
 85 90 95
 Gln Thr Leu Leu Asp Phe Leu Ala Glu Leu Ala Asn Lys Tyr Asp Val
 100 105 110
 Gln Tyr Leu Leu Gln Ser Arg Val Leu Asn Thr Lys Arg Lys Arg
 115 120 125

320

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

```

Met Asn Ile Asp Gly Leu Asp Ala Leu Leu Asn Gln Phe His Asp Met
 1             5             10             15
Lys Asn Asn Ile Asp Asp Asp Val Asp Asp Thr Leu Gln Glu Lys Ala
      20             25             30
Lys Glu Tyr Val Val Arg Ala Lys Leu Lys Ala Arg Glu Val Met Asn
      35             40             45
Lys Gly Tyr Trp Thr Gly Asn Leu Ser Arg Asn Ile Arg Tyr
 50             55             60

```

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

```

Met Val Gly Val Xaa Gly Lys Ile Arg Asp Glu Met Val Ile Pro Ala
 1             5             10             15
Pro Gly Asp Ile Arg Asn Val Ile Ala Ala Leu Ser Asp Ser Glu Ser
      20             25             30
Val Leu Ser Gln Leu Phe Gln Tyr Arg Phe Glu Glu Asn Gln Ile Ser
      35             40             45
Gly His Ser Leu Gly Asn Leu Leu Ile Ala Gly Met Thr Xaa Ile Thr
 50             55             60
Asn Asp Phe Gly His Ala Ile Lys Ala Leu Ser Lys Ile Leu Asn Ile

```

65 70 75 80
 Lys Gly Arg Val Ile Pro Ser Thr Asn Thr Lys Trp Cys Asn
 85 90

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Met Gly Leu Lys Gly Gln Gly Val Leu Leu Val Asn His Xaa Gln Asn
 1 5 10 15
 Val Asp Pro Ser Xaa His Gly Gly Gly Gln Glu Tyr Gly Val Arg Ser
 20 25 30
 Gly Thr Val Asn Val Gln Met Ile Leu Gln Trp Xaa Xaa Arg
 35 40 45

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

Met Asp Glu Gln Gln Gln Leu Thr Asn Ala Tyr His Ser Asn Lys Leu
 1 5 10 15
 Ser His Ala Tyr Leu Phe Glu Gly Asp Asp Ala Gln Thr Met Lys Gln
 20 25 30
 Val Ala Ile Asn Phe Ala Lys Leu Ile Leu Cys Gln Thr Asp Ser Gln
 35 40 45
 Cys Glu Thr Lys Val Ser Thr Tyr Asn His Pro Asp Phe Met
 50 55 60

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

```

Met Gly Pro Asn Gly Ala Gly Lys Ser Ser Leu Ile Lys Ser Leu Ile
 1             5             10             15
Gly Glu Phe Asn Ala Thr Gly Thr Lys Xaa Xaa Tyr Asn Lys Pro Ile
          20             25             30
Gln Gln Gln Xaa Gln Gln Ile Thr Tyr Ile Pro Gln Lys Ala His Ile
          35             40             45
Asp Leu Asp Phe Pro Ile Ser Val Glu Gln Val Ile Leu Ser Gly Cys
          50             55             60
Tyr Lys Glu Ile Gly Trp Phe Arg Arg Pro Asn Lys Ser Ala Arg Asp
65             70             75             80

```

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

```

Met Asp Asp Leu Arg Lys Ile Asn Gln Glu Leu Gly Ile Thr Ile Leu
 1             5             10             15
Ile Asn Leu His Phe Val Asp Leu Ala Lys Glu Tyr Gly Thr Arg Ile
          20             25             30
Ile Gly Leu Arg Asp Gly Glu Val Gly Leu
          35             40

```

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

```

Met Asp Ala Tyr Lys Glu Val Arg Gln Ser Ala Thr Ala Arg Lys Ala
 1             5             10             15
His Asn Ala Thr Val Ser Asn Ala Thr Asp Glu Glu Val Xaa Glu Ala
      20             25             30
Asn Ala Ala Val Asp Ala Ala Gln Thr Glu Gly Leu His Asp Ile Gln
      35             40             45
Val Val Lys Ser Gln Gln Glu Val Ala Asp Thr Lys Ala Lys Val Leu
      50             55             60
Asp Lys Ile Asn Ala Ile Gln Thr Gln Ala Lys Val Xaa Pro Ala Ala
65             70             75             80
Asp Thr Glu Val Glu Asn Ala Tyr Xaa Tyr Thr
      85             90

```

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

```

Met Asp Xaa Lys Xaa Leu His His Xaa Ser Pro Leu Pro Met Phe Gly
 1             5             10             15
Thr Cys Ala Gly Leu Ile Val Leu Xaa Gln Asp Ile Xaa Gly Glu Glu
      20             25             30
Gly Tyr Leu Asn Lys Leu Xaa Ile Pro Val His Arg Asn Ser Phe Gly
      35             40             45

```

Arg Gln Val Xaa Xaa Phe Glu Thr Glu Leu Asp Ile Lys Gly Ile Xaa
 50 55 60
 Thr Asp Ile Val Gly Val Phe Ile Arg Ala Pro His Ile Glu Lys Val
 65 70 75 80
 Gly Gln Gly Val Xaa Ile Leu Cys Lys Val Asn Gly Lys Ile Val Ala
 85 90 95
 Val Gln Gln Gly Lys
 100

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Met Glu Leu Lys Xaa Leu Xaa Gln Asn Ser Thr Leu Pro Met Phe Gly
 1 5 10 15
 Thr Cys Ala Gly Val Ile Val Leu Ala Gln Asp Ile Xaa Xaa Glu Xaa
 20 25 30
 Gly Tyr Xaa Asn Lys Leu Asn Ile Thr Val Xaa Arg Xaa Ser Phe Gly
 35 40 45
 Arg Xaa Val Asp Ser Phe Glu Thr Xaa Leu Asp Ile Lys Gly Ile Ala
 50 55 60
 Thr Asp Ile Xaa Gly Val Phe Ile Arg Ala Pro His Ile Glu Lys Val
 65 70 75 80
 Gly Xaa Gly Val Asp Ile Leu Cys Xaa Xaa Asn Glu Lys Ile Val Xaa
 85 90 95
 Val Xaa Gln Gly Lys Tyr Leu Gly Val Ser Phe His Pro Glu Leu Thr
 100 105 110
 Asp Asp Tyr Arg Val Thr Asp Tyr Phe Ile Asn His Ile Val Xaa Lys
 115 120 125
 Ala

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

325

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

```

Met Lys Asn Val Pro Leu Ser Xaa Xaa Xaa Asn Val Xaa Xaa Met Ile
 1             5             10             15
Asp Lys Gln Glu Phe Met Xaa Val Ser Gly Met Asn Arg Met Ala Tyr
          20             25             30
Asn Asp Gln Tyr Ile Ile Gly Gln Arg Gly Asp Glu Phe Ile Leu Tyr
          35             40             45
Lys Phe Gly Asp Glu Ser Met Arg Val Tyr Asn Thr Glu Phe Glu Met
          50             55             60
Gln Gln Asp Leu Asn Glu Leu Gly Gln Asn Leu Gln Leu Lys Pro Glu
65             70             75             80
Asn Ala Tyr Gln

```

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

```

Met Ile Xaa Ala Leu Tyr Xaa Trp Ser Ser Xaa Xaa Thr Tyr Ile Ala
 1             5             10             15
Leu Gly Asn Met Met Xaa Thr Ala Ala Xaa Leu Gly Ile Asp Ser Tyr
          20             25             30
Pro Met Glu Gly Phe Ser Leu Asp Thr Val Thr Asp Xaa Leu Ala Xaa
          35             40             45
Xaa Gly Ile Leu Asp Thr Glu Gln Phe Gly Leu Ser Val Met Val Ala
          50             55             60
Phe Gly Tyr Arg Gln Gln Asp Pro Pro Lys Asn Lys Thr Arg Gln Ala

```

65 70 75
Tyr Glu Asp Val Asn Glu Gly Val Gly Pro Xaa Glu
85 90

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

Met	Leu	Leu	Ala	Ser	Phe	Val	Leu	Ile	Thr	Leu	Gly	Gln	Ser	Val	Glu
1				5					10					15	
Gln	Leu	Arg	Ala	Ala	Ile	Ile	Tyr	Val	Val	Leu	Asn	Ile	Ile	Gly	Ser
			20					25					30		
Trp	Leu	Phe	Leu	Leu	Gly	Ile	Gly	Leu	Leu	Tyr	Lys	Thr	Val	Gly	Thr
		35					40					45			
Leu	Asn	Phe	Ser	His	Ile	Ala	Met	Arg	Leu	Asn	Asp	Met	Gly	Asp	Asn
	50					55					60				
Arg	Thr	Val	Thr	Met	Ile	Ser	Leu	Ile	Phe	Leu	Val	Ala	Phe	Ser	Ala
65					70					75					80
Lys	Ala	Ala	Leu	Val	Leu	Phe	Met	Trp	Leu	Pro	Lys	Ala	Tyr	Ala	Val
			85						90					95	
Leu	Asn	Thr	Glu	Leu	Ala	Ala	Leu	Phe	Ala	Ala	Xaa	Met	Thr	Xaa	Val
			100					105					110		
Gly	Ala	Tyr	Ala	Leu	Ile	Arg	Ile	Leu	His	Phe	Thr	Ile	Trp	Ile	Lys
		115					120					125			
His	Asn	Asp	Leu	Ile	His	Pro	Leu	Leu	Ala	Thr	Met	Ala	Ala	Tyr	
	130					135					140				

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

```

Met Gln Pro Ser Met Gln Tyr Phe Asn Glu Trp Trp Lys Gln Leu Phe
 1             5             10             15
Gly Glu Ser Glu Gly Lys Asp Phe Lys Gly Ile Tyr Pro Ser Ser Ala
             20             25             30
Asn Tyr Thr Thr Asp Leu His Ser Leu Gly Gln Tyr Val Gln Glu Gly
             35             40             45
Arg Arg Phe Leu Phe Glu Thr Xaa Val Lys Val Asn His Pro Lys Tyr
             50             55             60
Asp Ile Thr Ile Glu Lys Asp Ser Asp Asp Leu Asp Gly Leu Asn Tyr
             65             70             75             80
Leu Ala Gly Lys Thr Ile Asp Asp Gly
             85

```

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

```

Met Thr Leu Ile Xaa Leu Ala Met Ile Ile Ile Glu Tyr Ser Phe Leu
 1             5             10             15
Leu Ile Lys Asn Ala Val Asp Ala Gly Val Ile Asn Asn Ala Thr Thr
             20             25             30
Arg Ile Asn Thr Tyr Xaa Met Glu Ser Leu Ala Thr Val Thr Thr Glu
             35             40             45
Ser Asn Asn His Ala Gln Cys Met
             50             55

```

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

```

Met Phe Tyr Gly Leu Tyr Glu Glu Met Xaa His Leu Leu Tyr Cys Ser
 1           5           10           15
Ser Ala Gly His Glu Pro Gly Tyr Ile Tyr Arg Ala Val Lys Glu Glu
          20           25           30
Phe Xaa Glu Ile Ser Val Arg Gly Arg Val Leu Gly Ile Ser Ser His
          35           40           45
Thr Arg Tyr Gln Gln Gln Glu Ile Pro Ile Tyr Leu Asp Asp Leu Ile
          50           55           60
Ile Ile Leu Thr Asp Gly Val Thr Glu Ala Arg Asn Ser Glu Gly Thr
          65           70           75           80
Phe Ile Asp Lys His Lys Leu Leu Glu Tyr Ile Lys Lys His Lys His
          85           90           95
Leu His Pro Gln Asp Ile Val Xaa Ile Ile Tyr Glu Ala Ile Leu Arg
          100          105          110
Leu Gln Asn Pro Asn Lys Lys Asp Asp Met Thr Ile Leu Ile Ile Lys
          115          120          125
Arg Val Asn
          130

```

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

```

Met Arg Asp Glu Ile Asp Pro Val Arg Arg Thr Gly Ile Lys Gln Leu
 1           5           10           15
Met Asn Lys Gln Tyr Gln Gln Asp His Leu Val Ala Ser Ser Asp Lys
          20           25           30
Gly Lys Glu Lys Leu Arg Asn Ser Asp Thr Val Ala Val Leu Leu Pro
          329

```

	35		40		45	
Ala Xaa Thr Phe Tyr Leu Gly Lys Glu Asp Tyr Ala Ala Ala Arg Gly						
50		55		60		
Met Leu Asp Asn Asn Gly Ala Ile Ala Leu Ala Thr Asp Tyr Asn Pro						
65		70		75		80
Gly Ser Ser Val Thr Asn Asn Leu Gln Leu Val Met Ala Ile Ala Ala						
	85		90		95	
Leu Lys Leu Lys Leu Ser Pro Ser Glu Val Trp Asn Ala Val Thr Val						
	100		105		110	
Asn Ala Ala Lys Ala Ile Asp Ile Asn Ala Gly Thr Ile Asn Thr Gly						
	115		120		125	
Asp Lys Ala Asn Leu Val Ile Trp Asp Ala Pro Asn His Glu Tyr Ile						
	130		135		140	
Pro Tyr His Xaa Gly Tyr Gln Ser Arg Arg Lys Lys Leu Leu Lys Thr						
145		150		155		160
Val Arg Xaa Ser Xaa Ile Thr His Tyr Leu Leu Lys His Lys Ile Ile						
	165		170		175	
Arg Lys Leu						

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Met Thr Ile Leu Ile Asp Thr Tyr Gln Gln Tyr Leu Xaa Xaa Phe Glu			
1	5	10	15
Ala His Xaa Xaa Arg Val Leu Gln Asp Asp Gln Tyr Ile Glu Ala Leu			
	20	25	30
Glu Thr Leu Met Asp Xaa Tyr Ser Glu Phe Ile Leu Asn Pro Ile Tyr			
	35	40	45
Glu Gln Gln Phe Asn Ala Trp Arg Asp Val Glu Glu Lys Ala Gln Leu			
	50	55	60
Ile Lys Ser Leu Gln Tyr Ile Thr Ala Gln Cys Val Lys Gln Val Glu			
65	70	75	80
Val Ile Arg Ala Arg Arg Leu Leu Asp Gly Gln Ala Ser Thr Thr Gly			

330

	85	90	95
Tyr Phe Asp Asn Ile Glu His Cys Ile Asp Glu Glu Cys Gly Gln Cys			
100	105	110	
Ser Ile Thr Ser Asn Asp Lys Leu Leu Leu Xaa Gly Xaa Gly Ala Tyr			
115	120	125	
Pro Met Thr Leu Xaa Gln Val Ala Lys Glu Thr Gly Ala Ser Val Ile			
130	135	140	
Gly Ile Asp Ile Asp Pro Thr Ser Arg Xaa Thr			
145	150	155	

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

Met Lys Leu Asn Asn Tyr Ser Leu Lys Val Lys Asn Lys Gln Leu Xaa			
1	5	10	15
Xaa Asn Cys Asp Leu Asn Phe Tyr Leu Gly Gln Ile Asn His Ile Xaa			
20	25	30	
Gly Lys Asn Gly Val Gly Lys Ser Leu Leu Ala Lys Asp Phe Leu Leu			
35	40	45	
Asn Asn Ser Gly Asn Ile Pro Lys Ser Ile Ser Gln Asn Gly Asn Leu			
50	55	60	
Asn Ile Lys Xaa His Gln Ile Phe Pro Asn Gly Tyr			
65	70	75	

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

```

Met Val Gln Leu His Gln Leu Phe Pro Lys His Glu Val Phe Xaa Arg
 1             5             10             15
Xaa Glu Tyr Met Xaa Pro Gly Gly Arg Met Lys Asp Arg Pro Ala Lys
          20             25             30
Xaa Ile Asn Xaa His Gly Ile Asn His Gly Leu Ile Thr Xaa Asn Thr
          35             40             45
Xaa Xaa Xaa Glu Ser Thr Ser Gly
 50             55

```

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

```

Met Glu Gly Gly Ile Ser Tyr Ile Val Arg Xaa Ser Lys Ile Asp Pro
 1             5             10             15
Val Asn Ile Val Gly Ile Gly Ile Asp Phe Thr Ser Ser Thr Ile Ile
          20             25             30
Phe Thr Asp Glu Asn Leu Asn Pro Val His Asn Leu Lys Gln Phe Lys
          35             40             45
Asn Asn Pro His Ala Tyr Val Lys Leu Trp Lys His His Gly Ala Tyr
          50             55             60
Lys Glu Ala Glu Lys Leu Tyr Gln Pro Ala Ile Glu Asn Asn Asn Xaa
          65             70             75             80
Trp Xaa Gly His Tyr Gly Tyr Asn Val Ser Ser Glu Trp Met Ile Pro
          85             90             95
Lys Ile Met Glu Val Met Asn Arg Ala Pro Asp Ile Met Glu Lys Thr
          100            105            110
Ala Tyr Ile Met Glu Ala Gly Asp Xaa Ile Val Xaa Xaa Leu Thr Asn
          115            120            125
Lys Asn Val Arg Ser Asn Cys Gly Leu Gly Phe Gln Ser Ile Val Gly
          130            135            140
Lys Lys Glu Thr Gly Ser Ser Ile Met Asp Leu Phe Gly
          145            150            155

```

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

```

Met Thr Ile Asn Leu Ser Glu Thr Phe Ala Asn Ala Lys Asn Glu Phe
 1           5           10           15
Ile Asn Ala Val Asn Asn Gly Glu Pro Gln Glu Arg Gln Asn Glu Leu
      20           25           30
Xaa Gly Asp Met Ile Asn Xaa Leu Phe Gly Gly Asn
      35           40

```

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

```

Met Leu Asp Glu Xaa Xaa Xaa Asn Leu Asp Asp Tyr Met Arg Tyr Leu
 1           5           10           15
Ile Thr Lys Lys Glu Xaa Leu Ser Lys Leu Ile Asp Ser Leu Met Leu
      20           25           30
Thr Leu Glu Asn Lys Tyr Ile Asp Ile Ala Glu Ala Phe Xaa Ile Gln
      35           40           45
Cys Ala Arg Glu Ile Asn Asn Gln Glu Ile Glu Asn Ile Xaa Ser Glu
      50           55           60
Leu Asn Lys Val Glu Ala Tyr Tyr Ala Gln Ile Glu Thr Gln Ile Gln
      65           70           75           80
Gln Thr Ser Thr Glu Lys Ile Ala Thr Glu Lys Thr Ser Tyr Leu Ile

```

85
Asn Tyr Met Asn Ala Val Ala
100

90

95

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

Met Xaa Arg Ile Glu Gln Ala Glu Val Arg Met Glu Glu Ile Asp Val
1 5 10 15
Leu Met Ile Glu Ala Ser Ala Asp Tyr Gly Lys Ile Lys Glu Leu Xaa
 20 25 30
Glu Glu Lys Xaa Xaa Leu Xaa Ile Pro Ile
 35 40

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

Met Glu Tyr Ile Tyr Cys Ala Arg Pro Asp Ser Thr Ile Ala Gly Lys
1 5 10 15
Asn Val His Ala Xaa Arg Lys Ala Ser Gly Lys Lys Leu Ala Gln Glu
 20 25 30
Ser Pro Val Asn Ala Asp Met Val Ile Gly Val Pro Xaa Ser Ser Leu
 35 40 45
Ser Ala Xaa Ser Gly Leu Cys
 50 55

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

```

Met Pro Cys Ile Asn Leu Glu Phe Gly Thr Gly Leu Gly Thr Lys Gly
 1             5             10             15
Xaa Gly Gly Ser Xaa Gln Gln Tyr Tyr Pro Leu Xaa Asp Glu Ile Asp
          20             25             30
Phe Lys Xaa Ile
          35

```

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

```

Met Ala Glu Leu Ile His His Phe Asn Gln Tyr Asp Cys Val Glu Glu
 1             5             10             15
Thr Glu Leu Phe Asn Ile Val Gln Gln Val Val Ala His Ala Ile Asn
          20             25             30
Pro Thr Leu Pro His Xaa Asn Glu Leu Lys Asp Ile Leu Phe Gly Pro
          35             40             45
Thr Ile Thr Val Lys Ala Leu Leu Asn Met Arg Met Glu Asn Lys Val
          50             55             60
Lys Gln Tyr Leu Asn Ile Glu Leu Asp Asn Pro Ile Lys Lys Glu Val
          65             70             75             80

```


(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

```

Met Ala Xaa Leu Ile His His Phe Asn Gln Tyr Asp Cys Val Val Glu
 1             5             10             15
Thr Glu Leu Phe Asn Ile Val Gln Gln Val Val Ala His Ala Ile Asn
          20             25             30
Pro Thr Leu Pro His Ala His Glu Xaa Lys Asp Ile Leu Phe Gly Pro
      35             40             45
Thr Ile Thr Val Asn Ser Val Val Lys Tyr Glu Asn Gly Lys
 50             55             60

```

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

```

Met Ala Pro Xaa Thr Lys Xaa Asn Xaa Lys Lys Glu Arg Ile Val Gly
 1             5             10             15
Thr Ala Gly Gly Gly Met Val Ala Val Thr Val Thr Gly His Lys Glu
          20             25             30
Val Val Asp Val Glu Ile Lys Glu Glu Xaa Val Asp Pro Asp Asp Ile
      35             40             45
Glu Met Leu Pro Lys Thr
 50

```

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

```

Met Leu Lys Glu Ile His Glu Gln Pro Ala Val Met Arg Arg Ile Ile
 1             5             10             15
Gln Glu Tyr Gln Asp Ala Glu Gly Xaa Leu Xaa Ile Gly Ser Lys Thr
      20             25             30
Xaa Ser Met Xaa Leu Xaa Lys Gln Asp Arg Ile Tyr Gly Tyr Cys Ser
      35             40             45
Arg Val Gln Ser Tyr Pro Cys Arg Val
 50             55

```

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

```

Met Ile Ala Val Asn Trp Asn Thr Gln Glu Asp Met Thr Asn Met Phe
 1             5             10             15
Trp Arg Gln Asn Ile Ser Gln Met Trp Val Glu Thr Glu Phe Lys Val
      20             25             30
Ser Lys Asp Ile Ala Arg Trp Lys Xaa Leu Ser Glu Ala Glu Pro Asp
      35             40             45
Pro Phe Lys Lys Ala Leu Ala Gly Leu Ala Gly Leu Asp Thr His Xaa
 50             55             60
Gly Asp Asp Gly Met Pro Leu Val Met Leu His Thr Thr Asp Leu Arg
 65             70             75             80
Lys Lys Ala Val Tyr Ser Phe Met Xaa Met Met Glu Gln Ile His Ala

```

	85	90	95
Arg Lys Ala Tyr Xaa His Ile Xaa Thr Thr Leu Leu Pro Ser			
100	105	110	

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Met Val Ser Asp Gln Gln Asp Phe Met Tyr Thr Leu Arg Met Met Ile			
1	5	10	15
Val Thr Leu Gly Gly His Val Leu Asp Phe Glu Val Glu Asp Val Lys			
20	25	30	
Val Glu Ile Gln Asn Ile Glu Thr Phe Glu Gln His Phe Pro Ile Gln			
35	40	45	
Asp Lys Asp Phe Thr Lys Ala Asn Ile Asp Tyr Lys Asp Ile Ala Asp			
50	55	60	
Glu Ile Arg Glu Ala Glu			
65	70		

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

Met Pro Pro Thr Asn Thr Ser Thr Ile Ile Pro Met Cys His Pro Leu			
1	5	10	15
Pro Leu Thr Xaa Ile Asp Val His Phe Ser Trp Asp Glu Thr Asn Ala			
20	25	30	
	338		

```

Pro Leu Tyr Thr Leu Asn Ile Gln Thr Thr Val Ser Thr Thr Ala Lys
   35                               40                               45
Thr Gly Val Glu Met Glu Ala Leu Thr Ala Ala Ser Ala Thr Ala Leu
   50                               55                               60
Thr Ile Tyr Asp Met Thr Lys Ala Val Asp Lys Gly Met Ile Ile Gly
  65                               70                               75                               80
Glu Thr Tyr Leu Glu Ser Lys Ser Gly Gly Lys Ser Gly Asp Phe Gln
                               85                               90                               95
Arg Gln Ser Gly Xaa
                               100

```

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

```

Met Thr Lys Phe Ile Cys Val Thr Gly Gly Val Val Ser Ser Leu Gly
  1                               5                               10                               15
Lys Gly Ile Thr Ala Ser Ser Leu Gly Arg Leu Leu Lys Asp Arg Gly
                               20                               25                               30
Leu Asn Val Thr Xaa Gln Xaa Phe Xaa Pro Tyr Leu Asn Val Asp Pro
                               35                               40                               45
Gly Thr Met Ser Pro Tyr Gln His Gly Glu Val Phe Arg Asn Gly
  50                               55                               60

```

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

Met Pro Pro Glu Glu Trp Ile Cys Thr Met Val Asn Ser Met Arg Ile
 1 5 10 15
 Gly Leu Pro Ala Ser Leu Asp Lys Val Gly Glu Val Leu Arg Leu Gln
 20 25 30
 Ser Gln Lys Asp Lys Ala Gly Lys Asn Leu Ile Arg
 35 40

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Met Thr Lys Glu Gln Gln Leu Xaa Glu Arg Ile Ile Ala Ala Xaa Gly
 1 5 10 15
 Gly Met Asp Asn Ile Asp Ser Val Met Asn Cys Met Thr Arg Val Arg
 20 25 30
 Ile Lys Val Leu Asp Glu Asn Lys Val Asp Asp Gln Glu Leu Arg His
 35 40 45
 Ile Asp Gly Val Met Gly Val Ile His Asp Glu Arg Ile Gln Val Val
 50 55 60
 Val Gly Pro Gly Thr Val Asn Lys Val Ala Asn His Met Ala Xaa Leu
 65 70 75 80
 Ser Gly Val Asn Leu Gly Asp Pro Ile Pro Gln His His Lys
 85 90

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

```

Met Lys Gln Lys Xaa Leu Pro Lys Val Arg Met Ser Glu Ile Gly Phe
 1             5             10             15
Ile Leu Gln Ala Thr Asn Leu Val Pro Phe Leu Thr Val Lys Gln Gln
      20             25             30
Phe Thr Leu Leu Lys Lys Lys Asn Lys Asn Val Met Ser Asn Glu Asp
      35             40             45
Tyr Gln Gln Leu Met Ser Gln Leu Gly Leu Thr Ser Leu Leu Asn Lys
      50             55             60
Leu Pro Ser Glu Ile Ser Gly Gly Gln Lys Gln Arg Val Ala Ile Ala
65             70             75             80
Gln Ser Val Ile Tyr Glu Ser Val Asp Tyr Phe Ser Gly
      85             90

```

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

```

Met Asn Met His Ile Leu Tyr Xaa Xaa Arg Xaa Lys His Asn Leu Glu
 1             5             10             15
Ile Asp Xaa Leu Ala Gln Gln Leu Xaa Glu Lys Tyr Gly Thr Lys Tyr
      20             25             30
Glu Ala His Xaa Met Gly Glu Trp Glu Asn His His His Asp Pro Lys
      35             40             45
Phe Xaa Asp Ala Met His Leu Xaa Asp Phe Cys Gly Cys Thr Ile
      50             55             60

```

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

```

Met Ala Phe Lys Asp Gly Thr Ile Asn Pro Arg Lys Ser Asn Gln Leu
 1             5             10             15
Lys Asp Tyr Val Phe Ile Asp Asp Gly Trp Ala Lys His Gly Thr Tyr
          20             25             30
Cys Val Val Arg Arg Ile Gln Ile His Ile Glu Thr Trp Asp Arg Thr
          35             40             45
Ala Leu Glu Glu Gln Glu Ala Thr Phe Gly Ser Gly Asn Asp Ile Val
          50             55             60
Gly Ala Pro Leu Thr Gly Gly Lys Glu Phe Gly
65             70             75

```

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

```

Met Asp Ser Phe Val Asn Ile Asp Gly Thr Asp Asn Leu Leu Val Leu
 1             5             10             15
Lys Thr Leu Pro Gly Asn Ala Gln Ser Ile Gly Ala Ile Leu Asp Gln
          20             25             30
Ile Asn Trp Glu Glu Val Leu Gly Thr Ile Cys Gly Asp Asp Thr Cys
          35             40             45
Leu Ile Ile Cys Arg Ser Lys Glu Ala Ser Asp Glu Ile Lys Ser Arg
          50             55             60
Ile Phe Asn Leu Leu
65

```

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- 342

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

```

Met Val Asp Asp Ala Leu His Thr Glu Met Ile Val Asp Gly Thr His
 1             5             10             15
Ser His Pro Ala Ser Val Ala Ile Ala Tyr Arg Met Lys Gly Asn Glu
      20             25             30
Arg Xaa Tyr Leu Ile Thr Asp Ala Met Arg Ala Lys Gly Met Pro Glu
      35             40             45
Gly Glu Tyr Asp Xaa Gly Gly Gln Lys Val Thr Val Xaa Ser Gln Gln
      50             55             60
Ala Arg Leu Ala Asn Gly Ala Leu Ala Gly Ser Ile Leu Lys Met Asn
65             70             75             80
His Gly Leu Arg Asn Leu Ile Ser Phe Thr Gly Asp Thr Leu Xaa His
      85             90             95
Leu Trp Arg Val Thr Ser Leu Asn Gln Ala Ile Ala Leu Gly Ile Arg
      100             105             110

```

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

```

Met Ala Pro Tyr Thr Asn Lys Gly Tyr Ala Val Lys Glu Leu Cys Ser
 1             5             10             15
Tyr Leu Gln Ile Asn Met Asp Asp Val Tyr Thr Ile Gly Asp Arg Lys
      20             25             30
Leu Ile Tyr Leu Cys Leu Ile Pro
      35             40

```

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

```

Met Val Lys Xaa Xaa Ile Tyr Pro Arg Asn Glu Ile His Phe Ser Tyr
 1             5             10             15
Thr His Ile Ala Phe Thr Ile Asp Asp Ser Glu Phe Lys Tyr Trp His
      20             25             30
Gln Arg Xaa Lys Asp Asn Asn Val Asn Ile Leu Gly Gly Arg Val Arg
      35             40             45
Asp Ile Arg Asp Arg Gln Ser Ile Tyr Phe Thr Asp Pro Asp Gly His
      50             55             60
Lys Leu Glu Leu His Thr Gly Thr Leu Glu Asn Arg Leu Asn Tyr Tyr
      65             70             75             80
Lys Glu Ala Lys Pro His Met Thr Phe Xaa Lys
      85             90

```

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

```

Met Leu Val Gln Ser Gly Lys Pro Val Ala Val Phe Lys Thr His Glu
 1             5             10             15
Glu Ala Pro Arg Val Leu Ile Ser Asn Ser Val Leu Val Pro Glu Trp
      20             25             30
Ala Asn Trp Asp His Phe Asn Glu Leu Asp Lys Lys Gly Leu Ile Met
      35             40             45
Tyr Gly Gln Met Thr Ala Gly Ser Trp Ile Tyr Ile Gly Xaa Ser Arg
      344

```

50 55 60
 Tyr Cys Ala Arg Tyr Leu
 65 70

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

Met His His Asp His Pro Asn Lys Leu Lys Ser Asp Glu Lys Ile Leu
 1 5 10 15
 Leu Asp Gln Met Val Ser His Phe Pro Asn Phe Glu Asp Asp Phe Lys
 20 25 30
 Asn Ala Ala Gln Gly Ala Trp Val Lys Asn Ala Thr Asp Glu Leu Lys
 35 40 45
 Asp Ile Ser Asn Asp Leu Glu Lys Ile Gln Asp Ile Lys Val
 50 55 60

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

Met Ser Leu Ala Glu Arg Xaa Lys Ala Xaa Lys Ala Phe Arg His Xaa
 1 5 10 15
 Val Lys Asn Met Asp Asp Val Arg Met Pro Phe Ser Ser Val His Asp
 20 25 30
 Ala Pro Ser Lys Ile Ile
 35

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

```

Met Lys Pro Asn Ser Lys Ser Asn Lys Lys Ile Met Lys Asn Tyr Asn
 1             5             10             15
Trp Glu Tyr Phe Lys Ala Gln Ile Asn Gln Lys Leu Ser Glu Pro Glu
      20             25             30
Thr Lys Lys Ile Tyr Ser Gln Arg Lys Ile Asp Val Glu Leu Val Phe
      35             40             45
Gly Ile Tyr Glu Gly Tyr Phe Gly Phe His Ser Asn Val Ser Ser Arg
      50             55             60
Asn
65

```

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

```

Met Trp Asn Phe Ile Lys Cys Val Phe Lys Phe Val Phe Ser Leu Val
 1             5             10             15
Ala Ile Thr Thr Leu Val Ala Gly Val Gly Val Val Ala Phe Ala Tyr
      20             25             30
Ile Phe Lys Lys Asp Phe Glu Asp Ile Glu Arg Lys Thr Lys Glu Ile
      35             40             45
Ile Ser Asp Ile Glu Ser Lys Asn Asn
                        346

```

50

55

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

```

Met Glu Ile Asp Met Leu Gly Asp Ala Tyr Glu Phe Leu Ile Gly Arg
 1             5             10             15
Phe Ala Ala Thr Ala Gly Lys Lys Ala Gly Glu Phe Tyr Thr Pro Gln
          20             25             30
Gln Val Ser Lys Ile Leu Ala Lys Ile Val Thr Asp Gly Lys Asp Lys
      35             40             45
Leu Arg His Val Tyr Asp Pro Thr Cys Gly Ser Gly Ser Leu Leu Leu
      50             55             60
Arg Val Gly Lys Glu Thr Gln Val Tyr Arg Tyr Phe Gly Gln Glu Arg
65             70             75             80
Asn Asn Thr Thr Tyr Asn Leu Ala Arg Met Asn Met Leu Leu His Asp
          85             90             95
Val Arg Tyr Glu Asn Phe Glu Ile Arg Asn Asp Asp Thr Leu Glu Asn
          100            105            110
Pro Ala Phe Leu Gly Asn Thr Phe Asp Ala Val Ile Ala Asn Pro Pro
          115            120            125
Tyr Arg Cys Glu Met Asp Ser Arg Phe Lys Ile
      130            135

```

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

```

Met Tyr Leu Lys Asp Thr Arg Ile Glu Ile Val Gly Val Asn Lys Lys
 1             5             10             15
Asp Pro Leu Gln Tyr Ala Glu Ala Ile Asp Lys Leu Val Ser Ser Gly
          20             25             30
Ser Phe Thr Arg Asn Glu Val Arg Ile Met Leu Gly Glu Glu Pro Ser
          35             40             45
Asp Asn Pro Glu Leu Asp Glu Tyr Leu Ile Thr Lys Asn Tyr Glu Lys
          50             55             60
Ala Asn Xaa Gly Glu Asn Asp Glu Lys Glu Lys Asp Glu Asn Thr Leu
65             70             75             80
Lys Gly Gly Asp Glu Asp Glu Ser Gly Asp
          85             90

```

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

```

Met Tyr Leu Ile Glu Pro Ile Arg Asn Gly Glu Tyr Ile Thr Asp Gly
 1             5             10             15
Ala Ile Ala Leu Ala Met Gln Val Tyr Val Asn Gln His Ile Phe Leu
          20             25             30
Asp Glu Asp Ile Leu Phe Pro Tyr Tyr Cys Asp Pro Lys Val Glu Ile
          35             40             45
Gly Arg Phe Gln Asn Thr Ala Ile Glu Val Asn Gln Asp Tyr Ile Asp
          50             55             60
Lys His Ser Ile Gln Val Val Arg Arg Asp Thr Gly Gly Gly Ala Val
65             70             75             80
Tyr Val Asp Lys Gly Ala Xaa Asn Met Cys Cys Ile Leu Glu Gln Asp
          85             90             95
Thr Ser Ile Tyr Gly Asp Phe His Arg Phe Tyr Gln Pro Ala Ile Lys
          100             105             110
Ala Leu His Thr Leu Gly Ala Thr Asp Val Ile Gln Ser Gly Arg Asn
          115             120             125

```

Asp Leu Thr Leu Asn Gly Lys Lys Val Ser Gly Asp Xaa Xaa Val Glu
 130 135 140
 Arg Cys
 145

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

Met Tyr Val Xaa Asp Asp Ala Leu Asn Asp Val Xaa Pro Ala Arg Xaa
 1 5 10 15
 Met Gly Met Val Ser Val Trp Tyr Lys Gln Glu Asp Ala Glu Ile Glu
 20 25 30
 Pro Leu Glu Glu Glu Val Asp Phe Thr Ile Thr Thr Val Glu Glu Leu
 35 40 45
 Leu Thr Ile Leu Pro Ile Lys Asn Asp Asn Xaa Arg Arg Lys Leu Trp
 50 55 60
 Ile Tyr Leu Leu Glu Lys Asp Gly Thr Ser Ile His Tyr Ser Thr Leu
 65 70 75 80
 Gly Glu Gly Tyr Pro Ile Val Leu Ile His Thr Val Leu Asp Asn Xaa
 85 90 95
 Ser Val Phe Asn Xaa Leu Ala Ala Gln Leu Pro Gln Ser Phe Gln Val
 100 105 110
 Val Leu Ile Asp Leu Pro Trp Thr Trp Leu Phe Leu Ile Asn Leu Val
 115 120 125
 Thr Leu Lys
 130

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

```

Met Gly Phe Gln Xaa Xaa Leu Ser Ile Lys Thr Xaa His Gly Gly Ala
 1           5           10           15
Ile Val Gln Ser Tyr Pro Leu Leu Met Arg Gln Glu Lys Ser Asn Asp
      20           25           30
Trp Asp Phe Lys Gln Ile Xaa Asp Glu Ile Leu Glu Asn Leu Asn Asn
      35           40           45
Glu Ser Ile Asp Thr Ile Gly Val Val Leu Arg Asn
      50           55           60

```

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

```

Met Gln Ser Tyr Pro Ser Thr Lys Phe Val Gln Phe Tyr Lys Asp Asp
 1           5           10           15
Val Ser Pro Ser Met Val Asp Gly Asn Gly Arg Leu Lys Ser Asp Thr
      20           25           30
Asn Val Ile Ser Ile Glu Gly Gly Lys Tyr Asp Glu Asn Lys
      35           40           45

```

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

```

Met Leu Lys Leu Arg Glu Ala Thr Asn Glu Tyr Ile Gly Ala Asn Leu
 1             5             10             15
Asp Pro Ser His Leu Trp Trp Gln Gly Ile Asp Pro Ile Ala Ala Ile
      20             25             30
Arg Ile Leu Gly Gln Ala Asn Ala Ile His His Phe His Ala Lys Asp
      35             40             45
Thr Tyr Ile Asn Gln Glu Asn Val Asn Met Tyr Gly Leu Thr Asp Met
      50             55             60
Gln Pro Tyr Gly Asn Val Ala Thr Arg Ala Trp Thr Phe Arg Thr Val
65             70             75             80
Gly Tyr Gly His Ser Pro Tyr Val Trp Ala Asp Ile Ile Ser Gln Leu
      85             90             95
Ile Ile Asn Gly Tyr Asp Tyr Val Leu Ser Ile Glu His Glu Asp Pro
      100            105            110
Ile Met Ser Val Glu Glu Gly Phe Gln Lys Ala Xaa Gln Thr Leu Lys
      115            120            125
Ser Val Asn Ile Tyr Asp Lys Pro Ala Asp Met Trp Trp Ala
      130            135            140

```

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

```

Met Val Gln Met His Leu Ile Gly Val Val Asn Ala Cys Ile Val Thr
 1             5             10             15
Phe Ser Gly Leu Val Ile Gly Val Lys Gly Met Pro Thr Pro Ile Ala
      20             25             30
Gly Ala Ile Val Leu Phe Gly Phe Asn Asn Ala Val Thr Ser Ile Val
      35             40             45
Thr Ile Ala Thr Val Ile Ile Val Ser Ile Val Leu Ala Tyr Ile Ile
      50             55             60
Gly Thr Leu Ile Asn Lys Phe Asn Leu Met Asn Ile Asn Phe Lys Met
65             70             75             80

```


Pro Ser Lys Lys Asn His Ile Lys Glu Ser Val
 85 90

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

Met	Leu	Ile	Leu	Ser	Lys	Trp	Gln	Gly	Val	Ile	Leu	Gln	Asp	Asp	Ile	1	5	10	15
Ala	Gln	Gly	Leu	Asn	Thr	Ser	Tyr	Glu	Thr	Ala	Glu	Lys	Val	Lys	His	20	25	30	
Gln	Tyr	Gly	His	Ala	Phe	Tyr	Asp	Ser	Ala	Ser	Asp	Gln	Asp	Ile	Phe	35	40	45	
Thr	Val	Glu	Gln	Val	Asp	Ser	Asp	Glu	Thr	Val	Gln	Tyr	Thr	His	Lys	50	55	60	
Asp	Leu	Ser	Asp	Phe	Ile	Glu	Ala	Arg	Val	Glu	Glu	Ile	Phe	Phe	Glu	65	70	75	80
Val	Phe	Asp	Val	Leu	Gln	Asp	Leu	Gly	Leu	Thr	Gln	Val	Asn	Gly	Gly	85	90	95	
Phe	Ile	Val	Thr	Gly	Gly	Ser	Thr	Asn	Leu	Leu	Gly	Val	Lys	Glu	Leu	100	105	110	
Leu	Ser	Asp	Met	Val	Ser	Glu	Lys	Val	Xaa							115	120		

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

```

Met Ile Phe His Gln Val Glu Val Asn Gln Tyr Ala Val Phe Gln Tyr
 1             5             10             15
Pro Pro Tyr Asp Ile Thr Leu Ser Thr Lys Ile Ala Glu Val Ile Lys
          20             25             30
Glu Tyr Asp Leu Asp Leu Leu His Met His Tyr Ala Val Pro His Ala
          35             40             45
Ile Cys Gly Ile Leu Ala Arg Glu Met Ser Gly Lys Asp Ile Lys Ile
          50             55             60
Met Thr Thr Leu His Gly Tyr
65             70

```

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

```

Met Xaa Xaa Thr Pro Thr Phe Xaa Phe Asn Asp Tyr His Ile Met Ile
 1             5             10             15
Val His Pro Trp Xaa Leu Asp Asp Val Leu His Ser Asp Tyr Gln Xaa
          20             25             30
Glu Val Asp Glu Glu Xaa Ile Ile Glu Ala Thr Xaa Xaa Leu Asp Tyr
          35             40             45
Tyr Ala Gly Leu Ser Phe Arg Thr Leu Val Pro Lys Tyr Pro Ala Met
          50             55             60
Ser Pro His Ile Asn Leu Ser Thr Thr Val His Ile Thr Gly
65             70             75

```

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

```

Met Thr His Tyr His Asn Val Ser Arg Lys Gln Gln Glu Val Xaa Leu
 1             5             10             15
Xaa Gly Gln Ile Xaa Pro Xaa Asn Thr Tyr His Asn Lys Glu Ile Tyr
      20             25             30
Ala Phe Ala Gly Tyr Leu Asn Xaa
      35             40

```

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

```

Met Gln Lys Pro Phe Tyr Thr Asn Val Leu Ile Ala Lys Leu Gln Ala
 1             5             10             15
Ile Tyr Arg Arg Val Tyr Glu Phe Thr Ala Glu Glu Lys Arg Thr Leu
      20             25             30
Thr Trp Gln Asp Ala Val Val Asp Leu Ser Gln Asp Ser Ile His Lys
      35             40             45
Gly Val Asp Thr Ile Phe Leu Ser Lys Thr Glu Met Xaa Ile Leu Glu
      50             55             60
Ile Leu Ile Ser Lys Lys Asn Gln Ile Gly Ser Arg Xaa Thr Ile Ile
      65             70             75             80
Thr Xaa Leu Trp Asp Asp Glu Ala Phe Val Ser Asp Asn Thr Leu Thr
      85             90             95
Val Asn Val Asn Arg Leu Arg Lys Lys Leu Ser Glu Ile Ser Met Asp
      100             105             110
Ser Ala Ile Glu Thr Thr Val Gly Lys Gly Tyr Met Ala His Glu
      115             120             125

```

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

354

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

```

Met Thr Leu Lys Asp Ile Ala His Val Gly Lys Phe Gly Cys Ala Asn
 1             5             10             15
Cys Tyr Ala Thr Phe Lys Asp Asp Ile Ile Asp Ile Val Arg Arg Val
          20             25             30
Gln Gly Gly Gln Phe Glu His Val Gly Lys Thr Pro His Ser Ser His
          35             40             45
Lys Lys Ile Ala Leu Lys Arg Lys Ile Glu Glu Lys Asn Glu Tyr Leu
          50             55             60
Lys Lys Leu Ile Glu Ile Gln Asp Phe Glu Glu Ala Ala Ile Val Arg
65             70             75             80
Asp Glu Ile Lys Ala Leu Lys Ala Glu Ser Glu Val Gln His Asp Asp
          85             90             95
Ala

```

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

```

Met Phe Ala Tyr Asp Gly Trp Ile His Val Gly Asn Val Ala Gly Glu
 1             5             10             15
Leu Lys Asn Pro Lys Arg Asp Leu Pro Leu Ala Ile Ser Val Gly Ile
          20             25             30
Gly Cys Ile Met Ala Val Tyr Leu Leu Ile Asn Ala Thr Phe Leu Leu
          35             40             45
Thr Leu Pro Ile Glu Leu Leu Ala Gly Asn Leu Asn Ala Ala Ser Arg
          50             55             60             65
          70             71
355

```

50 55 60
Tyr Ile Lys Asn Ile Ile Trp.
65 70

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

Met	Lys	Lys	Leu	Ala	Asn	Tyr	Leu	Trp	Val	Glu	Lys	Val	Gly	Asp	Leu
1				5					10					15	
Tyr	Val	Phe	Ser	Met	Thr	Pro	Glu	Leu	Gln	Asp	Asp	Ile	Gly	Thr	Val
			20					25					30		
Gly	Tyr	Val	Glu	Phe	Val	Ser	Pro	Asp	Glu	Val	Lys	Val	Asp	Asp	Glu
			35				40					45			
Ile	Val	Ser	Ile	Glu	Ala	Ser	Lys	Thr	Val	Ile	Asp	Val	Gln	Thr	Pro
			50				55				60				
Leu	Ser	Gly	Thr	Ile	Ile	Glu	Arg	Asn	Thr	Lys	Ala	Glu	Glu	Glu	Pro
65					70					75					80
Thr	Ile	Leu	Asn	Ser	Glu	Asn	Pro	Glu	Glu	Asn	Trp	Leu	Phe	Lys	Leu
				85					90					95	
Asp	Asp	Val	Asp	Lys	Glu	Ala	Phe	Leu	Ala	Leu	Pro	Glu	Ala		
				100					105				110		

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

```

Met Ile Gln Val His Gln Ala Arg Ile Ile Ala Gly Thr Gln Glu Gln
 1             5             10             15
Val Lys Ala Gln Leu Asp Asp Phe Ile Ala Thr Phe Glu Val Asp Glu
          20             25             30
Val Leu Val Ala Pro Leu Ile Pro Gly Ile Glu Gln Arg Cys Lys Thr
          35             40             45
Leu Lys Leu Leu Ala Glu Ile Tyr Leu
          50             55

```

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

```

Met Ile Gln Val His Gln Ala Arg Ile Ile Ala Gly Thr Gln Xaa Gln
 1             5             10             15
Gly Lys Ala Gln Leu Asp Asp Phe Ile Ala Xaa Xaa Xaa Val Asp Glu
          20             25             30
Val Leu Val Ala Pro Leu Ile Pro Gly Ile Val Gln Arg Cys Lys Thr
          35             40             45
Leu Lys Leu Leu Xaa Xaa Ile Tyr Leu
          50             55

```

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

```

Met Phe Asp Ser Ile Arg Glu Thr Ile Asp Tyr Ala Ala Glu Asn Asn
                                     357

```

1	5	10	15
Met Ser Phe Ala Asp Ile Met Val Lys Glu Glu Met Glu Leu Ser Gly			
20	25	30	
Lys Ser Arg Asp Glu Val Arg Ala Gln Met Lys Gln Asn Leu Asp Val			
35	40	45	
Met Arg Asp Ala Val Ile Lys Gly Thr Thr Gly Asp Gly Val Glu Val			
50	55	60	

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

Met Tyr Thr Gly Ser Asp Val Arg Thr Val Gly Asp Leu Gly Ser Ile			
1	5	10	15
Lys Gln Pro Leu Pro His Phe Leu Ile Pro Asn Val Pro Phe Asn Leu			
20	25	30	
Glu Thr Leu His Ile Ile Phe Pro Tyr Ser Leu Ser Met Ala Ile Val			
35	40	45	
Gly Leu Val Glu Ser Leu Leu Thr Ala Lys Ile Val Asp Asp Ala Thr			
50	55	60	
Asp Thr Tyr Ser Ser Lys Asn Arg Glu Ser Arg Gly Gln Gly Ile Ala			
65	70	75	80
Asn Met Ile Thr Gly Leu Phe Gly Gly Met Gly Gly Cys Ala Met Ile			
85	90	95	
Gly Gln Ser Val Ile Asn Val Lys Ser Gly Ala His Ser Arg Leu Ser			
100	105	110	
Thr Phe Thr Ala Gly Ile Val Leu Ile Phe Met Ile Ile Val Leu Gly			
115	120	125	
Gly Leu Val Val Gln Val Pro Met Pro Ile Leu Ala Gly Ile Met Val			
130	135	140	
Met Val Ser Val Gly Thr Phe Asp Trp Asn Ser Phe Lys Tyr Ile Lys			
145	150	155	160
Lys Ala Pro Xaa Asn Arg Cys Ser Cys Tyr Ala His Tyr Gly Asp Tyr			
165	170	175	
Arg Phe Asn Asp Ser			

180

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

```

Met Glu Gly Glu Thr Val Gly Ile Asn Asp Pro Asn Ile Glu Ile Tyr
 1              5              10              15
Ser Glu Thr Leu Asp Leu Tyr His Thr Leu Val Pro Leu Asn Gln Glu
      20              25              30
Leu His Lys Leu Arg Leu Lys Thr Gln Asn Leu Xaa Asn Glu Asn Tyr
      35              40              45
Asn Ile Asn Asp Val
50

```

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

```

Met Gln Xaa Xaa Asp Xaa Val Gly Phe Gly Lys Gly Tyr Met Ala Pro
 1              5              10              15
Leu Tyr Gly Ser Lys Lys Asn Xaa Val Tyr Asp Asn Lys Xaa Ser Asp
      20              25              30
Lys Asn Ser Val Gly Leu Pro Asn Ser Arg Ala Leu Ile Trp Gln Gln
      35              40              45
Phe Asp Tyr Asn Asn Ser Arg Glu Arg Xaa Asp Xaa Arg Pro Leu Val
50              55              60

```


(2) INFORMATION FOR SEQ ID NO:207:

(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

(2) INFORMATION FOR SEQ ID NO:208:

(A) LENGTH: 62 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

Met Cys Leu Arg Glu Asp Xaa Val Thr Asp Ala Asn Ile Val His His
1 5 10 15
Ile Ile Tyr Val Asp Glu Asp Phe Asn Lys Ala Leu Asp Leu Asp Asn
360

			20					25					30				
Leu	Met	Ser	Val	Cys	Tyr	Ser	Cys	His	Asn	Lys	Ile	His	Ala	Asn	Asp		
			35				40					45					
Asn	Asp	Lys	Ser	Asn	Leu	Lys	Lys	Ile	Arg	Val	Leu	Lys	Ile				
			50				55					60					

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

Met Lys Gln Ala Arg Ile Leu Phe Asp Glu Ser Lys Ala Met Ile Lys
1 5 10 15
Ala Ser Pro Xaa Leu Arg Glu Asn Phe Arg Pro Leu Arg Asp Glu Ile
20 25 30
His Tyr Asp Ala Leu Tyr Leu Lys Ile Cys Thr Gly Phe Arg Gln
35 40 45

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

Met	Lys	Asn	Ser	Tyr	Gln	Ala	Gln	Lys	Val	Ile	Glu	Glu	Val	Ile	Lys
1				5					10					15	
Glu	Lys	Pro	Lys	Ala	Arg	Trp	Leu	Phe	Leu	Thr	Leu	Pro	Thr	Lys	Asn
			20					25					30		
Ala	Ile	Asp	Gly	Asp	Thr	Leu	Glu	Gln	Ser	Leu	Lys	His	Leu	Thr	Lys
		35					40					45			

Ala Phe Asp Arg Leu Ser Arg Tyr Lys Lys Val Lys Gln Asn Leu Val
 50 55 60
 Gly Phe Met Arg Ser Thr Glu Val Thr Ala Asn Lys Asn Asp Gly Ser
 65 70 75 80
 Tyr Xaa Gln His Met His Val Leu Val Cys Val Glu Asn Ala Tyr Phe
 85 90 95
 Arg Lys Lys Glu Asn Tyr Leu Thr Gln Arg Arg Met Gly
 100 105

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

Met Tyr Gly Glu Leu Leu Lys Leu Lys Asn Val Glu Val Arg Leu Thr
 1 5 10 15
 Asp Ile Ala Gly Phe His Ala Lys Gly Tyr Ile Phe Glu His Lys Asp
 20 25 30
 Tyr Ser Ser Met Val Ile Gly Ser Ser Asn Leu Thr Ser Asn Ala Leu
 35 40 45
 Lys Val Asn Ser Glu His Asn Val Leu Leu Ser Thr Met Lys Asn Gly
 50 55 60
 Asp Leu Val Asp Ser Val Lys Asn Glu Phe Glu Leu Leu Trp Gln Lys
 65 70 75 80
 Ser Thr Pro Leu Thr Glu Gln Trp Ile Asn Ser Tyr Lys Glu Ser Xaa
 85 90 95
 Glu Tyr Arg Ser Leu Glu Lys Leu Ala Glu Val Glu Gln Thr Gln Met
 100 105 110
 Leu Leu Ala Asp Lys Val Lys Lys Ser Val Glu Ile Val Pro Asn Leu
 115 120 125
 Met Gln Ala Glu Ala Leu Arg Ser Leu Lys Ala Ile Arg Asp Lys Xaa
 130 135 140
 Lys Asp Lys Ala Leu Ile Ile Ser Cys Asn Trp Val Gln Gly Lys Thr
 145 150 155 160
 Ile Leu Cys Ala Leu Asp Cys
 165

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

```

Met Tyr Gln Gln Ser Ser Phe Lys Glu Asn Leu Ile His Trp Phe Asp
 1             5             10             15
Glu Asn Gln Arg Glu Met Pro Trp Arg Gln Thr Thr Asn Pro Tyr Tyr
      20             25             30
Ile Trp Leu Ser Glu Val Met Leu Gln Gln Thr Gln Val Lys Thr Val
      35             40             45
Ile Asp Tyr Tyr His Arg Phe Gly Xaa Arg Phe Pro Thr Val Glu Val
      50             55             60
Leu Ser Gln Ala Ser Glu Asp Glu Val Leu Lys Tyr Trp Glu Gly Leu
      65             70             75             80
Gly Tyr Tyr Ser Arg Ala Arg Asn Phe His Thr Ala Ile Lys Glu Val
      85             90             95
Xaa Asp Lys Tyr Glu Gly Leu Val Pro Lys Asp Pro Asp Gln Phe Lys
      100            105            110
Ala Leu Lys Gly Val Gly Pro Tyr Thr Gln Ala Ala Val Met Ser Ile
      115            120            125
Ala Tyr Asn Val Pro Leu Ala Thr Val Asp Gly Asn Val Phe Arg Val
      130            135            140
Trp Ser Arg Leu Asn Asp Asp Tyr Arg Asp Ile Lys Leu Gln Ser Thr
      145            150            155            160
Arg Lys Ser Tyr Glu Gln Glu Leu Leu Pro Tyr Val Thr Thr Glu Ala
      165            170            175
Gly Thr Phe Asn Gln Ala Met Met Glu Leu Gly Ala Leu Ile Cys Xaa
      180            185            190
Pro Lys Asn Pro Leu Cys Leu Phe Xaa Pro Val Gln Glu Asn Cys Glu
      195            200            205
Ala Phe Asp Lys Gly Pro Phe Glu Lys Leu Pro Val Lys Ser Lys Asn
      210            215            220
Val Ser Lys Xaa Val Ile Glu Gln Ser Val Xaa Leu Ile Arg Asn Asn
      225            230            235            240

```

Gln Gly Gln Tyr Leu Leu Gln Lys Arg Arg Glu Xaa Leu Xaa Tyr Gly
 245 250 255
 Met Trp Gln Xaa Pro Met Xaa Asp Ser Glu His Xaa Arg Arg Lys Met
 260 265 270
 Xaa Glu Lys Ile Gly His Asp Ile Xaa Pro Xaa Glu Thr Pro Ile Xaa
 275 280 285
 Glu Leu Thr His Gln Phe Thr His Leu Thr Trp Lys Ile Lys Val Tyr
 290 295 300
 Ala Ala Ser Gly Ala Ile Asn Ile Xaa Thr Leu Pro Asp Asp Met Xaa
 305 310 315 320
 Trp Val

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

Met Ser Asn Thr Asp Lys Tyr Leu Arg Asp Ile Ala Arg Glu Leu Lys
 1 5 10 15
 Gly Ile Arg Lys Glu Leu Gln Lys Arg Asn Glu Thr Val Ile Ile Asp
 20 25 30
 Ala Asn Leu Asp Ser Val Arg Ser Ala Val Leu Xaa Asn Lys Xaa Lys
 35 40 45
 Pro Lys Tyr Asn Glu Pro Leu Phe
 50 55

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

```

Met Lys His Phe Glu Ala Gly Ala Asp Gln Ser Ile Val Gln Gly Phe
 1             5             10             15
Gln Tyr Gln Gln Thr Val Thr Arg Val Asp Asn Pro Thr Ile Leu Leu
      20             25             30
Lys Leu Leu Arg Asn Leu Leu Gln Leu Thr Pro Ile Ser Tyr
      35             40             45

```

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

```

Met Thr Val Phe Val Met Gln Leu Gln Ser Asn Leu Asn Ser Ile Glu
 1             5             10             15
Glu Leu Ile Ser Gln Ser Arg Trp Ser Tyr Arg Xaa Xaa Pro Arg Thr
      20             25             30
Val Asn Tyr Xaa Tyr Asn Gln Asp Lys Leu Met His Xaa Leu Gly Asp
      35             40             45
Ile Xaa Ala Gln Tyr Gly Xaa Gln His Asp Thr Gly Leu Xaa Pro His
      50             55             60
Glu Trp Xaa Tyr His Ile Ala Pro Arg Gly Xaa Ala Asp Ile Ala Gln
      65             70             75             80
His Asn Arg Asp Gly Gln Pro Ile Tyr Val Ser Leu Ser Tyr Ser Tyr
      85             90             95
Pro Tyr Ile Val Cys Val Val Asp Lys Xaa Pro Gly Gly Ile Asp Ile
      100            105            110
Glu Lys Ile Ser Xaa Arg Leu Xaa Trp Arg Asn Arg
      115            120

```

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids

365

- (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

```

Met Asn Ala Leu Leu Asn His Met Asn Thr Glu Gln Xaa Glu Ala Val
 1             5             10             15
Lys Thr Thr Glu Gly Pro Leu Xaa Xaa Met Ala Gly Ala Gly Ser Gly
      20             25             30
Lys Thr Arg Val Leu Thr His Arg Ile Ala Tyr Leu Leu Asp Glu Lys
      35             40             45
Asp Val Ser Pro Tyr Asn Val Leu Ala Ile Thr Phe Thr Asn Lys Ala
      50             55             60
Ala Arg Glu Met Lys Glu Arg Val Gln Lys Leu Val Gly Asp Gln Ala
      65             70             75             80
Glu Val Met Arg Met Ser Thr Phe His Ser Met Cys Val Arg Ile Xaa
      85             90             95
Thr Ser
  
```

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

```

Met Lys Ile Ala Ile Val Gly Ser Gly Asn Gly Ala Val Thr Ala Ala
 1             5             10             15
Val Asp Met Val Ser Lys Gly His Asp Val Lys Leu Tyr Cys Arg Asn
      20             25             30
Gln Ser Ile Ser Lys Phe Gln Asn Ala Ile Glu Lys Gly Gly Phe Val
      35             40             45
Ala Arg Lys Met Thr Leu Leu Lys Asp Cys Gly Ile Ser Leu Arg Thr
      50             55             60
  
```

Ser Val Val Thr Phe Gly Thr Glu Ser
65 70

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

Met	Lys	Ile	Ala	Ile	Val	Gly	Ser	Gly	Asn	Gly	Ala	Val	Thr	Ala	Ala	1	5	10	15
Val	Asp	Met	Val	Ser	Lys	Gly	His	Asp	Val	Lys	Leu	Tyr	Cys	Arg	Asn	20	25	30	
Gln	Ser	Ile	Ser	Lys	Phe	Gln	Asn	Ala	Ile	Glu	Lys	Gly	Gly	Phe	Asp	35	40	45	
Phe	Asn	Asn	Glu	Gly	Asp	Glu	Arg	Phe	Val	Lys	Phe	Thr	Asp	Ile	Ser	50	55	60	
Asp	Asp	Met	Glu	Tyr	Val	Leu	Lys	Asp	Ala	Glu	Ile	Xaa	Gln	Val	Ile	65	70	75	80
Ile	Pro	Ser	Ser	Tyr	Ile	Glu	Tyr	Tyr	Ala	Asp	Gly	Asn	Gly	Arg	Ala	85	90	95	
Cys	Asn																		

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

Met Asn Pro Leu Leu Ile Ile Gly Lys Arg Ser Tyr Ser Leu Tyr Leu
367


```

      1             5             10             15
Trp His Tyr Pro Ile Ile Val Phe Val Asn Ser Tyr Tyr Xaa Gln Gly
      20             25             30
Gln Ile Pro Val Tyr Val Tyr Ile Ile Glu Ile Val Leu Thr Ala Leu
      35             40             45
Met Ala Glu Ile Ser Tyr Arg Phe Ile Glu Thr Pro Ile Arg Lys Lys
      50             55             60
Gly Phe Lys Ala Cys Ala Phe Xaa Pro Lys Lys Lys Gly Gln Cys Ala
      65             70             75             80
Arg Thr Xaa Leu Xaa Ile Leu Leu Leu Ala Pro Ser Phe Val Cys Ser
      85             90             95
Xaa Gly Gln Gly Gly Cys Thr Trp Gln Thr Thr
      100             105

```

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

```

Met Asp Gly Ser Gln Val Thr Gly Val Ile Val Thr Gly Thr Xaa Asn
      1             5             10             15
Arg Glu Asn Tyr Gly Ile Xaa Phe Thr Gln Ala Leu Glu Thr Gly Gly
      20             25             30
Val Met Leu Gly Lys Asp Gly
      35

```

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

```

Met Arg Leu Ser Cys Phe Ile Gln Lys Lys Xaa Xaa Pro Ile Asn Gln
 1             5             10             15
Met Leu Ile Asp Glu Ser Met Pro Phe Ile Val Ile Gly Lys Pro Thr
      20             25             30
Ser Asp Ile Asp His Gln Phe Thr His Ile Asp Asn Asp Asn Ile Leu
      35             40             45
Ala Ser Xaa Asn Leu Thr Arg His Val Ile Glu Gln Gly Val Asp Glu
      50             55             60
Leu Ile Phe Ile Thr Glu Lys Gly Asn Phe Glu Val Ser Lys Asp Arg
      65             70             75             80
Ile Pro Gly Phe Glu Thr Val Ala Ser Pro Phe Asn Leu Asp Tyr Gln
      85             90             95
Ile Ile Glu Thr Ser Asn Glu Arg Glu Val Ile Leu Asn Tyr Met Gln
      100            105            110
Asn Leu His Thr Arg Leu Lys Asp Pro Asn Ile Lys Gln Ala Ile Ile
      115            120            125
Ser Leu Asp Ala Met Leu His Leu Ala Ile Leu Ser Val Leu Tyr Glu
      130            135            140
Leu Asn Ile Glu Ile Pro Lys Asp Val Met Thr Ala Thr Phe Asn Asp
      145            150            155            160
Ser Tyr Leu Xaa Glu Ile Ala Ser Pro Pro Gln Xaa Cys Ile Asp Ile
      165            170            175
Lys Pro Arg Met Leu Gly Gln Gln Ala Gly Ser Ala Ile Leu Xaa Ile
      180            185            190
Leu Lys Asn Lys Ala Gln Asp Val Ile Glu Leu Val Ile Ile Asp Thr
      195            200            205
Arg Ile Xaa Asn Lys Lys Ile Asn Thr Ala Ile Ala Lys Gly Phe Ser
      210            215            220
Asn Glu Leu Ser Asn Gly Trp Glu Arg Ser Lys
      225            230            235

```

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

```

Met Xaa Xaa Asp Xaa Thr Xaa Ser Xaa Pro His Leu Xaa Ser Gln Thr
 1             5             10             15
Ile Xaa Xaa Pro Xaa Asp Gly Val Ser Leu His Leu Xaa Thr Xaa Xaa
      20             25             30
Xaa Tyr Ala Xaa Xaa Xaa Met Ala Xaa Pro Asp Arg Leu Ser Lys Ser
      35             40             45
Xaa Ser Arg Ser Arg Tyr Xaa
 50             55

```

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

```

Met Ile Thr Leu Gln Met Val Glu Ile Leu His Gly Phe Met Met Gln
 1             5             10             15
Ile Leu Glu Lys Leu Ser Lys Gln Gln Ile Glu Ala Ile Ile Val Thr
      20             25             30
Gly Thr Arg Ala Glu Glu Leu Gln Leu Arg Leu Lys Leu Ala Glu Val
      35             40             45
Glu Val Pro Ile Ile Val Glu Arg Asp Ile Tyr Lys Ala Thr Ala Lys
      50             55             60
Thr Met Asp Tyr Lys Val Ser Gln Leu Gln Tyr Gln Thr Ile His Gln
      65             70             75             80
Leu Ala Pro Met Leu Asp Asn
      85

```

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

```

Met Thr Asp Gly Pro Ile Lys Val Asn Ser Glu Ile Gly Ala Leu Lys
 1             5             10             15
Thr Val Leu Leu Lys Arg Pro Gly Lys Glu Leu Glu Asn Leu Val Pro
      20             25             30
Asp Tyr Leu Asp Gly Leu Leu Phe Asp Asp Ile Pro Tyr Leu Glu Val
      35             40             45
Ala Gln Lys Glu His Asp His Phe Ala Gln Val Leu Arg Glu Glu Gly
      50             55             60
Val Glu Val Leu Tyr Leu Glu Lys Leu Ala Ala Glu Ser Ile Glu Asn
      65             70             75             80
Pro Gln Val Arg Ser Glu Phe Ile Asp Asp Val Leu Ala Glu Ser Lys
      85             90             95
Lys Thr Ile Leu Gly His Glu Glu Glu Ile Lys Thr Leu Phe Ala Thr
      100             105             110
Leu Ser

```

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

```

Met Lys Ser Lys Leu Ser Asn Ser Gly Ile Asp Val Thr Val Lys Asp
 1             5             10             15
Val Glu Lys Tyr Met Asn Arg Tyr Asn Glu Val Met Met Gly Lys Xaa
      20             25             30
Gly Glu Lys Ala Lys Glu Leu Cys Leu Ser Leu Leu Pro Tyr
      35             40             45

```

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

```

Met Pro Ser Gly Leu Pro Ile His Glu Trp Leu Met Leu Lys Gln Phe
 1           5           10           15
Ser Lys Tyr Lys Ser Ala Pro Ser Leu Pro Ile Leu Arg Arg Gly Gln
          20           25           30
His Tyr Lys Leu His Phe Asp Phe Asp Ala Thr Pro Ala Gly Ser Val
          35           40           45
Tyr Phe Ile Ile Ile Phe Tyr Asn Lys Asn Gly Thr Asn
50           55           60

```

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

```

Met Met Asn Ala Ala Ser Thr Ser Leu Ile Phe Arg Cys Leu Thr Ile
 1           5           10           15
Thr Glu Met Thr His Gln Asp Asp Leu Glu Tyr Lys Ser Met Arg Val
          20           25           30
Thr Lys Ile Asp Asp Asn Gln Tyr Gly Asn Asp Arg Ile Asn Val Ile
          35           40           45
Ile Ala Glu Pro Ser Asp Thr Tyr Pro Thr Ile Ser Asn Asp Phe Leu
50           55           60
Lys Leu Phe Gly His Val Trp Leu Val Glu Arg Trp Met Asp Asp Asp
65           70           75           80
Ile Lys Glu Asn Ile Lys Gln Leu Lys Asp Asp Leu Gln Ser Gln Asp
          85           90           95

```

Thr Leu Thr Ala Ile Asn Leu Ile Ser Tyr Gly Ser Lys Ser Asn Val
 100 105 110
 Ser Ala Thr Tyr Val Ala Gln His Leu Asp Cys Lys Val Tyr Arg Thr
 115 120 125
 Ser His Glu Asp Asp Asp Leu Lys Glu Trp Leu Thr Glu His Val Pro
 130 135 140
 Arg Lys
 145

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

Met Asn Met Phe Gly Leu Gly Asn Met Met Met Arg Tyr Val Met Lys
 1 5 10 15
 Lys Lys Asn Val Asp Ser Leu Pro Thr Leu Ile Asn Gln Ala Ile Glu
 20 25 30
 Pro His Ile Lys Leu Ile Ala Cys Xaa Met Ser Met Asp Val Met Gly
 35 40 45
 Ile Gln Arg Glu Glu Leu Arg Asp Glu Val Glu Tyr Gly Gly Val Gly
 50 55 60
 Thr Tyr Ile Gly Ala Thr Glu Asn Ala Asn His Asn Leu Phe Ile
 65 70 75

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

```

Met Ser Pro Lys Leu Gly Ala Val Thr Gly Asn Pro Arg Ile Arg Asn
 1           5           10           15
Lys Ser Ser Ile Leu Gly Lys Ile Gln Thr Ile Glu Tyr Ala Ser Leu
          20           25           30
Ile Gly Cys Ile Lys Arg Ser Gln Thr Leu Ala Gly Ala Val Asn Thr
        35           40           45
Ile Ser Gly Val Phe Thr Leu Phe Lys Lys Ser Ala Val Val Asp Val
        50           55           60
Gly Tyr Trp Asp Thr Asp Met Ile Thr Glu Asp Ile Ala Val Ser Trp
65           70           75           80
Lys Leu His Leu Arg Gly Tyr Arg Ile Lys Tyr Glu Pro Leu Ala Met
          85           90           95
Cys Trp Met Leu Xaa Pro Glu Thr Leu Gly Gly Leu Trp Lys Gln Arg
        100           105           110
Val Arg Trp Ala Gln Arg Gly Asp Thr Lys Tyr Tyr Tyr Glu Thr Phe
        115           120           125
Xaa Ser Thr Xaa Thr Lys Thr Lys Gly Phe Pro Leu Tyr Ile Val Ile
        130           135           140
Val
145

```

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

```

Met Thr Asn His Asp Gly Asp Gly Glu Lys Gly Glu Glu Xaa Phe Leu
 1           5           10           15
Lys Lys Ile Leu Gly Glu Glu Tyr Thr Gly Asn Val Xaa Glu Gly Asn
          20           25           30
Gly Arg Asn Phe Val Thr Gln Pro Ala Ser Ser Xaa Thr Ala Val Lys
        35           40           45
Ser Val Asn Ile Pro Asp Ser Ile Lys Thr Leu Lys Val Gly Asp Thr
        50           55           60
Ile Arg Phe Lys Cys Cys Ser Arg Ala Ile

```

65

70

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

```

Met Tyr Val Pro Leu Ser Val Asn Ala Asn Lys Gln Tyr Arg Phe Asn
 1             5             10             15
Ile Met Leu Glu Asp Ile Lys Ala Tyr Leu Pro Lys Glu Lys Xaa Trp
      20             25             30
Asp Val Phe Leu Glu Val Gln Ile Gly Thr Glu Val Phe Xaa Val Arg
      35             40             45
Val Gly
      50

```

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

```

Met Asn Ile Glu Xaa Asp Ile Asn Gly Arg Pro Lys His Ile Tyr Ser
 1             5             10             15
Ile Tyr Arg Xaa Met Met Lys Gln Lys Lys Gln Phe Asp Gln Ile Phe
      20             25             30
Asp Leu Leu Ala Ile Arg Val Ile Val Asn Ser Ile Asn Asp Cys Tyr
      35             40             45
Ala Ile Leu Gly Leu Val His Thr Leu Trp Lys Pro Met Pro Gly Arg
      50             55             60

```



```

Phe Lys Asp Tyr Ile Ala Met Pro Lys Gln Asn Leu Tyr Gln Ser Leu
65          70          75          80
His Thr Thr Val Val Gly Pro Asn Gly Asp Pro Leu Glu Ile Gln Ile
          85          90          95
Arg Thr Phe Asp Met His Glu Ile Ala Glu His Gly Val Ala Ala His
          100         105         110
Trp Ala Tyr Lys Glu Gly Lys Lys Val Ser Glu Lys Asp Gln Thr Tyr
          115         120         125
Gln Asn Lys Leu Asn Trp Leu Lys Glu Leu Ala Glu Ala Asp His Thr
          130         135         140
Ser Ser Asp Ala Gln Glu Phe Met Glu Thr Leu
145          150          155

```

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

```

Met Lys Leu Lys Gly Lys Asn Xaa Ile Ile Leu Thr Gly Leu Asp Arg
1          5          10          15
Gly Tyr Val Phe Glu Glu Gly Met Ala Ser Val Val Leu Lys Asp Asp
          20          25          30
Met Ile Met Gly Met Leu Ser Pro Xaa Val Arg Lys Arg Ser Gly Asn
          35          40          45
Arg Thr
50

```

(2) INFORMATION FOR SEQ ID NO:234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

```

Met Ala Ile Gly Ser Ser Lys Ile Asn Phe Ser Asp Ile Xaa His Tyr
 1             5             10             15
Val Thr Gly Xaa Thr Asp Thr Lys Ala Thr Phe Leu Leu His Asn Val
          20             25             30
Arg Met Pro Arg Met Ile Ala Gly Leu Phe Ile Gly Gly Ala Leu Ala
      35             40             45
Val Ser Gly Leu Gly
      50

```

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

```

Met Gly Pro Ser Ser Ser Gly Gly Ile Thr Val Ile Gln Ile Leu Lys
 1             5             10             15
Leu Leu Glu His Val Asp Leu Pro Ser Met Gly Pro Arg Ser Val Asp
          20             25             30
Tyr Leu His His Leu Ile Gln Ala Met His Leu Ala Tyr Ser Asp Arg
      35             40             45
Ala Gln Tyr Leu Ala Asp Asp Asn Phe His Glu Glu Cys Arg Tyr Ser
      50             55             60
His
      65

```

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

```

Met Pro Ser Lys Leu Leu Lys Gln Lys Lys Ile Lys Thr Ile His Arg
 1           5           10           15
Leu Thr Leu Ile Thr Thr Gln Leu Val Ala Gly Glu Gly Gly Tyr Val
      20           25           30
Asp Gly Tyr Ile Glu Thr Ile Glu Glu Thr Asp Ser Ser Ala Ile Asp
      35           40           45
Ile Asp Tyr His Thr Ala Val Xaa Cys Glu Xaa Xaa His Val Gly Gly
      50           55           60
Ile His
65

```

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

```

Met His Phe Thr Leu Val Phe Ile Leu Phe Leu Gly Gly Ile Tyr Met
 1           5           10           15
Thr Phe Glu Lys Glu Xaa Val Leu Glu Thr Leu Phe Pro Glu Asp Val
      20           25           30
Leu Ser Ile Ala Lys Gly Leu Thr Asp Gly Glu Val Glu Phe Leu Gln
      35           40           45
Gln Val Asp Ser Leu Leu Glu Ser Lys Tyr Arg Glu Asn Ile Asn Xaa
      50           55           60
His Trp Ile Asp Ala Thr Val Pro Glu Asp Tyr Phe Lys Asp Leu Gly
      65           70           75           80
Glu Leu Asn Tyr Phe Asn Asn Pro Leu Leu Tyr Lys Asp Arg Pro Asn
      85           90           95
Ala Lys Met Pro Ser Gln Leu Phe Gln Phe Phe Met Ser Tyr Leu Leu
      100           105           110
Ala Arg Phe Asp Ile Ser Leu Ala Thr Leu Leu Gly Val His Gln Gly
      115           120           125
378

```

Leu Gly His Asn Thr Phe Tyr Phe Gly Gly Ser Lys Glu Gln Ile Ala
 130 135 140
 Lys Tyr Val Pro Lys Leu Gln Ser His Glu Leu Arg Thr Cys Phe Ala
 145 150 155 160
 Leu Thr Glu Pro Glu His Gly Ser Asp Val Ala Gly Gly Leu Glu Thr
 165 170 175
 Val Xaa Glu Arg Gln Gly Asp Thr Trp Val Ile Asn Gly Glu Lys Lys
 180 185 190
 Trp Ile Gly Gly Ala His Val Ser Asp Val Ile Pro Val Phe Ala Val
 195 200 205
 Asn Lys Lys Thr Gly Lys Pro His Cys Phe Val Val Arg Pro Glu Gln
 210 215 220
 Asp Gly Val Asp Ile Glu Val Asn
 225 230

(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

Met Asn Leu Thr Asn Ser Phe Leu Ile Trp Lys Met Xaa Arg Thr Met
 1 5 10 15
 Val Val Phe Gly Gln Thr Lys Ala Xaa Phe Ala Lys Leu Gly Asn Ser
 20 25 30
 Gln Gly Lys Ser Val Xaa Glu Ala Asn Asn Val Glu Asp Ala Val Asp
 35 40 45
 Lys Val Gln Asp Ile Ile Xaa Pro Asn Asp Val Val Leu Leu Ser Pro
 50 55 60
 Ala Cys Ala Ser Trp Asp Gln Tyr Ser Thr Phe Glu Glu Arg Gly Glu
 65 70 75 80
 Lys Phe Ile Glu Arg Phe Arg Xaa His Leu Pro Ser Tyr
 85 90

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

```

Met Lys Ser Phe Thr Asp Leu Glu Lys Xaa Asn Leu Glu His Thr Tyr
 1             5             10             15
Val Asp Gly Gln Leu Val Val Ser Gly Arg Met Pro Ala Arg Lys Pro
      20             25             30
Asn Ile Gln Glu Asp His Tyr Phe Gly Ala Ile Ser Lys His Asp Ser
      35             40             45
Ser Asp Glu Phe Val Met Phe Ile Leu Arg Ala Asn Gln Asp Gly Ile
      50             55             60
Thr Leu Val Glu Lys Thr Asn Phe Leu Gly Val Asn Gly Ser Ala Thr
65             70             75             80
Tyr Xaa Ile Thr Leu Asn Gln Val Val Val Pro Gln Ser Gln Ile Ile
      85             90             95
Thr His Asp Ala Lys Pro Val Cys Gly Asn Leu Phe Ala Arg Asn Leu
      100            105            110
Leu Leu Thr Lys Phe Gln
      115

```

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

```

Met Lys Glu Asn Asp Val Val Leu Arg Xaa Val Thr Lys Leu Val Val
 1             5             10             15
Phe Ile Leu Leu Thr Phe Gly Phe Tyr Val Phe Phe Ala Gly His Asn
      20             25             30
Asn Pro Gly Gly Gly Phe Ile Gly Gly Leu Ile Phe Ser Ser Ala Phe
      380

```

```

          35          40          45
Ile Leu Met Phe Leu Ala Phe Asn Val Glu Glu Val Leu Glu Ser Leu
  50          55          60
Pro Ile Asp Phe Arg Ile Leu Val Ile Ile Gly Ala Leu Val Ser Ser
  65          70          75          80
Ile Thr Ala Ile Ile Pro Met Phe Leu Gly Lys Pro Phe Gly Ala Gln
          85          90          95
Tyr

```

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

```

Met Gln His His Lys Val Ala Ile Ile Gly Ala Gly Ala Ala Gly Ile
  1          5          10          15
Gly Met Ala Ile Thr Leu Lys Asp Phe Gly Ile Thr Asp Val Ile Ile
          20          25          30
Leu Glu Lys Gly Thr Val Gly His Ser Phe Lys His Trp Pro Lys Ser
          35          40          45
Thr Val Arg Ser Arg His His Leu Arg Leu Met Asp Leu Ala Cys Leu
          50          55          60
Ile
  65

```

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

```

Met Lys Tyr Lys Lys Leu Lys Val Leu Lys Gly Val Thr His Gly Ser
 1             5             10             15
Ser Val Phe Ile Asp Val Thr Ile Val Val Asp Ala Asn Leu Ser Leu
          20             25             30
Val Glu Ala His Gln Ile Cys Asp Asn Val Glu His His Leu His Xaa
          35             40             45
Lys Gly Ile Ser Ser Val Tyr Val His Pro Glu Pro Asp His Leu
 50             55             60

```

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

```

Met Met Leu Leu Ile Phe Asn Asn Ile Gly Ile Ile Ser Ile Thr Asp
 1             5             10             15
Phe Thr Asn Arg Ala Thr Met Gln Asn Glu Asn Lys Asp Pro Tyr Gly
          20             25             30
Glu Lys Leu Ala Tyr Gly Ile Ala Phe Asn Gly Ser Val Asp Met Gln
          35             40             45
Gly Asp Lys Gln Val Thr Ile Pro Lys Tyr Ser Val Val Thr Ile Thr
 50             55             60
Gly Glu Asn Ser Lys Asn Tyr Arg Val Thr Ala Asp Asn Lys Thr Tyr
 65             70             75             80
Tyr Val Ser Lys Asp Lys Leu Glu Tyr Phe Asn Pro Ala Gly Leu Tyr
          85             90             95
Gln Thr His Ser Phe Lys Lys Leu Ala Pro Tyr Met Lys Ser Asn Tyr
          100            105            110
Ser Asn Tyr Tyr Ala Tyr Phe Asn Ser Gln Leu His Lys Lys His Arg
          115            120            125
Phe Ser Tyr Lys Thr Leu Val Pro Asp Asp Asp Asn Arg Xaa Arg Leu
          130            135            140
Xaa Pro Xaa Thr Gln Xaa Pro Xaa Gln Leu Xaa Xaa Xaa Arg Trp Xaa
145            150            155            160

```

(2) INFORMATION FOR SEO ID NO:244:

(A) LENGTH: 40 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

(2) INFORMATION FOR SEQ ID NO:245:

(A) LENGTH: 84 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

```

Met Met Ala Leu Lys Thr Lys Val Leu Pro Lys Thr Val Val Ile Ile
 1              5              10              15
Thr Val Ile Ser Ala Leu Thr Pro Lys Asp Cys Ile Asp Leu Phe His
      20              25              30
Lys Thr Ile Pro Gly Met Val Ala Asn Asn Ala Asn Ile Ser Pro Lys
      383

```


35 40 45
 Pro Gly Thr Arg Tyr Lys Ala Lys Ala Thr Asn Thr Asn Val Ile Gly
 50 55 60
 Ala Ile Ile Val Gly Leu Gly Leu Gly Phe Trp Lys His Ile Xaa His
 65 70 75 80
 Ser Pro Tyr Phe

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

Met Ser Gln Leu Leu Ala Val Cys Pro Met Gly Leu Glu Ala Gly Val
 1 5 10 15
 Ala Arg Glu Ile Gln Glu Leu Gly Tyr Glu Thr Asn Cys Trp Lys Met
 20 25 30
 Gly Arg Xaa Phe Cys Gly Arg Arg Thr Gln Xaa Ala Ile Gly Xaa Gly
 35 40 45
 Lys Phe Met Gly Trp Ala Gln Glu Asp Pro Ser Lys Leu Trp Gly Gly
 50 55 60
 Pro Val Leu Thr Gln Gln Thr Val Asp Gly Phe Ile Arg Thr Asn Pro
 65 70 75 80
 Arg Ala Pro Leu Gly Ile Phe Tyr Trp
 85

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

```

Met Ser Tyr Ile Trp Thr Asp Gln Asn Arg Tyr Glu Gly Trp Leu Glu
 1             5             10             15
Val Glu Ile Leu Ala Cys Glu Gly Trp Ser Glu Leu Gly His Ile Pro
      20             25             30
Lys Ala Asp Val Gln Lys Ile Arg Gln Asn Ala Lys Val Asn Val Glu
      35             40             45
Arg Ala Gln Glu Ile Glu Gln Glu Thr Arg His Asp Val Val Ala Phe
      50             55             60
Thr Arg Gln Val Ser Glu Thr Leu Gly Glu Glu Arg Lys Trp Val His
      65             70             75             80
Tyr Gly Leu Thr Ser Thr Asp Val Val Asp Thr Ala Leu Ser Phe Val
      85             90             95
Ile Lys Gln Ala Asn Asp Ile Ile Glu Lys Asp Leu Glu Arg Phe Ile
      100            105            110
Asp Val Leu Ala Glu Lys Ala Lys Asn Tyr Lys Tyr Thr Leu Met Met
      115            120            125
Gly Arg Thr His Gly Val His Ala Glu Pro Asn Tyr Ile Trp Val Ser
      130            135            140
Lys Met Ala Leu Trp Tyr Thr Glu Met Gln Xaa
145            150            155

```

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

```

Met Xaa Ala Leu Leu Ser Ile Xaa Xaa Ile Xaa Thr Pro Glu Ser Ala
 1             5             10             15
Leu Ser Ala Pro Lys Asp Lys Tyr Ile Thr His Pro Xaa Ile Xaa Gly
      20             25             30
Ser Val Glu Gly Tyr Xaa Thr Met Asp Leu Xaa Xaa Ala Leu Ala Phe
      35             40             45
Xaa Gly Xaa Ile Asp Asn Gly Tyr Lys Phe Lys Gly Leu Thr Gly Ser
      50             55             60

```

Xaa Glu Asn Xaa Lys Ile Leu Ser Ala Ser Gln Val Phe Ile Gly Gly
 65 70 75 80
 His Ile Thr Trp Gly Leu Ile Tyr Phe Trp Xaa Leu Gln Tyr Gly Xaa
 85 90 95
 Gly His Gln Gln Leu Pro Gly Asn Phe
 100 105

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

Met Thr Gln Ser Ile Leu Asn Ile Ala Ile Ile Thr Leu Ser Gln Lys
 1 5 10 15
 Lys Cys Ser Glu Asn Met Leu Gly Arg Val Asn Ser Val Phe Lys Thr
 20 25 30
 Met Val Phe Ala Phe Arg Pro Ile Ala Leu Phe Leu Gly Gly Ile Leu
 35 40 45
 Leu Glu Asn Lys Gly Gly Phe Tyr Ala Leu Thr Ile Ser Ala Val Leu
 50 55 60
 Phe Ile Pro Leu Val Leu Tyr Ile Leu Lys Asn Arg Phe Tyr Gln Val
 65 70 75 80
 Glu Glu Tyr

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

```

Met Lys Leu Ser Asn Gly Val Lys Arg Leu Leu Lys His Ser Pro Thr
 1           5           10           15
Thr Phe Xaa Asp Pro Xaa Asn Ala Ala Met Xaa Ala Asp Thr Asp Gly
          20           25           30
Leu Ala Gly Leu Gln His Met Xaa Gly Asp Pro Thr Leu Leu Tyr Tyr
          35           40           45
Thr Thr Asp Glu Ala Lys Glu Ala Arg Asp Ala Phe Lys Glu Lys Arg
          50           55           60
Asp Pro Asp Phe Asp Gln Phe Pro Lys Phe Pro
65           70           75

```

(2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

```

Met Glu Asp Phe Asp Tyr Ile Ile Glu Leu Arg Glu Asn Glu Asn Gln
 1           5           10           15
Glu Ile His Tyr Glu Glu Met Lys Lys Gln Thr Val Gln Ser Lys Asn
          20           25           30
Asn Leu Asp Phe Gly Asp Pro Phe Gly Gly Gly Phe Gly Phe Phe Glu
          35           40           45

```

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

Met Gly Val His Ser Met Lys Met Lys Arg Phe Ile Ala Ile Val Met
 1 5 10 15
 Ala Leu Phe Leu Val Leu Xaa Gly Cys Ser Asn Ser Asn Asp Asn Asn
 20 25 30
 Glu Ser Lys Lys Asp Asp Ala Asp Asn Gly Lys Lys Gln Glu Ile Gln
 35 40 45
 Val Ala Ala Ala Ala Ser Leu Thr Asp Val Thr Lys Lys Arg Ala Ser
 50 55 60
 Glu Phe Lys Lys Glu His Lys Asn Ala Asp Ile Lys Phe Asn Tyr Gly
 65 70 75 80
 Gly Ser Gly Ala Xaa Arg Lys Gln Ile Xaa Ser Gly Ala Pro Leu Val
 85 90 95
 Asp Val Xaa Met Xaa Xaa Xaa Xaa Leu Lys Met
 100 105

(2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

Met Pro Ile Ile Thr Ser Tyr Ile Thr Gln Asp Xaa Gly Thr Xaa Thr
 1 5 10 15
 Val Val Ile Ser Gly Val Glu Leu Gly Asn Lys Glu Thr Leu Leu Leu
 20 25 30
 Asp Asn Gly Phe Asp Val Glu Val Asp Val Ser Val Ile Asp Pro Phe
 35 40 45
 Gln Ile Thr Gly Lys Gln Arg Arg Lys Ile Phe Ala Leu Val Lys Asp
 50 55 60
 Ile Glu Glu
 65

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear.

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

```

Met Met Ile Tyr Leu Gly Leu Phe Ile Phe Ser Ile Ser Val Gln Tyr
 1             5             10             15
Ile Ile Tyr Leu Phe Ile Asn Ile Met Ile Ser Gly Val Asn Ile Pro
      20             25             30
Gly Tyr Phe Ser Thr Ile Ala Ala Ile Leu Leu Leu Gly Gly Ile Gln
      35             40             45
Leu Ile Ser Ile Gly Val Val Gly Glu Tyr Ile Gly Arg Ile Tyr Tyr
      50             55             60
Glu Val Lys Ala Arg Pro Lys Tyr Ile Ile Gln Ala Thr Asn Leu Ser
65             70             75             80
Ser Ile Glu Asn Asp Glu Lys Asp Thr His Lys Val Tyr Ser Lys
      85             90             95

```

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

```

Met Ala Gln Met Gly Ala Tyr Val Pro Cys Lys Glu Ala Val Leu Pro
 1             5             10             15
Ile Phe Asp Gln Ile Phe Thr Arg Ile Gly Ala Ala Asp Asp Leu Val
      20             25             30
Ser Gly Lys Ser Thr Phe Met Val Glu Met Leu Glu Ala Gln Lys Ala
      35             40             45
Leu Thr Tyr Ala Thr Glu Asp Ser Leu Ile Ile Phe Asp Glu Ile Gly
      50             55             60
Arg Gly Thr Ser Thr Tyr Asp Gly Leu Ala Leu Ala Gln Ala Met Ile
65             70             75             80
Glu Tyr Cys Ser Trp Lys His Arg Met Leu Lys Arg Tyr Phe Gln His
                        389

```

Ile Ile Met Asn
100

85

90

95

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

```

Met Thr Gln Thr Asn Pro Ser Phe Asn Pro Ser Pro Arg Tyr Lys Ser
 1             5             10             15
Lys Lys Gly Trp Tyr Lys Asp Lys Pro Pro Lys Glu Lys Gly Gly Met
      20             25             30
Pro Ile Glu Val Glu Ile Ala Gly Pro Ile Val Ile Glu Asn Lys Phe
      35             40             45
Ile Asp Pro Lys Thr Asn Thr Glu Lys Val Ile Ile Thr Xaa Glu Gly
      50             55             60
Leu Xaa Lys
65

```

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

```

Met Ile Leu Leu Lys Arg Gln His Gln Leu Val Lys Glu Ala Gln Glu
 1             5             10             15
Gln Thr Pro Phe Ile Phe Val Asp Phe His Ala Glu Thr Thr Ser Glu
      20             25             30
                        390

```

Lys Tyr Ala Met Gly Trp His Leu Asp Gly Arg Ala Ser Ala Val Val
 35 40 45
 Gly Thr His Thr His Ile Gln Thr Glu Val Asn Val Phe Tyr Gln Arg
 50 55 60
 Gly Gln Gly Ile Leu Arg Met Leu Val
 65 70

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

Met Ile Thr Gly Ala Ala Gln Met Asp Gly Gly Ile Leu Val Val Ser
 1 5 10 15
 Ala Ala Asp Gly Pro Met Pro Gln Thr Arg Glu His Ile Leu Leu Ser
 20 25 30
 Arg Asn Val Gly Val Pro Ala Leu Val Val Phe Leu Asn Lys Val Asp
 35 40 45
 Met Val Asp Asp Glu Glu Leu Leu Glu Leu Val Glu Met Glu Val Arg
 50 55 60
 Asp Leu Leu Ser Glu Tyr Asp Phe Pro Gly Asp Asp Val Pro Val Ile
 65 70 75 80
 Ala Gly Ser Ala Leu Lys Ala Leu Glu Gly Asp Ala Gln Tyr Glu Glu
 85 90 95
 Lys Ile Leu Glu Leu Met Glu Ala Val Asp Thr Tyr Ile Pro Leu Gln
 100 105 110
 Thr

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

```

Met Ile Asn Glu Gln Arg Leu Leu Asn Thr Phe Leu Glu Leu Val Gln
 1             5             10             15
Ile Asp Ser Glu Thr Gly Asn Glu Ser Thr Ile Gln Pro Ile Leu Lys
      20             25             30
Glu Lys Phe Ile Ala Leu Gly Leu Arg Cys
      35             40

```

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

```

Met Asn Gln Leu Leu Val Arg His Phe Leu Asn Arg Gln Gln Arg Asp
 1             5             10             15
Asp Ile Phe Ile Gly Thr Lys Val Gly Asn Arg Leu Thr Lys Asp Gly
      20             25             30
Ser Thr Thr Trp Asp Pro Ser Lys Ser Tyr Ile Lys Glu Ala Val Lys
      35             40             45
Gly Ser Leu Lys Arg Leu Gly Ile Asp His Ile Asp Leu Tyr Gln Leu
      50             55             60
His Gly Gly Thr Ile Asp Asp Pro Leu Asp Glu Thr Ile Ser Ala Cys
      65             70             75             80
Asp Glu Leu Lys Gln Glu Gly Ile Ile Arg Ala Tyr Gly Ile Ser Ser
      85             90             95
Ile Arg Pro Asn Val Ile Asp Tyr Tyr Leu Lys His Ser Gln Ile Glu
      100            105            110
Thr Ile Met Ser Gln Phe Asn Leu Ile Asp Asn Arg Pro Glu Ser Leu
      115            120            125
Leu Asp Ala Ile His Asn Asn Asp Val Lys Val Leu Ala Arg Gly Pro
      130            135            140
Val Ser Lys Gly Leu Leu Thr Ser Asn Ser Gly

```

145

150

155

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

```

Met Ala Ile Gln Leu His Glu Ser Gly Val Leu Gln Asp Asn Asn Val
 1             5             10             15
Gln Leu Leu Gly Thr Glu Leu Thr Ser Ile Gln Gln Ala Glu Asp Arg
      20             25             30
Glu Met Phe Arg Thr Leu Met Asn Asp Leu Asn Val Pro Val Pro Glu
      35             40             45
Ser Asp Ile Val Asn Thr Val Glu Gln Ala Phe Lys Phe Lys Glu Gln
      50             55             60
Val Gly Tyr Pro Leu Ile Val Arg Pro Ala Phe Thr Met Gly Gly Tyr
      65             70             75             80
Arg Arg Arg Tyr Leu Val Ile Met Met Lys Asn Tyr Met Lys Ser Val
      85             90             95
Ser Asn Gly Leu Pro Leu
      100

```

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

```

Met Tyr Ile Cys Xaa Gln Lys Lys Asp Asp Asp Gly Ile Tyr Xaa Tyr
 1             5             10             15

```

Tyr Leu Gly Thr Ala Gly Tyr Ile Glu Gly Ser Glu Lys Gln Asp Lys
 20 25 30
 Met Pro Asn Gly Ser Asn Val Val Thr Met Asp Leu Ala Leu Asp Lys
 35 40 45
 Ala Val Arg Asp Asp Ile Tyr Arg Tyr Ile Thr Asn
 50 55 60

(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

Met Glu Lys Arg Thr His Arg Ile Phe Met Ile Gly Gln Arg Gly Ile
 1 5 10 15
 Leu Glu Ile Pro His Ser Arg Gly Val Pro Phe Ile Met Ser Asp Thr
 20 25 30
 Ala Gly Arg Asp Lys Pro Leu Pro Met Arg Pro Asp Lys Leu Lys Asn
 35 40 45
 Leu Gly Met Leu Thr Glu Pro Gly Leu Tyr Tyr Leu Tyr Thr Asp His
 50 55 60
 Thr Ala Gln Ile Asp Asp Phe Pro Xaa Pro Arg Glu Trp Arg Asp Ala
 65 70 75 80
 Ala Trp Phe Leu Glu Val Lys Pro Pro Gln Thr Gly Gly Asp Val Ile
 85 90 95
 Gln Ile Leu Thr Arg Asn Ser
 100

(2) INFORMATION FOR SEQ ID NO:264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

```

Met Leu Lys Arg Lys Ser Leu Gln Lys Xaa Ser Glu Arg Lys Thr Ala
 1             5             10             15
Ile Glu Ala Met Asn Asp Ser Thr Thr Glu Glu Gln Gln Ala Ala Lys
      20             25             30
Asp Lys Val Asp Gln Ala Val Val Thr Ala Asn Ala Asp Ile Asp Asn
      35             40             45
Ala Thr Ala Asn Thr Asp Val Asp Asn Ala Lys Thr Thr Asn Glu Ala
      50             55             60
Thr Arg Ala Ala Ile Thr Pro Asp Ala Asn Val Lys Pro Ala Ala Lys
      65             70             75             80
Gln Ala Xaa Ala Asp Lys Val Gln Ala Gln Glu Thr Ala Ile Asp Ala
      85             90             95
Asn Asn Gly Ser Thr Thr Glu Glu Lys Glu Ala Ala Lys Gln Gln Val
      100            105            110
Gln Ser Glu Lys Thr Ala Ala Asp Ala Ala Ile Asp Ala Ala His Ser
      115            120            125
Asn Val Glu Val Glu Ala Ala Lys Asn Ala Glu Ile Ala Lys Ile Glu
      130            135            140
Ala Ile Gln Pro Ala Thr Thr Ser Lys Asp Asn Ala Thr Gln Ala Ile
      145            150            155            160
Ala Thr Lys Ala Asn Glu Arg Lys Thr Ala Leu Ala Gln Thr Gln Asp
      165            170            175
Ile Thr Ala Glu Glu Ile Ala Ala Ala Asn Ala Asp Val Asp Asn Ala
      180            185            190
Val Thr Gln Ser Lys
      195

```

(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

```

Met Thr Lys Ile Ile Phe Met Gly Thr Arg Ala Phe Ser Thr Thr Val
                        395

```

1	5	10	15
Leu Glu Met	Leu Ile Ala Glu His Asp Val	Ile Ala Val Val Thr Gln	
20	25	30	
Pro Asp Arg	Pro Val Gly Arg Lys Arg Val Met Thr	Pro Pro Pro Val	
35	40	45	
Lys Lys Val Xaa Met Lys Tyr Asp Leu Pro Val Tyr Gln Pro Glu Lys			
50	55	60	
Leu Ser Gly Ser Glu Glu Leu Glu Gln Leu Xaa Gln Leu Asp Val Asp			
65	70	75	80
Leu Ile Val Thr Ala Ala Phe Gly Thr Ile Ile Thr			
85	90		

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

Met Cys Tyr Gly Ile Lys Glu Gln Val Asn Thr Phe Ile Gln Asn Gly	
1	5 10 15
Arg Val Glu His Leu Xaa Ile Asp Phe Lys Pro His Ser Tyr Gln Lys	
20	25 30
Tyr Ala Ile Asp Lys Val Ile Asp Asn Glu Lys Xaa Gly Leu Phe Leu	
35	40 45
Asp Met Gly Leu Gly Lys Thr Val Ser Thr Leu Thr Ala Phe Ser Glu	
50	55 60
Leu Gln Leu Leu Asp Thr Lys Lys Met Leu Val Ile Ala Pro Lys Gln	
65	70 75 80
Val Ala Lys Asp Thr Trp Val Asp Glu Val Asp Lys Trp Asn His Leu	
85	90 95
Asn His Leu Lys Val Ser Leu Val Leu Gly Thr Pro Lys Glu Arg Asn	
100	105 110
Asp Ala Leu Asn Thr Glu Ala Asp Ile Tyr Gly Thr Asn Lys Glu Xaa	
115	120 125
Thr Lys Trp Leu Cys Asp Gln Tyr Lys Lys Glu Trp Pro Xaa	
130	135 140

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

```

Met Xaa Leu Lys Glu Lys Thr Ile Asp Val Val Leu Glu Val Gly Glu
 1             5             10             15
Gln Val Arg Ile Lys Ser Gly Pro Phe Ala Asn Gln Val Gly Xaa Val
      20             25             30
Gln Glu Ile Val Thr Asp Lys Phe Lys Leu Thr Val Leu Val Asp Met
      35             40             45
Phe Xaa Arg Glu Thr Pro Val Glu Xaa Val Phe Asp His Ile Glu Lys
 50             55             60
Leu
65

```

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

```

Met Leu Gly Lys Ile Val Gly Xaa Glu Asp Lys Val Lys Ala Trp Lys
 1             5             10             15
Xaa Asp Trp Glu Glu Thr Thr Pro Lys Asp Gly Lys Glu Ile Lys Lys
      20             25             30
Ala Ile Gly Gln Asp Thr Pro Val Ser Leu Phe Asp Glu Phe Asp Lys
      35             40             45
Lys Leu Tyr Thr Tyr Gly Asp Asn Trp Gly Arg Gly Gly Glu Val Leu
 50             55             60

```

Tyr Gln Ala Phe Gly Leu

65

70

(2) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 93 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

```

Met Thr Glu His Lys Ser Gly Phe Val Ser Ile Ile Gly Arg Pro Asn
 1             5             10            15
Val Gly Lys Ser Thr Phe Val Asn Arg Val Ile Gly His Lys Ile Ala
      20             25            30
Ile Met Ser Asp Lys Ala Gln Thr Thr Arg Asn Lys Ile Gln Gly Val
      35             40            45
Met Thr Arg Asp Asp Ala Gln Ile Ile Phe Asn Asp Thr Pro Gly Ile
      50             55            60
His Lys Pro Lys His Lys Leu Gly Asp Tyr Thr Asp Glu Ser Arg Leu
65             70             75            80
Lys Tyr Ile Ser Glu Ile Asp Ala Ile Met Val Tyr Gly
      85             90

```

(2) INFORMATION FOR SEQ ID NO:270:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

```

Met Ala Lys Gln Lys Lys Phe Met Lys Ile Tyr Glu Ala Leu Lys Glu
 1             5             10            15
Asp Ile Leu Asn Gly Gln Ile Gln Tyr Gly Glu Gln Ile Pro Ser Glu
                        398

```

	20		25		30
His Asp Leu Val Gln Leu Tyr Gln Ser Ser Arg Glu Thr Xaa Arg Lys					
35		40		45	
Ala Leu Asp Xaa Xaa Ala Leu Asp Gly Met Ile Gln Lys Ile His Gly					
50		55		60	
Lys Gly Ser Leu Val Ile Tyr Gln Glu Val Thr Glu Phe Pro Phe Ser					
65		70		75	80
Glu Leu Val Ser Phe Xaa Glu Met Gln Glu Glu Met Gly Val Ala Tyr					
	85		90		95
Leu Thr Glu Val Val Val Asn Glu Val Val Glu Ala His Glu Val Pro					
	100		105		110
Glu Val Gln His Ala Leu Asn Ile Asn Ser Arg					
115		120			

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

Met Arg Leu Val Val Lys Val Ser Ser Leu Lys Ala Val Ile Gln Met			
1	5	10	15
Ile Leu Asp Ile Ala Lys Asp Tyr Leu Phe Thr Xaa Glu Val Val Gln			
20	25	30	
Thr Phe Glu Asn Glu Arg Phe Lys Thr Lys His Thr His Gly Thr Gly			
35	40	45	
Cys Thr Phe Ser Ala Val Ile Thr Ala Glu Leu Ala Lys Gly Arg Pro			
50	55	60	
Leu Phe Glu Ala Val His Lys Ala Lys Lys Phe Ile Ser Met Ser Ile			
65	70	75	80
Gln Tyr Thr Pro Glu Ile Xaa Arg Gly Arg Gly Pro Val Asn His Phe			
	85	90	95
Ala Tyr Leu Lys Lys Glu Gly Leu Asp Asp Glu Leu Ser Lys			
100	105	110	

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

```

Met Lys Arg Phe Ile Tyr Ile Asp Pro Glu Ile Tyr Asn Leu Gly Ile
 1           5           10           15
Pro Val Leu Gly Ile Cys Tyr Gly Met Gln Leu Thr Thr Lys Leu Leu
          20           25           30
Gly Gly Lys Val Xaa Arg Ala Asn Glu Arg Glu Tyr Gly Lys Ala Ile
          35           40           45
Ile Asn Ala Lys Ser Asp Glu Leu Phe Ala Gly Leu Pro Ala Glu Gln
          50           55           60
Thr Val Trp Met Ser His Ser Asp Lys Val Ile Glu Ile Pro Glu Gly
65           70           75           80
Phe Glu Val Ile Ala Asp Ser Pro Ser Thr Asp Tyr Ala Ala Ile Glu
          85           90           95
Asp Lys Lys Arg Arg Ile Tyr Gly Val Gln Phe His Pro Glu Val Pro
          100          105          110
Ser Tyr Arg Ile Trp
          115

```

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

```

Met Glu Ile Ile Val Xaa Glu Asn Leu Val Leu Lys Glu Lys Glu Arg
 1           5           10           15
Leu Gln Val Leu Tyr Lys Asp Ile Pro Ser Asn Lys Leu Lys Val Val
          20           25           30
                                400

```

Asp Gly Leu Ile Ile Gln Ala Ala Arg Leu Arg Val Met Leu Asp Tyr
 35 40 45
 Met Trp Glu Asp Ile Lys Glu Lys Gly Asp Tyr Asp Leu Phe Thr Gln
 50 55 60
 Ser Glu Lys Ala Pro Pro Tyr Glu Arg Glu Arg Pro Val Gly Lys Leu
 65 70 75 80
 Phe Xaa Ala Arg Asp Ala Ala Tyr Gln Lys Ile Ile Lys Gln Leu Ser
 85 90 95
 Asp Leu Leu Ala Xaa Glu Lys Glu Asp Thr Glu Thr Pro Ser Asp Asp
 100 105 110
 Tyr Leu

(2) INFORMATION FOR SEQ ID NO:274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

Met Thr Ser Tyr Tyr Ala Asn Gln Pro Phe Val Arg Ile Arg Asp Ile
 1 5 10 15
 Gly Thr Phe Pro Thr Thr Lys Glu Val Leu Gly Ser Asn Tyr Cys Asp
 20 25 30
 Ile Gly Ile Tyr Val Asp Glu Thr Thr Gln Thr Ala Ile Leu Val Ser
 35 40 45
 Val Ile Asp Asn Leu Val Lys Gly Ala Ser Gly Gln Ala Ile Gln Asn
 50 55 60
 Leu Asn Ile Leu Tyr Asp Phe Glu Val Thr Thr Gly Leu Asn Gln Ser
 65 70 75 80
 Pro Val Tyr Pro

(2) INFORMATION FOR SEQ ID NO:275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

```

Met Val Val Thr Gly Asp Gln Thr Gln Ile Asp Leu Pro Lys Gly Val
 1             5             10             15
Lys Ser Gly Leu Lys Glu Ala Xaa Ser Arg Leu His Asn Val Lys Gly
             20             25             30
Ile Ser Ile Leu Lys Leu Ala Gln Ser Asp Val Xaa Arg His Pro Leu
             35             40             45
Val Ser Lys Xaa Ile Glu His Tyr Glu Gly Glu Asn
 50             55             60

```

(2) INFORMATION FOR SEQ ID NO:276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

```

Met Lys Phe Ile Ile Leu Xaa Glu Glu Asn Ile Asp Ser Val Ile Phe
 1             5             10             15
Lys Gly Tyr Ser Asp Gln Asp Glu Val Arg Phe Gln Glu Leu Phe Glu
             20             25             30
Asn Met Lys Gln Asn Leu Asp Ser Glu Ile Gln Arg Gly Glu Val Thr
             35             40             45
Pro Gln
 50

```

(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

```

Met Met Ser Asn Lys Leu Asp Gly Ile Asn Lys Met Ile Thr Ala Lys
 1           5           10           15
His Lys Xaa Met Asp Asp Leu Tyr Asp Val Lys Arg Glu Val Lys Ala
      20           25           30
Leu Ile Asp Glu Ser Asp Glu Leu Asn His Ser Ile Glu Gln Leu Tyr
      35           40           45
Gln His Leu Gly Xaa Arg Tyr His Ser Ser Asn Met Ala Ser Arg Met
      50           55           60
Glu Gln Phe Arg Asp Xaa Phe His Phe Ala Lys Arg Arg Ser Xaa Glu
      65           70           75           80
Ala Leu Tyr Glu Gln Gln Gln His Ile Gln His Xaa Ile Arg Lys Ala
      85           90           95
Glu Glu Glu Met Ile Asp Leu Glu Met Arg Arg Asn Val Glu Ile Glu
      100          105          110
Thr Val Thr Lys Glu Glu Asn Lys Trp Lys Gln
      115          120

```

(2) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

```

Met Ile Phe Gly Lys Gly Thr Ala Lys Ala Thr Ser Tyr Gly Ala Gly
 1           5           10           15
Ile Ile His Phe Leu Gly Gly Ile His Glu Ile Tyr Phe Pro Tyr Val
      20           25           30
Leu Met Arg Pro Leu Leu Phe Ile Ala Val Ile Leu Gly Gly Met Thr
      35           40           45
Gly Val Ala Thr Tyr Gln Ala Thr Gly Phe Gly Phe Lys Ser Pro Ala
      50           55           60

```

```

Ser Pro Gly Ser Phe Ile Val Tyr Cys Leu Asn Ala Pro Arg Gly Glu
65          70          75          80
Phe Leu His Met Leu Leu Gly Val Phe Leu Ala Ala Leu Val Ser Phe
          85          90          95
Val Val Ala Ala Leu Ile Met Lys Phe Thr Arg Glu Pro Lys Gln Asp
          100          105          110
Leu Glu Ala Ala Thr Ala Gln Met Glu Asn Thr Lys Gly Lys Lys Ser
          115          120          125
Ser Val Ala Ser Lys Leu Val Ser Ser Asp Lys Asn Val Asn Thr Glu
          130          135          140
Glu Asn Ala Ser Gly Asn Val Ser Glu Thr Ser Ser Ser Asp Asp Asp
145          150          155          160
Pro Glu Ala Leu Leu Asp Asn Tyr Asn Thr Glu Asp Val Asp Ala His
          165          170          175
Asn Tyr Asn Asn Ile Asn His Val Ile Phe Gly Cys Asp Ala Gly Met
          180          185          190
Gly Ser Ser Ala Met Gly Ala Ser Met Leu Arg Asn Lys Phe Lys Lys
          195          200          205
Ala Gly Ile Asn Asp Ile Thr Gly Tyr Lys Tyr Cys Asp
          210          215          220

```

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

```

Met Glu Asp Thr Ala Met Leu Leu Ser Thr Arg Glu Lys Glu Met Ile
1          5          10          15
Ala Leu Leu Ile Lys Tyr His Ser Gln Tyr Ile Thr Ile His Asp Ile
          20          25          30
Ala Gln Gln Leu Ala Val Ser Ser Arg Thr Ile His Arg Glu Leu Lys
          35          40          45
Gly Val Glu Ala Tyr Leu Thr Ser Phe Ser Leu Thr Leu Glu Arg Ala
          50          55          60
Asn Lys Lys Gly Leu Arg Ile Ala Gly Ala Asp Ser Asp Leu Asn Asp
65          70          75          80

```

```

Leu Lys Gln Ser Ile Ala Gln His Gln Thr Ile Asp Leu Ser Val Glu
      85                      90                      95
Glu Gln Lys Val Ile Ile Ile Tyr Ala Leu Ile Gln Ala Lys Glu Pro
      100                    105                    110
Val Lys Gln Tyr Ser Leu Ala Gln Glu Ile Gly Val Ser Val Gln Thr
      115                    120                    125
Leu Ala Lys Met Leu Asp Asp Leu Glu Leu Asp Leu Asn Lys Tyr Gln
      130                    135                    140
Leu Ser Leu Ser Arg Lys Arg Gly Glu Gly Ile Tyr Leu Val Gly Thr
      145                    150                    155                    160
Glu Ser Lys Lys Arg Glu Phe Leu Ser Gln Leu Met Val Asn Asn Leu
      165                    170                    175
Asn Ser Thr Ser Val Tyr Ser Ser Asn
      180                    185

```

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

```

Met Pro Ala Ser Val Ile Gly Leu Val Leu Leu Phe Val Leu Leu Cys
  1              5              10              15
Thr Gly Ala Val Lys Leu Gly Glu Val Glu Lys Val Gly Ala Thr Leu
      20              25              30
Thr Asn Asn Ile Gly Leu Leu Phe Val Pro Ala Gly Ile Ser Val Val
      35              40              45
Asn Ser Leu Gly Val Ile Ser Gln Ala Pro Phe Leu Ile Ile Gly Leu
      50              55              60
Ile Ile Val Ser Thr Ile Leu Leu Leu Ile Cys Thr Gly Tyr Val Thr
      65              70              75              80
Gln Ile Ile Met Lys Val Thr Ser Arg Ser Lys Gly Asp Lys Val Thr
      85              90              95
Thr Lys Ile Asn Asp Arg Gly Gly Thr Ser Ser Cys Leu Thr Thr
      100             105             110

```

(2) INFORMATION FOR SEQ ID NO:281:

405

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

```

Met Leu Gly Lys Xaa Met Xaa Arg Ala Thr Ala Asp Thr Asn Asp Thr
 1           5           10           15
Gln Lys Ser Val Gly Pro Val Xaa Asn Asn Lys Ala Lys Asp Met Gln
      20           25           30
Thr Asn Asp Thr Gln Lys Ser Val Gly Ser Ala Ala Asn Asn Lys Ala
      35           40           45
Thr Gln Asn Asp Gly Ala Asn Ala Ser Pro Ala Thr Val Ser Asn Gly
      50           55           60
Ser His Ser Met His Gln Asp Met Leu Asn Val Thr Lys Pro Glu Glu
65           70           75           80
Asn Lys Ala Asn Ala Lys Ser Asp Gln Gln Gly Lys Val Asn Lys Pro
      85           90           95
Lys Gln Gln Ala Lys Thr Leu Pro Asp Thr Gly Met Ser Gln
      100           105           110

```

(2) INFORMATION FOR SEQ ID NO:282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

```

Met Xaa Xaa Ala Lys Phe Xaa Xaa Leu Ile Ala Thr Pro Glu Asn Thr
 1           5           10           15
Gly Xaa Pro Asn Val Ser Glu Thr Thr Asp Asn Gly Lys Ala Asp Ala
      20           25           30
Ser Pro Pro Thr Xaa Asn Asn Ser Asp Ala Xaa Thr Gly Xaa Thr Thr

```

35	40	45													
Val	Thr	Ser	Ala	Thr	Asp	Asp	Ala	Xaa	Asp	Lys	Pro	Gln	Ala	Asn	Asn
50						55					60				
Asn	Ser	Ser	Ala	Asp	Ala	Ser	Thr	His	Ser	Pro	Thr	Met	Asp	Asn	Ala
65					70					75				80	
Val	Thr	Ser	Lys	Pro	Glu	Val	Glu	Ser	Thr	Asn	Asn	Gly	Thr	Thr	Asp
					85					90				95	
Lys	Pro	Val	Thr	Glu	Thr	Asp	Asn	Ala	Xaa	Pro	Ala	Glu	Ser	Thr	Thr
			100					105						110	
Ile	Asn	Asn	Ser	Thr	Pro	Thr	Ala	Thr	Xaa	Glu	Asn	Ala	Arg	Pro	Gly
	115						120					125			
Ser	Xaa	Ala	Pro	Ala	Pro	Thr	Thr	Ala	Ser	Thr	Glu	Ala	Ala	Ser	Ser
	130					135					140				
Ala	Asp	Ser	Lys	Asp	Asn	Ala	Ser	Val	Asn	Asp	Ser	Lys	Gln	Asn	Ala
145					150					155				160	
Glu	Val	Xaa	Asn	Ser	Ala	Xaa	Ser	Gln	Ser	Thr	Asn	Gly	Lys	Val	Ala
					165					170				175	
Gln	Pro	Xaa	Ser	Glu	Xaa	Lys	Ala	Lys	Ala	Glu	Lys	Asp	Gly	Arg	Asp
					180					185				190	
Ser	Thr	Ile	Gln	Xaa	Met	Val	Xaa	Ser	Thr	Thr	Glu	Thr	Leu	Pro	Ser
	195						200						205		
Ala	Asp	Ile	Thr	Glu	Pro	Xaa	Val	Pro	Ser	Asn	Thr	Ser	Lys	Asp	Lys
	210						215						220		
Glu	Glu	Ser	Thr	Thr	Asn	Gln	Xaa	Asp	Ala	Gly	Gln	Leu	Lys	Ser	Glu
225					230					235				240	
Thr	Asn	Val	Ala	Ser	Asn	Glu	Ala	Xaa	Xaa	Ser	Pro	Ser	Lys	Ala	Asp
					245					250				255	
Thr	Glu	Val	Ser	Asp	Lys	Pro	Ser	Thr	Ser	Ala	Ser	Ser			
					260					265					

(2) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

Met Gln Asn Lys Ile Thr Glu Ile Leu Asn Asn Asn Glu Thr Thr Asn


```

1           5           10           15
Glu Glu Lys Gly Asn Asp Ile Gly Pro Val Arg Ala Ala Tyr Glu Glu
           20           25           30
Gly Xaa Xaa Xaa Ile Asn Ala Ala Xaa Thr Thr Gly Asp Val Thr Thr
           35           40           45
Ala Lys Asp Thr Ala Gly Thr Lys Ser Ser Thr Thr Ser Cys Lys Ser
           50           55           60
Cys
65

```

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

```

Met Lys Lys Lys Leu Leu Val Leu Thr Met Ser Thr Leu Phe Ala Thr
1           5           10           15
Gln Leu Ile Asn Ser Asn His Ala Lys Ala Ser Val Thr Glu Ser Val
           20           25           30
Asp Thr Lys Phe Val Val Pro Glu Ser Gly Ile Asn Lys Ile Ile Pro
           35           40           45
Ala Tyr Asp Glu Phe Lys Asn Ser Pro Lys Val Asn Val Ser Asn Leu
           50           55           60
Thr Asp Asn Lys Asn Phe Val Val Ser Glu Asp Lys Leu Asn Lys Ile
65           70           75           80
Val Asp Ser Ser Ala Ala Ser Lys Ile Val Asp Lys Asn Phe Ala Val
           85           90           95
Pro Glu Ser Lys Leu Gly Asn Ile Val Pro Glu Tyr Lys Glu Ile Asn
           100          105          110
Asn Arg Val Asn Val Ala Thr Asn Asn Pro Ala Ser Gln Gln Val Asp
           115          120          125
Lys His Phe Val Ala Lys Gly Pro Glu Val Asn Arg Phe Ile Thr Gln
           130          135          140
Asn Lys Val Asn His His Phe Ile Thr Thr Gln Thr His Tyr Lys Lys
145          150          155          160
Val Ile Thr Ser Xaa Lys Ile Asn Thr Cys Xaa Leu Thr Cys Xaa Ser

```

	165	170	175
Cys Lys Arg Ile Leu Leu Ile Xaa Thr Leu Leu Leu His Ile Arg Leu			
180	185	190	
Ala			

(2) INFORMATION FOR SEQ ID NO:285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

Met Gly Xaa Ile Pro Val Ser Xaa Pro Ala Glu Xaa Val Xaa Ser Asp			
1	5	10	15
Lys Gln Asn Tyr Asp Xaa Tyr Val Ala Lys Thr Gln Thr Ser Gln Asn			
20	25	30	
Lys Gln Leu Glu Gln Glu Lys Gln Phe Asp Ser Val Gly Lys Gln Gly			
35	40	45	
Thr Ala Ser Lys Ser Ser Asp Glu Xaa Val Ser Ser Thr Thr Xaa Ser			
50	55	60	
Met Pro Asn Tyr Ser Xaa Gly Gly			
65	70		

(2) INFORMATION FOR SEQ ID NO:286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

Met Tyr Ser Asn Xaa Thr Xaa His Arg Ala Ile Val Ser Xaa Pro Asp			
1	5	10	15

Xaa His Lys Glu Ser Phe Lys Thr Ser Glu Val Pro Pro Ala Ile Xaa
 20 25 30
 Gly Xaa Met Xaa Pro Xaa Xaa Leu Glu Asn Gly Arg Ile Pro Val Ser
 35 40 45
 Lys Pro Ser Glu Lys Val Glu Ser Asp Lys Gln Lys Tyr Asp Xaa Tyr
 50 55 60
 Val Ala Lys Thr Gln Thr Ser Gln Xaa
 65 70

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

Met Phe Leu Gly Asp Val Ala Leu Ser Ala Ile Arg Pro Pro Thr His
 1 5 10 15
 Ile Lys Ala Asp Gly Asp Ala Asp Val Thr Tyr Gly Val Ala Ile Val
 20 25 30
 Gly Asp Lys Val Thr Arg Lys Glu Leu Thr Ile Glu Ala Thr Val Thr
 35 40 45
 Pro Leu Cys Pro Cys Ser Gln Xaa Ile Ser Glu Tyr Ser Ala His Thr
 50 55 60
 Gln Arg Gly Val Val Thr Val Lys Thr Tyr Ile Asn Lys Asp Xaa Asn
 65 70 75 80
 Ile Val Asp Asp Tyr Lys Asn Lys Ile Leu Asp Ala Met Glu Ala Asn
 85 90 95
 Ala Ser Ser Ile Leu Tyr Pro Ile Leu Lys Arg Pro Asp Glu Lys Arg
 100 105 110
 Val Thr Glu Arg Ala Tyr Glu Asn Pro Arg Phe Val Glu Asp Leu Ile
 115 120 125
 Arg Leu Ile Ala Ala Asp Leu Val Glu Phe Asp Trp Leu Asp Gly Phe
 130 135 140
 Asp Ile Glu Cys Arg Asn Glu Glu Ser Ile His Gln His Asp Ala Phe
 145 150 155 160
 Ala Lys Leu Lys Tyr Arg Lys
 165

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

```

Met Thr Xaa Xaa Thr Pro Ala Gln Lys Xaa Asp Xaa Ser Xaa Xaa Val
 1             5             10             15
Asn Xaa Gly Thr Thr Xaa Ala Gly Val His Thr Ala Gln Ser Tyr Ala
          20             25             30
Thr Thr Leu His Gln Ala Xaa Ser Thr Xaa Lys Thr Ser Xaa Xaa Xaa
      35             40             45
Gln

```

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

```

Met Tyr Xaa His Trp Ile Leu Gly Asp Ile Asn Ser Ala Tyr Ile Ile
 1             5             10             15
Xaa Val Val Ser Lys Tyr Thr Pro Thr Ser Asp Gly Glu Leu Asp Ile
          20             25             30
Ala Gln Gly Thr Ser Met Arg Thr Thr Asp Lys Tyr Gly Tyr Tyr Asn
      35             40             45
Tyr Ala Gly Tyr Ser Asn Phe Ile Val Thr Ser Asn Asp Thr Gly Gly
      50             55             60
Gly Asp Gly Thr Val Lys Pro Glu Xaa Lys Leu Tyr Lys Ile Gly Asp

```

65		70		75		80									
Tyr	Val	Trp	Glu	Asp	Val	Asp	Lys	Asp	Gly	Val	Gln	Gly	Thr	Asp	Ser
			85						90						95
Lys	Glu	Lys	Pro	Met	Ala	Asn	Val	Leu	Val	Thr	Leu	Thr	Tyr	Pro	Asp
			100						105					110	
Gly	Thr	Thr	Lys	Ser	Val	Arg	Thr	Asp	Ala	Asn	Gly	His	Tyr	Glu	Phe
			115						120					125	
Gly	Gly	Leu	Lys	Asp	Gly	Glu	Thr	Tyr	Thr	Val	Lys	Phe	Glu	Thr	Pro
			130						135					140	
Ala	Gly	Tyr	Leu	Pro	Thr	Lys	Val	Asn	Gly	Thr	Thr	Asp	Gly	Glu	Lys
			145						150					155	
Asp	Ser	Asn	Gly	Ser	Ser	Val	Thr	Val	Lys	Ile	Asn	Gly	Lys	Asp	Asp
			165						170					175	
Met	Ser	Leu	Asp	Thr	Gly	Phe	Tyr	Lys	Glu	Pro	Lys	Tyr	Asn	Leu	Gly
			180						185					190	
Asp	Tyr	Val	Trp	Glu	Asp	Thr	Asn	Lys	Asp	Gly	Ile	Gln	Asp	Ala	Asn
			195						200					205	
Glu	Pro	Gly	Ile	Lys	Asp	Val	Lys	Val	Thr	Leu	Lys	Asp	Ser	Thr	Gly
			210						215					220	
Lys	Val	Ile	Gly	Thr	Thr	Thr	Thr	Asp	Ala	Ser	Gly	Lys	Tyr		
			225						230					235	

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

Met	Thr	Leu	Asp	Ser	Gly	Phe	Asp	Lys	Thr	Pro	Lys	Tyr	Ser	Leu	Gly
1				5					10					15	
Asp	Tyr	Val	Trp	Tyr	Asp	Ser	Asn	Lys	Asp	Gly	Lys	Gln	Asp	Ser	Thr
			20						25					30	
Glu	Lys	Gly	Ile	Lys	Asp	Val	Lys	Val	Thr	Leu	Leu	Asn	Glu	Lys	Gly
			35						40					45	
Glu	Val	Ile	Gly	Thr	Thr	Lys	Thr	Asp	Glu	Asn	Gly	Lys	Tyr	Arg	Phe
			50						55					60	
Asp	Asn	Leu	Asp	Ser	Gly	Lys	Tyr	Lys	Val	Ile	Phe	Glu	Lys	Pro	Ala

(2) INFORMATION FOR SEQ ID NO:291:

(A) LENGTH: 130 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

(2) INFORMATION FOR SEQ ID NO:292:

(A) LENGTH: 94 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

```

Met Ser Thr Ser Glu Ser Leu Ser Asp Ser Thr Ser Thr Ser Gly Ser
 1           5           10           15
Val Ser Gly Ser Leu Ser Ile Ala Ala Ser Gln Ser Val Ser Thr Ser
      20           25           30
Thr Ser Asp Ser Met Ser Thr Ser Glu Ile Val Ser Asp Ser Ile Ser
      35           40           45
Thr Ser Gly Ser Leu Ser Ala Ser Asp Ser Lys Ser Met Ser Val Ser
      50           55           60
Ser Ser Met Ser Thr Ser Gln Ser Gly Ser Thr Ser Glu Ser Leu Xaa
65           70           75           80
Asp His Lys Val His Leu Ile Leu Ile Val Ser His Tyr His
      85           90

```

(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

```

Met Thr Phe Gly Ser Val Phe Thr Ser Thr Pro Ser Xaa Ser Leu Thr
 1           5           10           15
Asp Arg Phe Cys Arg Leu Asp Gln Glu Arg Phe Gly Asp Ile Lys Asp
      20           25           30
Ile Thr Asp Lys Gly Tyr Tyr Gln Asn Ser Phe His Tyr Asp Val Arg
      35           40           45
Lys Asp Val Thr Pro Phe Glu Lys Leu Asp Phe Glu Lys Asp Tyr Pro
      50           55           60
Tyr Tyr Ala Ser Gly Gly Phe Ile His Tyr Cys Glu Tyr Pro Lys Leu
65           70           75           80
Gln His Asn Leu Lys Ala Leu Glu Xaa Gly Ile Gly Pro Xaa Ser Tyr
      85           90           95

```

Cys Xaa Ser Trp Leu Thr Leu Gly Xaa Lys Tyr Xaa Asp Leu Xaa His
 100 105 110
 Cys Tyr

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

Met Gly Gln Leu Glu Thr Ser Ile Arg Asp Lys Asp Thr Thr Leu Gln
 1 5 10 15
 Ser Gln Asn Tyr Gln Asp Ala Asp Asp Ala Lys Arg Thr Ala Tyr Ser
 20 25 30
 Gln Ala Val Asn Ala Ala Ala Thr Ile Leu Xaa Lys Thr Ala Gly Gly
 35 40 45
 Asn Thr Pro Xaa Ala Asp Val Asp Arg Ala Met Gln Ala Val Thr Gln
 50 55 60
 Ala Asn Thr Ala Leu Asn Gly Ile Gln Tyr Leu Arg Thr Cys Glu Thr
 65 70 75 80
 Arg Leu Arg Thr Gln Gln Xaa Thr Asn Ala Ser Val Xaa Xaa Ser Lys
 85 90 95
 Gln Thr Arg Xaa Ile Asp Xaa Thr Xaa
 100 105

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:


```

Met Leu Val Phe Thr Leu Xaa Asn Val Arg Arg Ser Met Val Glu Gln
 1             5             10             15
Leu Asn Glu Asp Tyr Val Leu Tyr Leu Arg Ala Ser Gly Val Lys Ser
      20             25             30
Ile Thr Leu Met Leu His Val Leu Arg Asn Ala Ile Gln Val Ala Val
      35             40             45
Ser Xaa Leu Cys Met Ser Ile Pro Met Ile Met Gly Gly Leu Val Val
      50             55             60
Ile Glu Tyr Ile Xaa Ala Trp Xaa Gly Leu Gly Gln Leu Ser Leu Xaa
65             70             75             80
Ala Xaa Thr Trp Asn Thr Ile Xaa Gln Xaa Xaa Lys His Met Tyr
      85             90             95

```

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

```

Met Asn Thr Leu Lys Leu Thr Ile Ile Ser Ser Val Met Val Met Ile
 1             5             10             15
Thr Ser Ile Ile Leu Gly Val Val Ser Ala Leu Lys Arg Gly Lys Phe
      20             25             30
Thr Asp Arg Ala Ile Arg Ser Val Ala Phe Phe Leu Thr Ala Leu Ala
      35             40             45
Ser Cys Arg Ile Arg His Glu Arg His
      50             55

```

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

```

Met Asn Phe Asn Asn Leu Asp Gln Leu Tyr Arg Ser Val Ile Met Asp
 1             5             10             15
His Tyr Lys Asn Pro Thr Asn Lys Gly Val Leu Xaa Asn Gly Ser Met
          20             25             30
Thr Val Asp Met Asn Asn Pro Thr Cys Gly Asp Arg Ile Arg Leu Thr
          35             40             45
Phe Asp Ile Glu Asp Gly Ile Ile Lys Asp Ala Lys Phe Glu Gly Glu
          50             55             60
Gly Cys Ser Ile Ser Met Ala Ser Ala Ser Met Met Thr Gln Ala Val
          65             70             75             80
Lys Gly Asn Pro Xaa Gly Glu Ala Ile Gln Xaa Asp Pro Arg Asn Leu
          85             90             95
Pro Xaa Met Met Leu Gly Trp Lys Pro Xaa Val Xaa Gln Gly Arg Met
          100            105            110
Gly Arg Tyr
          115

```

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

```

Met Ser Xaa Xaa Xaa Gly Xaa Thr Val Thr Ala Thr Xaa Xaa Lys Val
 1             5             10             15
Xaa Val Lys Pro Asp Asp Gln Val Leu Ala Gly Tyr Thr Asp Xaa Asn
          20             25             30
Lys Leu Val Asn Phe Lys Ala Pro Lys Glu Met Ile Gly
          35             40             45

```

(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:

417

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

```

Met Ile Asp Val Ile Ser Glu Gly Gly Asn Ile Val Pro His Ile His
 1             5             10             15
Leu Pro Val Gln Ser Gly Asn Asn Ala Val Leu Lys Ile Met Gly Arg
      20             25             30
Lys Tyr Thr Arg Glu Ser Tyr Leu Asp Leu Val Lys Arg Ile Lys Asp
      35             40             45
Arg Leu Pro Asn Val Ala Leu Thr Thr Asp Ile Ile Val Gly Tyr Pro
      50             55             60
Asn Glu Ser Glu Glu Gln Phe Glu Glu Thr Leu Thr Leu Tyr Asp Glu
65             70             75             80
Val Gly Phe Glu His Ala Tyr Thr Tyr Leu Tyr Ser Gln Arg Asp Gly
      85             90             95
Thr Pro Ala Ala Lys Met Lys Asp Asn Val Pro Leu Asn Val Lys Lys
      100            105            110
Glu Arg Leu Gln Arg Leu Asn Lys Lys Val Gly His Tyr Ser Gln Ile
      115            120            125
Ala Met Ser Lys Tyr Glu Gly Gln Thr Val Thr Val Leu Cys Glu Gly
      130            135            140
Ser Ser Lys Lys Asp Asp Gln Val Leu Ala Gly Tyr Thr Asp Lys Asn
145            150            155            160
Lys Leu Val Asn Phe Lys Ala Pro Lys Glu Met Ile Gly
      165            170

```

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

```

Met Ile Ala Met Ser Phe Leu Tyr Leu Gln Gly Gly Arg Leu Ile Asp
 1             5             10             15
Val Leu Thr Ala Ile Leu Ala Gly Ser Leu Gly Tyr Leu Val Thr Glu
      20             25             30
Ile Leu Asp Arg Lys Leu His Ala Gln Phe Ile Pro Glu Phe Ile Gly
      35             40             45
Ser Leu Val Ile Gly Ile Ile Ala Val Ile Gly His Thr Leu Ile Pro
      50             55             60
Thr Gly Asp Leu Ala Thr Ile Ile Ile Ala Ala Val Met Pro Ile Val
65             70             75             80
Pro Gly Val Leu Ile Thr Asn Ala Ile Gln Asp Leu Phe Gly Gly His
      85             90             95
Met Leu Met Phe Thr Thr Lys Ser Leu Glu Ala Leu Val Thr Ala Phe
      100            105            110
Gly Ile Gly Ala Gly Val Gly Ser Val Leu Ile Leu Val
      115            120            125

```

(2) INFORMATION FOR SEQ ID NO:301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

```

Met Phe Lys Ser Tyr Met Asp Ile Thr Pro Asn Glu Tyr Arg Asn Leu
 1             5             10             15
Ser Lys Tyr Asn Lys Cys Leu Met Leu Lys Pro Glu Pro Leu Val Gly
      20             25             30
Lys Met Val Gln Glu Val Lys Glu Ile Ile Leu Asn Tyr Ile Glu His
      35             40             45
Tyr Lys Asn His Pro Thr Asp Val Ile His Ile Gly
      50             55             60

```

(2) INFORMATION FOR SEQ ID NO:302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

```

Met Tyr Xaa Xaa Lys Ile Gly Pro Ser Ile Xaa Phe Lys Ala Xaa Tyr
 1           5           10           15
Ala Pro Phe Leu Phe Glu Lys Leu Met Met Pro Leu Ser Ile Leu Ile
      20           25           30
Pro Val Gly Ala Ile Ala Leu Ser Leu Leu Val Gly Tyr Gly Leu Leu
      35           40           45
Glu Phe Val Gly Val Tyr Met Glu Pro Ile Met Arg Pro Ile Phe Lys
      50           55           60
Thr Pro Gly Lys Ser Ala Val Asp Ala Val Ala Ser Phe Val Gly Ser
65           70           75           80
Tyr Ser Leu Gly Leu Leu Ile Thr Asn Arg Val Tyr Lys Gln Gly Met
      85           90           95
Tyr Asn Lys Arg Glu Ala Thr Ile Ile Ala Thr Gly Phe Ser Thr Val
      100          105          110
Ser Ala Thr Phe Met Ile Ile Val Ala Lys Xaa Pro
      115          120

```

(2) INFORMATION FOR SEQ ID NO:303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

```

Met Lys Lys Phe Asn Val Gln Ile Thr Tyr Thr Gly Met Ile Glu Glu
 1           5           10           15
Thr Ile Glu Ala Glu Ser Leu Glu Glu Ala Glu Asn Glu Ala Arg Asp
      20           25           30
Ile Ala Met Met Glu Val Pro Phe Asp Cys Asp Glu Tyr Glu Ile Asn
      35           40           45

```

420

Val Glu Glu Lys Glu

50

(2) INFORMATION FOR SEQ ID NO:304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

```

Met Thr Asn Thr Leu Gln Val Lys Leu Leu Ser Lys Asn Ala Arg Met
 1           5           10           15
Pro Glu Arg Asn His Lys Thr Asp Ala Gly Tyr Asp Ile Phe Ser Ala
          20           25           30
Glu Thr Val Val Leu Glu Pro Gln Glu Lys Ala Val Ile Lys Thr Asp
          35           40           45
Val Ala Val Ser Ile Pro Glu Gly Tyr Val Gly Leu Leu Thr Ser Arg
          50           55           60
Ser Gly Val Ser Ser Lys Thr His Leu Val Ile Glu Thr Gly Lys Ile
          65           70           75           80
Asp Ala Gly Tyr His Gly Asn Leu Gly Ile Asn Ile Lys Asn Asp Ala
          85           90           95
Ile Ala Ser Asn Gly Tyr Ile Thr Pro Gly Val Phe Asp Ile Lys Gly
          100          105          110
Glu Ile Asp Leu Ser Asp Ala Ile Arg Gln Tyr Gly Thr Tyr Gln Ile
          115          120          125
Asn Glu Gly Asp Lys Leu Ala Gln Leu Val Ile Val Pro Ile Trp Thr
          130          135          140
Pro Glu Leu Lys Gln Val Glu Glu Phe Glu Cys Val Ser Glu Arg Gly
          145          150          155          160
Ala Lys Gly Phe Gly Ser Ser Gly Val
          165

```

(2) INFORMATION FOR SEQ ID NO:305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid

421

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

```

Met Thr Phe Thr Leu Ser Asp Glu Gln Tyr Lys Asn Leu Cys Thr Asn
 1             5             10             15
Ser Asn Lys Leu Leu Asp Lys Leu His Lys Ala Leu Lys Asp Arg Glu
      20             25             30
Glu Tyr Lys Lys Gln Arg Asp Glu Leu Ile Gly Asp Ile Ala Lys Leu
      35             40             45
Arg Asp Cys Asn Lys Glu Leu Glu Lys Lys Ala Ser Ala Trp Asp Arg
      50             55             60
Tyr Cys Lys Ser Val Glu Lys Asp Leu Ile Asn Glu Phe Gly Asn Asp
65             70             75             80
Asp Glu Arg Val Lys Phe Gly Met Glu Leu Asn Asn Lys Ile Phe Met
      85             90             95
Glu Asp Asp Thr Asn Glu
      100

```

(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

```

Met Asn Pro Pro Tyr Gly Arg Ser Ile Lys Arg Trp Val Lys Lys Ala
 1             5             10             15
Tyr Glu Glu Ser Leu Lys Gly Ala Thr Val Val Cys Leu Ile Pro Ala
      20             25             30
Arg Thr Asp Thr Thr Tyr Trp His Asp Tyr Ile Phe Asn Lys Ala Asp
      35             40             45
Asp Ile Arg Phe Leu Arg Gly Arg Leu Lys Phe Gly Asp Ser Lys Asn
      50             55             60
Arg Ala Pro Phe Pro Ser Ala Ile Ile Val Tyr Arg Gly Ala Gln Met

```

65		70		75		80									
Ser	Lys	Tyr	Asn	Ala	Lys	Lys	Val	Xaa	Ser	Thr	Lys	Gly	Ile	Xaa	Phe
		85		90		95									
Trp	Ile	Ala	Lys	Xaa	Glu	Cys	Xaa	Ile	Phe	Thr	Lys	Tyr	Leu	Glu	Ser
		100		105		110									
Asn	Ile	Glu	Trp	His											
		115													

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

Met	Tyr	Pro	Ile	Lys	Asn	Leu	Glu	Asn	Leu	Tyr	Asp	Lys	Glu	Gly	Tyr
1				5					10					15	
Arg	Asp	Gly	Glu	Phe	Lys	Lys	Gly	Asp	Lys	Gly	Thr	Trp	Thr	Ile	Ser
		20						25					30		
Thr	Asp	Phe	Ala	Lys	Ser	Asn	Lys	Gln	Gly	Glu	Met	Asn	Ser	Glu	Gly
		35					40					45			
Met	Val	Leu	His	Phe	Asn	Arg	Asn	Thr	Gly	Ala	Ala	Thr	Gly	Tyr	Tyr
		50				55					60				
Thr	Val	Arg	Ala	Thr	Tyr	Asp	Val	Val	Asp	Lys	Leu	Xaa	Arg	Ser	Xaa
65					70				75					80	
Gln	Ile	Ser	Cys	Cys	Xaa										
					85										

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

```

Met Cys Val Val Tyr Arg Thr Ser Val Leu Ile Leu Leu Ala Ser Gly
 1             5             10             15
Cys Ser Gly Val Phe Asp Thr Pro Glu Asp Ser Lys Glu Thr Gln Ile
          20             25             30
Lys Lys Ser Phe Ala Lys Thr Leu Asp Met Tyr Pro Ile Lys Asn Leu
          35             40             45
Glu Asp Leu Tyr Asp Lys Glu Gly Tyr Arg Asp Gly Glu Phe Lys Lys
          50             55             60
Gly Asp Lys Gly Thr Trp Val Val Arg Ser Glu Met Ile Ile Gln Pro
65             70             75             80
Lys Arg

```

(2) INFORMATION FOR SEQ ID NO:309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

```

Met Lys Glu Asn Arg Thr Thr Met Lys Lys Asp Ile Arg Leu Lys Trp
 1             5             10             15
Ser Asp Asn Lys Ile Ile Pro Thr Lys Glu Ile Xaa Asp Xaa Asn Ile
          20             25             30
Lys Lys Glu Xaa Glu Asn Phe Lys Phe Phe Val Gln Tyr Gly Asn Phe
          35             40             45
Lys Asp Leu Ser Lys Tyr Lys Asp Gly Asp Ile Ser Tyr Asn Pro Glu
          50             55             60
Val Pro Ser Tyr Ser Pro Lys Tyr Gln Val Thr Asn Asp Asp Tyr Asn
65             70             75             80
Val Xaa Gln Xaa Arg Lys Arg Tyr Arg Tyr Thr Asp Arg Ile Lys His
          85             90             95
Xaa Ser Tyr Cys
          100

```

(2) INFORMATION FOR SEQ ID NO:310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

```

Met Phe Leu Xaa Leu Asn Arg Xaa Thr Arg Ser Ala Xaa Gly Phe Tyr
 1           5           10           15
Tyr Val Asn Ala Ile Lys Lys Xaa Val Asn Gly Arg Pro Gln Asp Asn
          20           25           30
Gln Ile Glu Tyr Pro Val Glu Met Ile Asp Asn Lys Xaa Ile Pro Thr
        35           40           45
Lys Asp Ile Xaa Asp Xaa Xaa Ile Lys Lys Glu Ile Glu Asn Phe Lys
       50           55           60
Phe Phe Ala Gln Tyr Gly Asn Phe Lys Asp Leu Thr Lys Tyr Lys Gly
      65           70           75           80
Gly Asp Ile Ser Tyr Asn Pro Glu Ala Pro Ile Tyr Ser Ala Lys Tyr
          85           90           95
Xaa Leu Xaa Asn Asp Asp Tyr Asn Val Lys Gln Leu Arg Lys Arg Tyr
        100          105          110
Asp Ile Pro Thr Asn Lys Ala Pro Lys Leu Leu Leu Xaa Gly Thr Gly
       115          120          125
Asn Leu Asp Gly Thr Ser Ile Gly Xaa Xaa Lys Ile Glu Xaa Thr Xaa
      130          135          140
Gly Xaa Lys Xaa Gly Glu Asn Xaa His Phe Thr Xaa Asn Leu His Phe
     145          150          155          160
Lys Pro Ser Asn Asp Glu Xaa Ser
          165

```

(2) INFORMATION FOR SEQ ID NO:311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

```

Met Lys Asn Asn Lys Ile Ile Leu Leu Asp Glu Val Lys Asp Asp Lys
 1             5             10             15
Leu Lys Gln Lys Ile Glu Asn Phe Lys Phe Phe Gly Gln Tyr Ala Asn
      20             25             30
Leu Lys Glu Leu Arg Lys Tyr Asn Asn Gly Asp Val Ser Ile Asn Glu
      35             40             45
Asn Val Pro Ser Tyr Asp Val Glu Tyr Lys Met Ser Asn Lys Asp Glu
      50             55             60
Ile Val Lys Glu Leu Arg Ser Arg Tyr Asn Ile Ser Thr
65             70             75

```

(2) INFORMATION FOR SEQ ID NO:312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

```

Met Gly Ile Ser Lys Ala Met Met Glu Lys Val Phe Val Ala Lys Ser
 1             5             10             15
Arg Asn Ile Arg Ser Glu Gln Thr Leu Ile Cys Gly Thr Arg Tyr Gly
      20             25             30
Asn Val Met Ala Ser Arg Gly Ser Val Ile Pro Leu Phe Ile Asp Lys
      35             40             45
Ile Lys Ala Gly Glu Pro Leu Thr Ile Thr Asp Pro Asp Met Thr Arg
      50             55             60
Phe Leu Met Ser Leu Glu Asp Ala Val Glu Leu Val Val His Ala Phe
65             70             75             80
Lys His Ala Glu Thr Gly Asp Ile Met Val Gln Lys Ala Pro Ser Ser
      85             90             95
Thr Val Gly Asp Leu Ala Thr Ala Leu Leu Glu Leu Phe Glu Ala Asp
      100             105             110
Asn Ala Ile Glu Ile Ile Gly Xaa Leu Val Pro Trp Arg Glu Lys Ala
      115             120             125
Xaa Thr Xaa Leu Pro Xaa Glu Glu Tyr Xaa Pro Xaa

```

130

135

140

(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

```

Met Met Gln Gln Leu Ser Leu Lys His Arg Leu Asn Asn Gly Asp Ser
 1             5             10             15
Val Tyr Gly Ile Ser Asn Ser Ile Pro Asp Pro Leu Met Ile Glu Val
          20             25             30
Ile Ala Ala Ser Gly Tyr Asp Xaa Val Val Xaa Asp Thr Glu His Val
      35             40             45
Ala Xaa Xaa Asp Glu Thr Leu Ala His Ser Xaa Ser Arg Ser
 50             55             60

```

(2) INFORMATION FOR SEQ ID NO:314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

```

Met Ser Phe Thr Ala Pro Thr Lys Gln Pro Ile Val Lys Pro Lys Glu
 1             5             10             15
Lys Thr Lys Tyr Glu Phe Lys Ser Gly Gly Lys Lys Lys Met Val Ile
          20             25             30
Ala Glu Ala Asn Lys Val Thr Pro Ile Gly Asn Phe Ile Pro Gly Thr
      35             40             45
Tyr Arg Ile Pro Ala Met Lys Ser Thr Glu Asn Gly Asp Phe Xaa Gly
 50             55             60

```

Tyr Leu Lys Phe Asp Phe Arg Gln Ser Asn Ser Glu Thr Val Asp Val
 65 70 75 80
 Thr Glu Asp Phe Glu Glu Ala Asn Ile Thr Val Thr Leu Lys Gly Asp
 85 90 95
 Thr Lys Leu Asn Asp Ser Ser Lys Lys Val Thr Ile Asn Asp Arg Glu
 100 105 110
 Met Ala Phe Ser Ser Ser Lys Thr Tyr Gly Pro Tyr Pro Gln Asn Lys
 115 120 125
 Asp Ile Thr Ile Ser Ala Ser Gly Lys Ala Lys Gly Lys Thr Phe Thr
 130 135 140
 Thr Gln Thr Lys Thr Ile Lys Ala Ser Asp Leu Xaa Tyr Asn Thr Glu
 145 150 155 160
 Asp Asn Phe Glu Phe Trp Asp Xaa Glu Asp Ile Xaa Gly Leu Cys
 165 170 175

(2) INFORMATION FOR SEQ ID NO:315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

Met Met Ile Ser Ser Pro Gln Ile Ile Asp Ala Glu Lys His Gly Asp
 1 5 10 15
 Lys Ile Thr Ala Thr Val Arg Leu Ile Asn Glu Asn Gly Lys Gln Val
 20 25 30
 Asp Lys Glu Tyr Glu Leu Glu Gln Gly Ser Gln Asp Arg Leu Gln Leu
 35 40 45
 Ile Lys Thr Ser Glu Lys
 50

(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

```

Met Xaa Lys Pro Thr Gln His Tyr Ile Phe Asn Leu Pro Asn Asn Glu
 1           5           10           15
Gly Leu Ser Ser Leu Leu Leu Asn Trp Ser Thr Tyr Gln Asp Ser Ile
          20           25           30
Ile Ser Thr Glu Ile Gln Asp Leu Asp Val Leu Thr Ser Gly Pro Ile
          35           40           45
Pro Pro Asn Pro Ser Glu Leu Ile Thr Ser Arg Ala Phe Ala Asn Leu
          50           55           60
Tyr Asp Thr Leu Leu Met Asn Tyr Tyr Leu Val Ile Ile Asp Thr Pro
65           70           75           80
Gln

```

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

```

Met Ser Lys Lys Glu Asn Thr Thr Thr Thr Leu Phe Val Tyr Glu Asn
 1           5           10           15
Pro Asn Ser Thr Ile Ser Glu Lys Xaa Arg Gly Ile Arg Xaa Asn Ile
          20           25           30
Met Phe Ser Lys Ala Asn Gly Glu Val Lys Arg Leu Leu Xaa Thr Ser
          35           40           45
Glu Lys Pro Gly Ala Gly Lys Ser Thr Val Val Ser Asn Val Ala Ile
          50           55           60
Thr Tyr Ala Gln Ala Gly Tyr Lys Thr Leu Val Ile Asp Gly Asp Met
65           70           75           80
Arg Lys Pro Thr Gln Asn Tyr Ile Phe Asn Glu His Asn Asn Asn Gly
          85           90           95
Leu Ser Ser Leu Ile Ile Gly Arg Xaa Thr Met Ser Glu Xaa Ile Thr
          429

```

```

          100              105              110
Ser Thr Glu Ile Glu Asn Leu Asp Leu Leu Thr Ala Xaa Pro Val Pro
          115              120              125
Pro Asn Pro Ser Glu Leu Ile Gly Ser Glu Arg Phe Lys Glu Leu Val
          130              135              140
Asp Leu Phe Asn Lys Arg Tyr Asp Ile Ile Ile Val Xaa Thr Pro Pro
          145              150              155              160
Val Ile Thr Val Thr Xaa Ala Gln Leu Xaa Ala Leu Val Leu Leu Lys
          165              170              175
Ile Val Leu Leu Val Ile Asp Ser Glu Lys Asn Asp Lys Asn Glu Val
          180              185              190
Lys Lys Ala Lys Ala Leu Met Glu Lys Ala Gly Arg
          195              200

```

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

```

Met Thr Xaa Asn Thr Val Thr Leu His Thr Ala His Ile Val Ser Leu
 1              5              10              15
Gly Asp Ile Glu Ala Lys Ala Ser Ile Lys Pro Phe Ile Arg Arg
          20              25              30
Thr Pro Leu Ile Lys Ser Met Tyr Leu Ser Xaa Asn Ile Thr Lys Gly
          35              40              45
Asn Val Tyr Leu Lys Leu Glu Asn Met Gln Phe Thr Gly Ser Phe Lys
          50              55              60
Phe Arg Gly Ala Ser Asn Lys Ile Asn His Leu Ser Asp Xaa Xaa Lys
          65              70              75              80
Ala Lys Gly Ile Ile Gly Ala Ser Ala Gly Asn His Ala Gln Gly Val
          85              90              95
Ala Leu Thr Ala Lys Leu Leu Gly Ile Asp Ala Thr Ile Val Met Pro
          100              105              110
Glu Thr Ala Pro Ile Ala Lys Gln Asn Ala Thr Lys Gly Tyr Gly Ala
          115              120              125
Lys Val Ile Leu Lys Gly Xaa Asn Phe Asn Glu Thr Arg Leu

```

130

135

140

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

```

Met Xaa Xaa Thr Arg Xaa Arg Ser Xaa Xaa Xaa Thr Xaa Leu Asn Xaa
 1             5             10             15
Arg Lys Ser Ala Val Met Ser Xaa Glu Ile Thr Ser Xaa Asp Trp Xaa
      20             25             30
Val Thr Xaa Pro His Glu Xaa Ile Ser Xaa Gly Xaa Xaa Xaa Arg Val
      35             40             45
Lys His Arg Asp Phe Asp Pro Pro Leu Tyr Val Glu Ala Glu Val Ile
      50             55             60
Ala Glu Glu Tyr Asn Ile Ile Ser Glu Asn Ser Thr Tyr Thr Phe Gly
      65             70             75             80
Gln Pro Lys Glu Phe Lys Glu Ser Glu Leu Arg Glu Glu Phe Asn Lys
      85             90             95
Arg Leu Asn Ile Ile His Gln Lys Leu Asn Asp Asn Ile Ser Asn Ile
      100            105            110
Asn Thr Ile Val Lys Asp Val Val Asp Ser Glu Leu Glu Tyr Phe Glu
      115            120            125
Arg Lys Ile His Lys Ser Asp Thr Pro Pro Glu Asn Pro Val Asn Asp
      130            135            140
Met Leu Trp Tyr Asp Thr Ser Asn Pro Asp Val Ala Val Leu Arg Arg
      145            150            155            160
Tyr Trp Asn Gly Arg Trp Ile Glu Glu Thr Pro Asn Asp Val Xaa Lys
      165            170            175
Leu Gly Gly Ile Thr Arg Glu Glu Ser Ala Ile Gln
      180            185

```

(2) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids

431

- (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

```

Met Ala Lys Glu Leu Glu Ser Gly Lys Lys Leu Ser Asp Asp Thr Phe
 1           5           10           15
Lys Leu Ser Arg His Thr Gly Leu Ile Ala Glu Glu Val Glu Glu Leu
      20           25           30
Gly Phe Asn Glu Phe Val Ile Tyr Asp Asp Asn Gly Glu Ile Glu Gly
      35           40           45
Ile Ala Tyr Asp Arg Leu Trp Val His Leu Xaa Pro Ile Ile Thr Xaa
      50           55           60
Lys Pro Xaa Xaa Lys Xaa Arg Lys Thr Xaa Trp Xaa Xaa
65           70           75
  
```

(2) INFORMATION FOR SEQ ID NO:321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

```

Met Val Gly Glu Gly Leu Ala Ile Lys Ala His Glu Glu Ser Lys Val
 1           5           10           15
Ile Ala Pro Phe Asn Gly Leu Ile Ser Met Ile Val Pro Thr Lys His
      20           25           30
Ala Val Gly Ile Gln Ser Glu Asp Gly Val Asp Ile Val Ile His Ile
      35           40           45
Gly Val Lys Xaa Val Asp Leu Glu Gly Lys Gly Phe Lys Tyr Phe Val
      50           55           60
Asn Gln Asn Asp His Val Glu Ala Gly Gln Thr Xaa Leu Gln Phe Asp
65           70           75           80
Gln Gln Tyr Ile Gln Gln Xaa Gly Tyr Asn Ala Asp Xaa Ile Val Val
      85           90           95
  
```

Ile Ser Asn Ser Ala Asp Leu Gly Lys Val Glu Leu Thr Met Asn Glu
 100 105 110
 Ile Ile Thr Thr Glu Asp Val Ile Phe Xaa Ile Phe Lys Asn
 115 120 125

(2) INFORMATION FOR SEQ ID NO:322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

Met Gly Leu Lys Cys Leu Arg Thr Ser Ile Ala Trp Thr Arg Ile Phe
 1 5 10 15
 Pro Asn Gly Asp Glu Asp Val Pro Asn Glu Glu Gly Leu Ala Phe Tyr
 20 25 30
 Asp Arg Ile Phe Asp Glu Leu Ile Ala Gln Gly Ile Glu Pro Val Val
 35 40 45
 Thr Leu Ser His Phe Glu Met Pro Leu His Leu Ala Lys His Tyr Gly
 50 55 60
 Gly Phe Arg Asn Arg Glu Val Val Asp Tyr Phe Val His Phe Ala Arg
 65 70 75 80
 Val Val Phe Glu Arg Tyr Lys Asp Lys Val Thr Tyr Trp Met Thr Phe
 85 90 95
 Asn Glu Ile Asn Asn Gln Met Asp Thr Ser Asn Pro Ile Phe Leu Trp
 100 105 110
 Thr Asn Ser Gly Val Ala Leu Thr Glu Asn Asp Asn Pro Glu Glu Val
 115 120 125
 Leu Tyr Gln Val Ala His His Glu Leu Leu Ala Ser Ala Leu Ala Val
 130 135 140
 Arg Leu Gly Lys Glu Ile Asn Pro Lys Phe Lys Ile Gly Thr Met Ile
 145 150 155 160
 Ser His Val Pro Ile Tyr Pro Tyr Ser Cys His Pro Lys Asp Met Met
 165 170 175
 Glu Ala Gln Ile Ala Asn Arg Leu Arg Phe Phe Phe Pro Asp Val Gln
 180 185 190
 Val Arg Gly Tyr Tyr Pro Ser Tyr Ala Lys Lys Met Leu Ala Arg Lys
 195 200 205

Gly Tyr Asp Val Gly Trp Gln Glu Gly Asp Asp Ser Ile Leu Gln Gln
 210 215 220
 Gly Thr Xaa Asp Tyr Ile Gly Phe Ser Tyr Tyr Met Ser Thr Ala Val
 225 230 235 240
 Lys His Asp Val Asp Thr Thr Xaa Glu Asn Asn Ile Val Asn Gly Gly
 245 250 255
 Phe Gly Phe Ile Cys Gly Glu Ser Ala Tyr Arg Asn Glu
 260 265

(2) INFORMATION FOR SEQ ID NO:323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

Met Tyr Xaa Arg Val Met Asp Leu Gly Val His Cys Ser Val Gly Gly
 1 5 10 15
 Gly Ala Ile Thr Arg Pro Xaa Glu Ile Thr Lys Arg Phe Gly Xaa Val
 20 25 30
 Met Glu Asp
 35

(2) INFORMATION FOR SEQ ID NO:324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

Met Xaa Asn Leu Ile Pro Lys Asn Pro Gln Xaa Pro Thr Gln Asp Glu
 1 5 10 15
 Leu Lys His Lys Ser Lys Pro Ala Gln Ser Phe Asn Xaa Asp Val Asn

	20		25		30										
Gln	Lys	Asp	Thr	Arg	Ala	Thr	Ser	Leu	Phe	Glu	Thr	Asp	Pro	Ser	Ile
	35		40		45										
Ser	Asn	Asn	Asp	Asp	Ser	Gly	Gln	Phe	Asn	Val	Val	Asp	Ser	Lys	Asp
	50		55		60										
Thr	Arg	Gln	Phe	Val	Lys	Ser	Ile	Ala	Lys	Asp	Ala	His	Arg	Ile	Gly
	65		70		75									80	
Gln	Asp	Asn	Asp	Ile	Tyr	Ala	Ser	Val	Met	Ile	Ala	Gln	Ala	Ile	Leu
		85			90									95	
Glu	Ser	Asp	Ser	Gly	Arg	Ser	Ala	Leu	Ala	Lys	Ser	Pro	Asn	His	Asn
		100			105									110	
Leu	Phe	Gly	Ile	Lys	Gly	Ala	Phe	Glu	Gly	Asn	Ser	Val	Pro	Phe	Asn
		115			120									125	
Thr	Leu	Gly	Ser												
	130														

(2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

Met	Cys	Val	Gly	Leu	Ala	Ile	Met	Thr	Trp	Val	Ile	Ser	Leu	Xaa	Asn
1		5		10		15									
Val	Ser	Val	Lys	His	Pro	Gly	Thr	His	Xaa	Thr	Ile	Tyr	Ile	Lys	Asn
		20		25		30									
Ile	Ile	Ser	His	Asp	Gly	Xaa	Thr	Met	Ile	Met	Asn	Asp	Thr	Ile	Lys
		35		40		45									
Xaa	Phe	Ser	Glu	Xaa	Pro	Ala	Leu	Gly	Leu	Val	Leu	Ala	Xaa	Met	Ile
		50		55		60									
Gly	Ile	Gly	Val	Ala	Glu	Xaa	Asn	Arg	Ile	Leu	Arg				
65		70		75											

(2) INFORMATION FOR SEQ ID NO:326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- 435

- (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

```

Met Ser Lys Ser Glu Gln Ala Asp Ile Lys Asp Val Gly Gly Phe Val
 1             5             10             15
Gly Gly Tyr Leu Lys Glu Gly Lys Arg Arg Ala Gly Gln Val Met Asn
      20             25             30
Arg Ser Met Leu Thr Leu Asp Ile Asp Tyr Ala Ala Gln Asp Met Thr
      35             40             45
Asp Ile Leu Ser Met Phe Tyr Asp Phe Ala Tyr Cys Leu Tyr Ser Thr
      50             55             60
His Lys His Arg Glu Ile Ser Pro Arg Leu Arg Leu Val Ile Pro Leu
65             70             75             80
Lys Arg Asn Val Asn Ala Asp Glu Tyr Glu Ser Tyr Trp Ala Leu Ser
      85             90             95
Pro Gln Ile Ser Leu Gly Met Asp Tyr Phe Asp Asp Thr Thr Tyr Gln
      100            105            110
Pro His Arg Leu Asn Val Ile Gly Leu Pro Pro Ser
      115            120

```

(2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

```

Met Met Lys Leu Ile Lys Asn Gly Lys Val Leu Gln Asn Gly Glu Leu
 1             5             10             15
Gln Gln Ala Asp Ile Leu Ile Asp Gly Lys Val Ile Lys Gln Ile Ala
      20             25             30
Pro Ala Ile Asp Pro Ser Asn Gly Val Gly His His Arg Cys Glu Arg
      35             40             45

```

Ser Leu Gly Gly His Leu Asp Leu Val Asp Val Gln Val Pro Phe Pro
 50 55 60

(2) INFORMATION FOR SEQ ID NO:328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

Met Thr Ile Tyr Glu Glu Tyr Gly Tyr Phe Glu Gly Leu Asp Val Leu
 1 5 10 15
 Ile Cys Gly Asp Ile Lys Asn Ser Arg Val Ala Arg Ser Asn Tyr His
 20 25 30
 Ser Leu Lys Ala Leu Gly Ala Asn Val Met Phe Asn Ser Pro Asn Ala
 35 40 45
 Trp Ile Asp Asp Ser Leu Glu Ala Pro Tyr Val Asn Ile Asp Asp Val
 50 55 60
 Ile Glu Thr Val Asp Ile Val Met Leu Leu Arg Ile Gln His Glu Arg
 65 70 75 80
 His Gly Leu Ala Glu Glu Thr Arg Phe Ala Ala Asp Asp Tyr His Gln
 85 90 95
 Lys His Gly Leu Asn Glu Val Arg Tyr Asn Lys Leu Gln Glu His Ala
 100 105 110
 Ile Val Met His Pro Ala Pro Val Asn Arg Gly Val Glu Ile Gln Ser
 115 120 125
 Asp Leu Val Glu Ala Ser Lys Ser Arg Ile Phe Lys Gln Met Glu Asn
 130 135 140
 Gly Val Tyr Leu Arg Met Ala Val Ile Asp Glu Leu Leu Lys
 145 150 155

(2) INFORMATION FOR SEQ ID NO:329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

```

Met Asn His Leu Leu Ser Met Glu His Leu Ser Thr Asp Gln Ile Tyr
 1           5           10           15
Lys Leu Ile Gln Lys Ala Ser Gln Phe Lys Ser Gly Glu Arg Gln Leu
      20           25           30
Pro Asn Phe Glu Gly Lys Tyr Val Ala Asn Leu Phe Phe Glu Asn Ser
      35           40           45
Thr Arg Thr Lys Cys Ser Phe Glu Met Ala Arg Ala Ala Leu Glu Leu
      50           55           60
Gly Leu Lys Thr Ile Ser Phe Glu Thr Ser Thr Ser Ser Val Ser Lys
65           70           75           80
Gly

```

(2) INFORMATION FOR SEQ ID NO:330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

```

Met Met Met Ser Thr Ile Xaa Val Xaa Gly Arg Arg Asp Xaa Ile Ile
 1           5           10           15
Ile Arg Ser Asp Tyr Thr Xaa Gly Pro Val Glu Asp Glu Asp Xaa Leu
      20           25           30
Xaa Xaa His Pro Xaa Val Lys Glu Cys Ala Val Val Xaa Xaa Pro His
      35           40           45
Asp Ile Arg Gly Asn Ile Val Lys Ala Phe Val Ile Leu Gln Asp His
      50           55           60
Thr Ala Gly Asp Asp Thr Leu Val Lys Glu Leu Gln Gln Phe Val Lys
65           70           75           80
Asn Glu Val Ala Pro Tyr Lys Tyr Pro Arg Glu Ile Glu Phe Pro Phe
      85           90           95
Val Ile Ser Gly Ile Phe

```

100

(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

```

Met Thr Met Ile Gln Ile Ile Gly Val Ile Leu Val Thr Ile Val Leu
 1             5             10             15
Leu Asn His Trp Asn Phe Trp Ile Leu Ala Ile Gly Phe Ile Ile Leu
      20             25             30
Ile Ala Pro Xaa Thr Gly Val Ala Thr Leu Gly Phe Xaa Ile Ala Met
      35             40             45
Asp Glu Ser Ser Ser Gly Arg Gly Ser Ser Ser Ser Leu Leu Gly Leu
      50             55             60
Val Gln Phe Leu Phe Gly Gly Val Ala Ser Pro Leu Val Gly Val Lys
      65             70             75             80
Gly Glu Asp Asn Pro Ile Pro Tyr Ile Ile Ile Ile Ala Thr Ala
      85             90             95
Xaa Ile Leu Ile Ile Xaa Gln Ile Tyr Asn Met Lys Val Xaa
      100             105             110

```

(2) INFORMATION FOR SEQ ID NO:332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

```

Met Asn Asp Tyr Ser Thr Thr Val Ala Asn Lys Gln Leu Tyr Val Thr
 1             5             10             15

```


Tyr Ile Ile Gly Gly Gln Xaa Gly Val Phe Ile Asn Trp Leu Ser Xaa
 20 25 30
 Gly Cys Xaa Glu Ser Pro Glu Glu Val Ala Asp Ile Leu Leu Ala Asn
 35 40 45
 Thr Xaa Lys Leu Gln Xaa Gln
 50 55

(2) INFORMATION FOR SEQ ID NO:333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

Met Lys Lys Met Ile Leu Ile Asn Val Ile Thr Val Val Val Leu Leu
 1 5 10 15
 Ala Ile Gly Ile Ala Gly Phe Tyr Phe Trp Asn Lys Thr Thr Ser Tyr
 20 25 30
 Val Thr Thr Asp Asn Ala Lys Val Asn Gly Asp Gln Ile Lys Ile Ala
 35 40 45
 Ser Pro Ala Ser Gly Gln Ile Lys Ser Leu Asn Val Lys Gln Gly Asp
 50 55 60
 Lys Leu Asp Lys Gly Asp Lys Val Ala Thr Val Thr Val Gln Gly Gln
 65 70 75 80
 Asp Gly Glu Thr Lys Asp Met Asp Leu Lys Met Pro Gln Lys Gly Thr
 85 90 95
 Ile Gly Lys Leu Asp Gly Met Glu Gly Ser Met Arg Ala Ser Trp
 100 105 110

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

```

Met Xaa Gln Ala Asn Ile Asp Glu Lys Asp Ile Lys Asp Val Glu Val
 1             5             10             15
Gly Lys Asp Val Asp Val Thr Ile Asp Gly Gln Lys Ala Ser Ile Lys
          20             25             30
Gly Lys Val Asp Ser Ile Gly Lys Ala Thr Ala Ala Ser Phe Ser Leu
          35             40             45
Met Pro Ser Ser Asn Ser Asp Gly Asn Tyr Thr Lys Val Ser Gln Val
          50             55             60
Ile Pro Val Lys Ile Thr Leu Glu Ser Glu Pro Ser Lys Gln Val Val
          65             70             75             80
Pro Gly Met Asn Ala Glu Val Lys Ile His Lys Asn Xaa Gly Gly Ser
          85             90             95
Leu Asn Asp Tyr Asp Leu His Tyr
          100

```

(2) INFORMATION FOR SEQ ID NO:335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

```

Met Ile Pro Gly Ile Asp Leu Ala Gly Thr Ile Val Glu Ser Glu Ala
 1             5             10             15
Pro Gly Phe Glu Lys Gly Glu Gln Val Ile Val Thr Ser Tyr Asp Leu
          20             25             30
Gly Val Ser His Tyr Gly Gly Phe Ser Glu Tyr Ala Arg Val Lys Ser
          35             40             45
Glu Trp Ile Ile Lys Leu Pro Asp Thr Leu Thr Leu Glu Glu Ser Met
          50             55             60
Ile Tyr Gly Thr Ala Gly Tyr Thr Ala Gly Leu Ala Ile Glu Arg Leu
          65             70             75             80
Glu Lys Val Gly Met Asn Ile Glu Asp Gly Pro Val Leu Val Arg Gly
          85             90             95
Ala Ser Gly Gly Val Gly Thr Leu Ala Val Leu Met Leu Asn Glu Leu
          100

```

	100	105	110
Gly Tyr Lys Val Ile Ala Ser Thr Gly Lys Pro Arg Cys			
115	120	125	

(2) INFORMATION FOR SEQ ID NO:336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

Met	Ile	Ile	Lys	Asn	Pro	Leu	Ala	Ser	Ser	Thr	Cys	Gln	Ala	Xaa	Glu
1				5					10					15	
Asp	Pro	Val	Gly	Gly	Glu	Gly	Ile	Asn	Tyr	Val	Thr	Lys	Arg	Leu	Asn
			20					25					30		
His	Ser	Gly	Ser	Ile	Ala	Val	Ile	Gly	Met	Thr	Ala	Gly	Asn	Thr	Tyr
			35					40					45		
Thr	Asn	Ser	Val	Phe	Pro	His	Ile	Leu	Arg	Gly	Val	Asn	Ile	Leu	Gly
			50					55				60			
Ile	Asp	Ser	Val	Phe	Thr	Ala	Met	Lys	Leu	Arg	His	Glu	Arg	Leu	Ala
65					70					75				80	
Ser	Ser	Arg	Lys	Arg	Phe	Lys	Ala								

(2) INFORMATION FOR SEQ ID NO:337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

Met	Val	Lys	Val	Thr	Tyr	Asp	Ile	Pro	Thr	Cys	Glu	Asp	Tyr	Cys	Ala
1				5					10					15	

```

Leu Arg Ile Asn Ala Gly Met Ser Pro Lys Thr Arg Glu Ala Ala Glu
      20                      25                      30
Lys Gly Leu Pro Asn Ala Leu Phe Thr Val Thr Leu Tyr Asp Lys Asp
      35                      40                      45
Arg Leu Ile Gly Met Gly Arg Val Ile Gly Asp Gly Gly Thr Val Phe
      50                      55                      60
Gln Ile Val Asp Ile Ala Val Ser Lys Ser Tyr Gln Gly Gln Asp Tyr
      65                      70                      75                      80
Gly Arg Leu Ile Met Glu His Ile Met Lys Xaa Tyr
      85                      90

```

(2) INFORMATION FOR SEQ ID NO:338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

```

Met Thr Leu Asn Lys Arg Asn Thr Pro Gly Ser Leu Xaa Pro Lys Phe
 1              5              10              15
Leu Asn Val Ser Ser Leu Ile Gln Tyr Ile Gln Ala Ala Tyr His Glu
      20                      25                      30
Pro Leu Arg Glu Glu Phe Lys Asn Leu Thr Pro Tyr Val Thr Lys Leu
      35                      40                      45
Ser Lys Val His Gly Pro Asn His Pro Tyr Leu Val Glu Leu Lys Glu
      50                      55                      60
Thr Tyr Asp Thr Phe Lys Ser Gly Met Leu Glu His Ile Gln Lys Glu
      65                      70                      75                      80
Asp Asp Val Asp Phe Gln Asn
      85

```

(2) INFORMATION FOR SEQ ID NO:339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

```

Met His Lys Leu Ile Ile Lys Tyr Asn Lys Gln Leu Lys Met Leu Asn
 1             5             10             15
Leu Arg Asp Gly Lys Thr Tyr Thr Ile Ser Glu Asp Glu Arg Ala Asp
      20             25             30
Ile Thr Leu Lys Ser Leu Gly Glu Val Ile His Leu Glu Gln Asn Asn
      35             40             45
Gln Gly Thr Trp Gln Ala Asn His Thr Ser Ile Asn Lys Val Leu Val
      50             55             60
Arg Lys Gly Asp Leu Asp Asp Ile Thr Leu Gln Leu Xaa Thr Glu Ala
65             70             75             80
Asp Tyr Ala Ser Phe Gly Tyr Pro Ser Ile Pro Arg Ile Arg
      85             90

```

(2) INFORMATION FOR SEQ ID NO:340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

```

Met Arg Glu Ile Pro Lys Ser Ser Ile Xaa Pro Glu His Phe His Leu
 1             5             10             15
Met Tyr Leu Leu Glu Gln His Ser Pro Tyr Phe Ile Asp Ala Glu Leu
      20             25             30
Thr Glu Leu Arg Asp Ser Phe Gln Ile His Tyr Asp Leu Asn Asp Asn
      35             40             45
His Thr Pro Cys Asp Asn Leu Lys Ser Phe Thr Lys Asn Glu Lys Leu
      50             55             60
Arg Tyr Leu Leu Asn Ile Lys Asn Leu Glu Glu Val Asn Arg Thr Arg
65             70             75             80
Tyr Thr Phe Val Trp Ala Pro Asp Glu Leu Phe Phe Thr Arg Asp Gly
      85             90             95
Leu Pro Ile Ala Lys Thr Arg Gly Leu Gln Asn Val Val Asp Pro Xaa

```

```

      100              105              110
Pro Val Ser Glu Ala Glu Phe Leu Thr Arg Tyr Lys Ala Leu Val Ile
      115              120              125
Cys Ala Phe Asn Glu Lys Gln Ser Phe Asp Ala Leu Val Glu Gly Asn
      130              135              140
Leu Glu Leu His Lys Gly Thr Pro Phe Glu Thr Lys Val Ile Glu Ala
      145              150              155              160
Ala Thr Leu Asp Leu Leu Thr Ala Phe Leu Asp Glu Gln Tyr Gln Lys
      165              170              175
Gln Glu Gln Asp Tyr Ser Gln Asn Tyr Ala Tyr Val Arg Lys Val Gly
      180              185              190
His Thr Val Phe Lys Trp Val Ala Ile Gly Met Thr Thr Leu Ser Val
      195              200              205
Leu Leu Ile Ala Phe Leu Ala Phe Xaa Tyr Xaa Ser Val Met Lys His
      210              215              220
Asn Glu Arg Ile Glu Lys Gly Xaa His Ala Xaa Val Arg Asp Asp Tyr
      225              230              235              240
Thr Gln Val Leu Asn Thr Cys Asp Asp Leu Asp Gly Lys Lys Leu Ala
      245              250              255
Arg Gly Xaa Leu Xaa Ile Tyr Ala Arg Gly Tyr Phe His Pro Thr Xaa
      260              265              270
Leu Gly Xaa Xaa Xaa Arg
      275

```

(2) INFORMATION FOR SEQ ID NO:341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

```

Met Ala Thr Asp Thr Leu Xaa Lys Ala Arg Val Leu Asp Ile Thr Gly
  1              5              10              15
Pro Leu Gly Asn Xaa Ile His Phe Ala Asn Ser Ala Val Asp Arg Ile
      20              25              30
Val Pro Leu Gln Xaa Xaa Glu Asn Ile Leu Asp Val Met Val Glu Pro
      35              40              45
Phe Tyr Glu Trp Val Val Glu Lys Asp Ala Trp Tyr Gly Pro Glu Leu
      445

```

50	55	60
Asn His Ile Lys Tyr Val Asp Asp Leu Thr Pro Tyr Ile Glu Arg Lys		
65	70	75
Leu Leu Thr Val Asn Thr Gly His Ala Tyr Leu Ala Tyr Ala Gly Lys		80
	85	90
Phe Ala Gly Lys Ala Thr Val Leu Asp Ala Val Lys Asp Ser Ser Ile		95
	100	105
Glu Ala Gly Leu Arg Arg Val Leu Ala Glu Thr Ser Gln Tyr Ile Thr		110
	115	120
Asn Glu Phe Asp Phe Thr		125
130		

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

Met Gly Pro Gln Asp Ile Ala Val Ala Lys Gly Ala Asp Ser Pro Leu		
1	5	10
Ile Lys Pro Xaa Ala Phe Ala Ser Glu Ile His Gly Glu Ser Gly Leu		15
	20	25
Asp Gly Pro Lys Leu Pro Ser Thr Pro Ser Arg Gln Ala Val Ala Met		30
	35	40
Pro Ala Ser Asp Val Ile Ile Asn Lys Val Met Thr Ser Asp Thr Pro		45
	50	55
Val Thr Ile Val Ala Thr Gly Pro Leu Thr Asn Val Ala Thr Ala Leu		60
	65	70
Ile Arg Glu Pro Arg Ile Ala Glu His Ile Glu Ser Ile Thr Leu Met		75
	85	90
Gly Gly Gly Thr Phe Gly Asn Trp Thr Pro Thr Ala Gly Ile Ser Ile		95
	100	105
Phe Gly		110

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

```

Met Leu Lys Ala Ala Lys Arg Val Leu Glu Ser Gly Ile Thr Ile Asn
 1             5             10             15
Val Phe Gly Leu Asp Val Thr His Gln Val Leu Ala Asp Asn His Val
      20             25             30
Ile Glu Arg Phe Glu Ser Ile Asn Asn Pro Val Ala Gln Phe Val Val
      35             40             45
Glu Leu Leu Gln Phe Phe Lys Lys Thr Tyr Lys Thr His Phe Asn Met
 50             55             60
Asp Gly Gly Pro Ile His Asp Ala Cys Thr Asn Leu Tyr Leu Leu Gln
65             70             75             80
Pro Glu Leu Phe Thr Met Val Pro Val Asn Xaa Asp Ile
      85             90

```

(2) INFORMATION FOR SEQ ID NO:344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

```

Met Ala Lys Thr Tyr Ile Phe Gly His Lys Asn Pro Asp Thr Asp Ala
 1             5             10             15
Ile Ser Ser Ala Ile Ile Met Ala Glu Phe Glu Gln Leu Arg Gly Asn
      20             25             30
Ser Gly Ala Lys Ala Tyr Arg Leu Gly Asp Val Ser Ala Glu Thr Gln
      35             40             45
Phe Ala Leu Asp Thr Phe Asn Val Pro Ala Pro Glu Leu Leu Thr Asp
 50             55             60

```



```

Asp Leu Asp Gly Gln Asp Val Ile Leu Val Asp His Asn Glu Phe Xaa
65              70              75              80
Pro Ser Ser Asp Thr Ile Val Ser Ala Thr Ile Lys His Val Ile Asp
              85              90              95
Pro His Arg Ile Ala Asn Phe Glu Thr Ala Gly Pro Leu Cys Tyr Arg
              100             105             110
Ala Glu Pro Val Gly Cys Thr Ala Thr Ile Leu Tyr Lys Met Phe Arg
              115             120             125
Glu Arg Gly Xaa Glu Ile Asn Pro Glu Ile Gly Gly Leu Met Leu Ser
              130             135             140
Ala Ile Ile Ser Asp Ser Leu Leu Xaa Asn Ser Pro Thr Cys Thr Gln
145             150             155             160
Gln Arg Arg Xaa Xaa Arg Trp Lys Asn
              165

```

(2) INFORMATION FOR SEQ ID NO:345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

```

Met Thr His Arg Ala Leu Leu Val Val Asp Tyr Ser Tyr Asp Phe Ile
1              5              10              15
Ala Asp Asp Gly Leu Leu Thr Cys Gly Lys Pro Gly Gln Asn Ile Glu
              20              25              30
Asp Phe Ile Val Ser Arg Ile Asn Asp Phe Asn Tyr Tyr Gln Asp His
              35              40              45
Ile Phe Phe Leu Met Asp Leu His Tyr Leu His Asp Ile His His Pro
              50              55              60
Glu Ser Lys Leu Phe Pro Pro His Asn Ile Val Asp Thr Ser Gly Arg
65              70              75              80
Glu Leu Tyr Gly Lys Val Gly Lys Leu Xaa Asp Thr Ile Lys Ala Gln
              85              90              95
Pro Asn Val His Phe Ile Asp Lys Thr Arg Tyr Asp Ser Phe Phe Gly
              100             105             110
Thr Pro Leu Asp Ser Leu Phe Glu Arg Lys Lys Tyr
              115             120

```

(2) INFORMATION FOR SEQ ID NO:346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

```

Met Leu Leu Xaa Arg Leu Leu Ala Tyr Pro Pro Thr Asn Leu Pro Lys
 1             5             10             15
Ile Gly Gln Glu Ile Gly Asn Val Phe Ala Gly Ile Gly Xaa Leu Met
          20             25             30
Ile Ala Phe Ala Gln Asn Ser Ser Asn Ile Phe Asp Trp Leu Val Lys
      35             40             45
Leu Thr Ser Gln Phe Arg Ala Trp Ser Glu Gln Val Gly Gln Ser Gln
      50             55             60
Gly Phe Lys Asp Phe Ile Ser Tyr Val Gln Glu Asn Gly Pro Thr Ile
65             70             75             80
Met Gln Leu Ile Gly Asn Ile Ile Lys Ala Leu Val Ala Phe Gly Thr
          85             90             95
Ala Met Ala Pro Ile Ala Ser Lys Leu Leu Asp Phe Ile Thr Asn Leu
          100             105             110
Ala Gly Phe Ile Ala Lys Leu Phe Glu Thr His Pro Ala Ile Ala Gln
          115             120             125
Val Ala Gly Val Met Gly Ile Leu Gly Gly Val Phe Trp Ala Leu Met
          130             135             140
Ala Pro Ile Val Ala Ile Ser Ser Val Leu Thr Asn Val Phe Gly Leu
          145             150             155             160
Ser Leu Phe Ser Val Val Glu Lys Ile Leu Glu Phe Val Arg Thr Ser
          165             170             175
Ser Leu Val Thr Gly Ala Leu Glu Ala Leu Thr Gly Val Phe Gly Thr
          180             185             190
Ile Ser Ala Pro Ile Leu Ala Val Ile Ala Val Ile Gly Ala Phe Ile
          195             200             205
Gly Val Leu Val Tyr Leu Trp Lys Thr Asn Glu Asn Phe Arg Asn Thr
          210             215             220
Ile Thr Glu Ala Trp Asn Gly Val Lys Thr Ala Val Ser Gly Ala Ile
          225             230             235             240

```

Gln Gly Val Val Gly Trp Leu Thr Glu Leu Trp Gly Lys Ile Gln Ser
 245 250 255
 Thr Leu Gln Pro Ile Met Pro Ile Leu Gln Val Leu Gly Gln Ile Phe
 260 265 270
 Met Gln Val Leu Gly Val Val Val Ile Gly Ile Ile Thr Asn Val Met
 275 280 285
 Asn Ile Ile Gln Gly Leu Trp Thr Leu Ile Thr Ile Ala Phe Gln Ala
 290 295 300
 Ile Gly Gln Val Ile Ser Arg Gly Lys Ser Lys Ser
 305 310 315

(2) INFORMATION FOR SEQ ID NO:347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

Met Glu Glu Ser Glu Arg Phe Asn Glu Trp Ile Glu Gln Gly Ala Ala
 1 5 10 15
 Ile Tyr Ile Cys Gly Asp Glu Lys Cys Met Ala Lys Asp Val His Gln
 20 25 30
 Ala Ile Lys Asp Val Leu Val Lys Glu Arg His Ile Ser Gln Glu Glu
 35 40 45
 Ala Glu Leu Leu Leu Arg Gln Met Lys Gln Gln Gln Arg Tyr Gln Arg
 50 55 60
 Asp Val Tyr
 65

(2) INFORMATION FOR SEQ ID NO:348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

```

Met Glu Ser Lys Asp Gln Leu Ile Gln Met Leu Glu Ser Leu Lys Asp
 1             5             10             15
Gln Gln Gln Phe Arg Asp Ala Leu Leu Ala Gln Lys Ala His Ala His
          20             25             30
Gly Thr Ser Val Asn Asn Ser Ser Lys Phe Leu Asn Arg Arg Ser Lys
      35             40             45
Ala Lys Lys Lys Lys Gln Ser Lys Ile Lys His His Leu Ile
    50             55             60

```

(2) INFORMATION FOR SEQ ID NO:349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

```

Met Met Ala Ser Ser Ile Ile Leu Thr Asn Ile Leu Pro Tyr Asp Ala
 1             5             10             15
Gln Ala Ala Ser Glu Lys Asp Thr Glu Ile Ser Lys Glu Ile Leu Ser
          20             25             30
Lys Gln Asp Leu Leu Asp Lys Val Asp Lys Ala Ile Arg Gln Ile Glu
      35             40             45
Gln Leu Lys Gln Leu Ser Ala Ser Ser Lys Ala His Tyr Lys Ala Gln
    50             55             60
Leu Asn Glu Ala Lys Thr Ala Ser Gln Ile Asp Glu Ile Ile Lys Arg
 65             70             75             80
Ala Asn Glu Leu Asp Ser Lys Glu Asn Lys Ser Ser His Thr Glu Met
          85             90             95
Asn Gly Gln Ser Asp Ile Asp Ser Lys Leu Asp Gln Leu Leu Lys Asp
      100             105             110
Leu Asn Glu Val Ser Ser Asn Val Asp Arg Gly Gln Gln Ser Gly Glu
      115             120             125
Asp Asp Leu Asn Ala Met Lys Asn Asp Met Ser Gln Thr Ala Thr Thr
      130             135             140
Lys Tyr Gly Glu Xaa Asp Asp Lys Asn Asp Glu Ala Met Val Asn Lys
                        451

```

145 150 155 160
 Ala Leu Glu Glu Leu Glu His Leu Asn Pro Ala Asn Thr Pro Ile Arg
 165 170 175
 Lys Met His

(2) INFORMATION FOR SEQ ID NO:350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

Met Lys Ser Thr Ala Gln Leu Thr Lys Glu Asn Asn Val Lys Ser Leu
 1 5 10 15
 Arg Leu Ser Asn Thr Asp Arg Glu Ile Phe Glu Asn Tyr Met Thr Tyr
 20 25 30
 Met Arg Ser Asp Phe Arg Val Asn Pro His Asp Thr Glu Leu Ile Ile
 35 40 45
 Asn Arg Ile Leu Lys Gln Leu Leu Ser Ala Glu Gln His Gly Leu Leu
 50 55 60
 Ala Leu Asp Phe Phe Asn His Asp Pro Lys Ala His Ala Ile Lys Glu
 65 70 75 80
 Leu Lys Ala Met Pro Asn Glu Thr Phe Lys Asn Ile Phe Lys Tyr Ile
 85 90 95
 Tyr Gln His Ile Val Leu Leu Ile Gly Ile Val Ser Phe Leu Lys Gly
 100 105 110
 Phe Leu Gly Phe Phe His Gly Lys Lys Trp Lys
 115 120

(2) INFORMATION FOR SEQ ID NO:351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

```

Met Phe Xaa Lys Phe Asp Arg Ile Glu Asp Ser Leu Arg Thr Gln Glu
 1             5             10             15
Lys Ile Tyr Asp Lys Leu Asp Arg Asn Phe Glu Glu Leu Arg His Glu
             20             25             30
Arg Gln Gly Arg Arg
             35

```

(2) INFORMATION FOR SEQ ID NO:352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

```

Met Arg Ile Asp Lys Phe Leu Ala Asn Met Gly Val Gly Thr Arg Asn
 1             5             10             15
Glu Val Lys Gln Leu Leu Lys Lys Gly Leu Val Asn Val Asn Glu Gln
             20             25             30
Val Ile Lys Ser Pro Lys Thr His Ile Glu Pro Glu Asn Asp Lys Ile
             35             40             45
Thr Val Arg Gly Glu Leu Ile Glu Tyr Ile Glu Asn Val Tyr Ile Met
             50             55             60
Leu Asn Lys Pro Lys Gly Tyr Ile Ser Ala Thr Glu Asp His His Ser
             65             70             75             80
Lys Thr Val Ile Asp Leu Ile Pro Glu Tyr Gln His Leu Asn Ile Phe
             85             90             95
Pro Val Gly Arg Leu Asp Lys Asp Thr Glu Gly Leu Leu Leu Ile Thr
             100            105            110
Asn Asp Gly Asp Phe Asn His Glu Leu Met Ser Pro Asn Lys His Val
             115            120            125
Ser Lys Lys Tyr Glu Val Ile Ser Gly Asn Pro Ile Thr Glu Asp Asp
             130            135            140
Asn Ser Ser Phe
145

```

(2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

```

Met Glu Ala Val Xaa Ser Gly Leu Gly Met Ile Gly Leu Asn Val Asn
 1             5             10             15
Tyr Gly Asn Pro Thr Phe Ile Arg Asp Gly Glu Asn Gly Tyr Leu Val
      20             25             30
Pro Phe Asp Thr Xaa Glu Asp Arg Val Asp Asp Val Ile Ala Lys Leu
      35             40             45
Ala His Ala Ile Val Met Tyr Phe Asn Asn Gly Pro Gln Ala Pro His
      50             55             60
Asp Ile Ser Tyr Glu Val Ala Gln Gln Phe Met Thr Gln Asp Ile Ile
65             70             75             80
Leu Lys Trp Glu Thr Leu Xaa Gln Glu Val Leu His Asp
      85             90

```

(2) INFORMATION FOR SEQ ID NO:354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

```

Met Asp Tyr Ala Ile Gln Leu Pro Asn Met Val Gln Gly Xaa Thr Gly
 1             5             10             15
Val Asn Pro Pro Val Gly Ala Val Val Val Asn Glu Gly Arg Ile Val
      20             25             30
Gly Ile Gly Ala His Leu Arg Lys Gly Asp Lys His Ala Glu Val Gln
      45

```

```

          35              40              45
Ala Leu Asp Met Ala Gln Xaa Asn Ala Glu Gly Ala Thr Ile Tyr Ile
  50              55              60
Thr Leu Glu Pro Cys Ser His Phe Gly Ser Thr Pro Pro Cys Val Asn
  65              70              75              80
Lys Ile Ile Asp Cys Lys Ile Ala Xaa Val Val Leu Xaa Asn Xaa Arg
          85              90              95
Gln Phe Arg

```

(2) INFORMATION FOR SEQ ID NO:355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

```

Met Gly Arg Pro Thr Phe Leu His Asn Ile Ile Phe Asp Val Ala Arg
  1              5              10              15
His His Arg Pro Asp Gln Ala His Met Tyr Leu Phe Asp Phe Gly Thr
          20              25              30
Asn Gly Leu Met Pro Val Thr Asp Ile Pro His Val Ala Asp Tyr Phe
          35              40              45
Thr Glu Asp Pro Arg Arg Pro Arg Leu Leu Arg Arg Tyr Val Tyr Leu
          50              55              60
Met Met Lys Ser Gly Ser Ser
  65              70

```

(2) INFORMATION FOR SEQ ID NO:356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

```

Met Met Ile Lys Met Thr Arg Glu Gly Leu Ala Leu Asp Met Gln Val
 1             5             10             15
Thr Leu Thr Ala Ser Arg Ala Asn Ala Met Lys Thr Pro Met Tyr Ile
      20             25             30
Asn Met Lys Thr Arg Ile Ala Met Phe Leu Tyr Asp Lys Ser Glu Val
      35             40             45
Ser Asn Val Val Gly Gln Xaa Xaa Xaa Ala Val Lys Asp Val Val Gly
      50             55             60
Arg Ala Leu Leu Ser Ser Asp Asp Asn Val Ser Phe His Ile Gly Gln
65             70             75             80
Pro Phe Lys His Asp Glu Thr Lys Ser Tyr Asn Asp His Asn
      85             90

```

(2) INFORMATION FOR SEQ ID NO:357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

```

Met Ile Ser Ser Glu Asn Pro Arg Glu Ile Ala His Ile Ala Glu Ile
 1             5             10             15
Met Met Lys Glu Ile Asp Ile Leu Asn Glu Lys Tyr Ala Ile Cys Ile
      20             25             30
Ala Asp Ser Ser Gly Glu Phe Lys Ala Tyr Arg His Gln Val Ala Asn
      35             40             45
Phe Ala Glu Glu Arg Glu Asp Ile Lys Ala Ile His Gln Leu Met Ile
      50             55             60
Glu Asp Leu Lys Gln Arg Glu Met Asp Gly Pro Phe Glu Lys Asp Ser
65             70             75             80
Leu Tyr Ile Ile Asn Asp Phe Lys Thr Tyr Ile Asp Cys Thr Tyr Ile
      85             90             95
Pro Glu Asp Asp Val Lys Lys Leu Ile Thr Lys Gly Pro Glu Leu Gly
      100             105             110
Leu Asn Ile Leu Phe Val Gly Ile His Lys Glu Leu Ile Asp Ala Tyr
      115             120             125

```

Asp Lys Gln Ile Asp Val Ala Arg Lys Met Ile Asn Gln Phe Ser Ile
 130 135 140
 Gly Ile Pro Tyr Phe Arg Pro Thr Ile Leu
 145 150

(2) INFORMATION FOR SEQ ID NO:358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

Met Lys Cys Val Gly Ala Thr Thr Val Ala Thr Thr Met Ile Cys Ala
 1 5 10 15
 Pro Met Ala Gly Ile Gln Phe Phe Val Thr Gly Gly Ile Gly Gly Val
 20 25 30
 His Lys Gly Ala Glu His Thr Met Asp Ile Ser Ala Asp Leu Glu Glu
 35 40 45
 Leu Ser Lys Thr Asn Val Thr Val Ile Cys Ala Gly Ala Lys Ser Ile
 50 55 60
 Leu Asp Leu Pro Lys Thr Met Glu Tyr Leu Glu Thr Lys Gly Val Pro
 65 70 75 80
 Val Ile Gly Tyr Gln Thr Asn Glu Leu Pro Ala Phe Phe Thr Arg Glu
 85 90 95
 Ser Gly Val Lys Leu Thr Ser Ser Val Glu Thr Pro Glu Arg Leu Ala
 100 105 110
 Asp Ile His Leu Thr Lys Gln Gln Leu Asn Leu Glu Gly Gly Ile Val
 115 120 125
 Val Ala Asn Pro Ile Pro Tyr Glu His Ala Leu Ser Lys Ala Tyr Ile
 130 135 140
 Glu Ala Ile Ile Asn Glu Ala Val Val Glu Ala Glu Asn Gln Gly Ile
 145 150 155 160
 Lys Gly Lys Asp Ala Thr Pro Phe Leu Leu Gly Lys Ile Val Glu Lys
 165 170 175
 Thr Asn Gly Lys Ser Leu Ala Ala Asn Ile Lys Leu Val Glu Asn Asn
 180 185 190
 Ala Ala Leu Gly Ala Lys Ile Ala Val Ala Val Asn Lys Leu Leu
 195 200 205

(2) INFORMATION FOR SEQ ID NO:359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

```

Met Lys Phe Gln Leu Glu Glu Leu Ser Glu Ala His Leu Lys Glu Gly
 1             5             10             15
Glu Ile Glu Gln Leu Glu Ile Asp Ile Lys Arg Ile His Asn Ser Glu
      20             25             30
Lys Leu Ser Leu Ala Leu Asn Asn Ala His Met Thr Leu Thr Asp Glu
      35             40             45
Asn Ala Ile Thr Asp Arg Leu Tyr Glu Leu Ser Asn His Leu Leu Thr
      50             55             60
Ile Asn Asp Ile Val Pro Asn Lys Tyr Asp Lys Leu Lys Glu Asp Ile
65             70             75             80
Asp Gln Phe Tyr Tyr Ile Leu Glu Asp Ala Lys His Glu Xaa Tyr Asp
      85             90             95
Glu Met Ala Xaa Thr Glu Phe Asp Glu Gln Val Leu Asn Glu Tyr Glu
      100            105            110
Ser Arg Met Asn Leu Leu Asn Asn Leu Lys Arg Lys Tyr Gly Lys Asp
      115            120            125
Ile Ser Glu Leu Ile Ala Tyr Gln Glu Lys Leu Asn Asn Glu Ile Asn
      130            135            140
Lys Ile Glu Asn Tyr Glu Gln Ser Thr Ser Gln Leu Arg Glu Glu Ile
145            150            155            160
Asn Ala Leu Tyr Asn Gln Val Ile Glu Val Gly Gln Ala Leu Ser Lys
      165            170            175
Gln Arg Arg Ile Val Ala Arg Glu Leu Arg Asp His Ile Val Ser Glu
      180            185            190
Ile Gln Asn Leu Gln Met Lys Asp Ala Asn Leu Glu Ile Ser Phe Lys
      195            200            205
Lys Leu Glu Glu Pro Asn Ile Asp Gly Ile Glu Phe Val Glu Phe Leu
      210            215            220
Xaa Thr Pro Asn Lys Gly Gly Thr Xaa Lys Lys Phe Xaa
225            230            235

```

(2) INFORMATION FOR SEQ ID NO:360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

```

Met Pro Lys Glu Met Leu Pro Ile Leu Asp Lys Pro Thr Ile Gln Tyr
 1             5             10             15
Ile Val Glu Glu Ala Ala Arg Ala Gly Ile Glu Asp Ile Ile Ile Val
      20             25             30
Thr Gly Arg His Lys Arg Ala Ile Ala Asp His Phe Asp Ser Gln Lys
      35             40             45
Glu Leu Glu Met Val Leu Lys Glu Lys Gly Lys Ser Glu Leu Leu Glu
      50             55             60
Lys Val Gln Tyr Ser Thr Glu Leu Ala Asn Ile Phe Tyr Val Arg Gln
      65             70             75             80
Lys Glu Xaa Lys Gly Leu Gly His Ala Ile Ser Ser Ala Leu Val Pro
      85             90             95
Ile Tyr Arg Gln
      100

```

(2) INFORMATION FOR SEQ ID NO:361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

```

Met Leu Thr Ile Pro Xaa Lys Glu Asn Arg Gly Ser Lys Glu Gln Glu
 1             5             10             15
Val Ala Ile Met Ile Asp Ala Leu Ala Asp Thr Gly Xaa Lys Ala Leu
                        459

```

	20		25		30										
Glu	Ala	Leu	Ser	Lys	Lys	Ser	Gln	Glu	Glu	Ile	Asp	His	Ile	Val	His
	35						40						45		
Gln	Met	Ser	Leu	Ala	Ala	Val	Asp	Gln	His	Met	Val	Leu	Ala	Gln	Leu
	50					55						60			
Ala	His	Glu	Glu	Thr	Gly	Arg	Gly	Ile	Tyr	Glu	Asp	Lys	Ala	Ile	Lys
65					70					75				80	
Asn	Leu	Tyr	Ala	Ser	Glu	Tyr	Ile	Trp	Asn	Xaa	Ile	Lys	Asp	Asn	Lys
				85				90					95		
Thr	Val	Gly	Ile	Ile	Gly	Glu	Asp	Lys	Glu	Lys	Gly	Leu	Thr	Tyr	Val
			100					105					110		
Ala	Glu	Pro	Ile	Gly	Val	Ile	Cys	Gly	Val	Thr	Pro	Thr	Thr	Asn	Pro
	115						120					125			
Thr	Ser	Thr	Thr	Ile	Phe	Lys	Ala	Met	Ile	Ala	Ile	Lys	Thr	Gly	Asn
	130					135						140			
Pro	Ile	Ile	Cys	Ala	Phe	His	Pro	Ser	Ala	Gln	Glu	Ser	Ser	Lys	Arg
145					150					155				160	
Ala	Ala	Glu	Val	Val	Leu	Glu	Ala	Ala	Met	Lys	Ala	Gly	Ala	Pro	Lys
				165				170					175		
Asp	Ile	Ile	Gln	Trp	Ile	Glu	Val	Pro	Ser	Ile	Glu	Ala	Thr	Lys	Gln
			180				185					190			
Leu	Met	Asn	His	Lys	Gly	Ile	Ala	Leu	Val	Leu	Ala	Thr	Gly	Gly	Ser
	195						200					205			
Gly	Met	Val	Lys	Ser	Ala	Tyr	Ser	Thr	Gly	Asn	Arg	His			
	210						215					220			

(2) INFORMATION FOR SEQ ID NO:362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

Met	Tyr	Asn	Leu	Asp	Arg	Ile	Xaa	Val	Tyr	Met	Arg	Leu	Arg	Arg	Val
1			5					10				15			
Gly	Asn	Lys	Phe	Ser	Ile	Lys	Thr	Trp	Lys	Phe	Asp	His	Ile	Lys	Asp
		20					25				30				
Pro	Asp	Arg	Arg	Lys	Pro	Ile	Asp	Met	Asp	Glu	Lys	Glu	Trp	Ile	Asp
								460							

```

          35          40          45
Gly Gly Lys Phe Tyr Gln Arg Pro Ala Ser Ile Ile Ala Ile Tyr Ser
  50          55          60
Ala Lys Tyr Xaa Gly Tyr Lys Trp Met Glu Met Asn Gly Leu Gly Ser
  65          70          75          80
Phe Asn Thr Glu Ile Leu Pro Xaa Pro Lys Gly Ala Arg Asp Val Ile
          85          90          95
Ile Gln Lys Gly Asp Leu Val Lys Ile Asp Xaa Gln Ala Xaa Ser Val
          100          105          110
Val Ile Lys
          115

```

(2) INFORMATION FOR SEQ ID NO:363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

```

Met Asp Val Asp Thr Thr Ser Lys Lys Gly Ala His Glu Lys Leu Leu
  1          5          10          15
Thr Glu Phe Glu Lys Gly Asn Gly Asp Ile Leu Leu Gly Thr Gln Met
          20          25          30
Ile Ala Lys Gly Leu Asp Tyr Pro Asn Ile Thr Leu Val Gly Val Leu
          35          40          45
Asn Ala Asp Thr Met Leu Asn Leu Pro Asp Phe Arg Ala Ser Glu Arg
          50          55          60
Thr Tyr Gln Leu Leu Thr Gln Val Ala Gly Arg Ala Gly Arg His Glu
          65          70          75          80
Lys Ala Gly Gln Val Ile Ile Gln Thr Tyr Asn Pro Asp His Tyr Ser
          85          90          95
Ile Leu Asp Cys Ser Lys Lys
          100

```

(2) INFORMATION FOR SEQ ID NO:364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids

- (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

```

Met Asn Leu Asp Ser Gln Ile Leu Val Lys Tyr Lys Ser Glu Pro Gly
 1             5             10             15
Leu Leu Gln Ala Xaa Gln Phe Leu Asp Asp Tyr Tyr His Glu Lys Phe
      20             25             30
Ile Lys Glu Lys Leu Ala Leu Lys Ile Asp Ile Gly Xaa Thr Asp Asp
      35             40             45
Asp Val Thr Leu Leu Ile Ile Arg Asn Lys Xaa Lys Tyr Cys Thr Ser
      50             55             60
Ile
65
  
```

(2) INFORMATION FOR SEQ ID NO:365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

```

Met Lys Val Leu Asn Leu Gly Ser Lys Lys Gln Ala Ser Phe Tyr Val
 1             5             10             15
Ala Cys Glu Leu Tyr Lys Glu Met Ala Phe Asn Gln His Cys Lys Leu
      20             25             30
Gly Leu Ala Thr Gly Gly Thr Met Thr Asp Leu Tyr Glu Gln Leu Val
      35             40             45
Lys Leu Leu Asn Lys Asn Gln Leu Asn Val Asp Asn Val Ser Thr Phe
      50             55             60
Asn Leu Asp Glu Tyr Val Gly Leu Thr Ala Ser His Pro Gln Ser Tyr
      65             70             75             80
His Tyr Tyr Met Asp Asp Met Leu Xaa Lys Gln Tyr Pro Tyr Phe Xaa
      85             90             95
  
```

```

Arg Lys Asn Ile His Ile Pro Asn Gly Asp Ala Asp Asp Met Asn Ala
      100                      105                      110
Glu Ala Ser Lys Tyr Asn Asp Val Leu Glu Gln Gln Gly Gln Arg Asp
      115                      120                      125
Ile Gln Ile Leu Gly Ile Gly Glu Asn Gly His Ile Gly Phe Asn Glu
      130                      135                      140
Pro Gly Thr Pro Phe Asp Ser Val Thr His Ile Val Asp Leu Thr Glu
      145                      150                      155                      160
Ser Thr Ile Lys Ala Asn Ser Arg Tyr Phe Lys Asn Glu Asp Asp Val
      165                      170                      175
Pro Lys Gln Ala Ile Ser Met Gly Leu Ala Asn Ile Leu Gln Ala Lys
      180                      185                      190
Arg Ile Ile Leu Leu Ala Phe Gly
      195                      200

```

(2) INFORMATION FOR SEQ ID NO:366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

```

Met Met Leu Phe Tyr Gln Cys Tyr Leu Lys Gln Gln Leu Gln Xaa Ile
  1              5              10              15
Ala Leu Pro Val Ser Ala Gly Ile Gly Gly Ile Lys Glu Leu Thr Ser
      20              25              30
Leu Ala Xaa Ile Leu Asn Gly Val Ile Ile Tyr Ala Leu Gly Asn Lys
      35              40              45
Phe Xaa Lys Leu Phe Arg Ile Thr Asn Pro Ile Ala Arg Gly Leu Ala
      50              55              60
Leu Gly Thr Ser Gly His Thr Leu Gly Val Ala Pro Ala Lys Glu Leu
      65              70              75              80
Gly Pro Val Glu Glu Ser Met Ala Ser Ile Ala Leu Val Leu Val Gly
      85              90              95
Val Val Val Val Ala Val Val Pro Val Phe Val Ala Ile Phe Phe
      100              105              110

```

(2) INFORMATION FOR SEQ ID NO:367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

```

Met Asn Ala Gly Thr Gln Leu Tyr His Ile Val Ala Ser Asn Ala Tyr
 1           5           10           15
His Lys Asp Thr Glu Asp Phe Tyr Ile Ser Leu Lys Ile Val Asp Val
          20           25           30
Lys Gln Pro Glu Gly Asp Gln Arg Val Tyr Arg Thr Ser Thr Tyr Asp
          35           40           45
Leu Thr Thr Asp Glu Ile Ser Lys Val Lys Gln Ala Phe Ile Asn Ala
          50           55           60
Asn Arg Asp Val Ile Thr Leu Ala Glu Gly Asp Ile Ser Val Thr Asn
65           70           75           80
Thr Pro Asn Gly Ala Asn Val Ser Thr Ile Thr Val Asn Ile Asn Lys
          85           90           95
Gly Arg Leu Thr Lys Ser Phe Ala Ser Asn Leu Ala Asn Met Asn Phe
          100          105          110
Leu Arg Trp Val Asn Phe Pro Gln Asp Tyr Thr Val Thr Trp Thr Asn
          115          120          125
Ala Lys Ile Ala Asn Arg Pro Thr Asp Gly Gly Leu Ser Trp Ser Asp
          130          135          140
Asp His Lys Ser Leu Ile Tyr Arg Tyr Asp Ala Thr Leu Gly Thr Gln
145          150          155          160
Ile Thr Thr Asn Asp Ile Leu Thr Met Leu Lys Ala Thr Thr Thr Val
          165          170          175
Pro Gly Leu Arg Asn Asn Ile Thr Gly Asn Glu Lys Ala Gln Ala Glu
          180          185          190
Ala Gly Gly Arg Pro Asn Tyr Arg Thr Thr Gly Tyr Ser Gln Ser Asn
          195          200          205
Ala Thr Thr Asp Gly Gln Arg Gln Phe Thr Leu Asn Gly Gln Val Ile
          210          215          220
Gln Ile Leu Asp Ile Ile Asn Pro Ser Asn Gly Tyr Gly Gly Gln Pro
225          230          235          240
Val Thr Asn Ser Asn Thr Arg Ala Asn His Ser Asn Ser Thr Val Val
          245          250          255

```

(2) INFORMATION FOR SEO ID NO:368:

(A) LENGTH: 59 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEO ID NO:368:

(2) INFORMATION FOR SEQ ID NO:369:

(A) LENGTH: 100 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

Met Thr Ala Ile Leu His Asn Lys Tyr His Lys Val Val Leu Pro Pro
1 5 10 15
Tyr Leu Gly Phe Phe Gly Gly Xaa Arg Phe Val Pro Ile Val Thr Ala
20 25 30
Phe Ala Ala Ile Phe Leu Gly Val Leu Met Phe Phe Ile Trp Pro Ser
465

```

          35              40              45
Ile Gln Ala Gly Ile Tyr His Val Gly Gly Phe Val Thr Lys Thr Gly
          50              55              60
Ala Ile Gly Thr Phe Val Tyr Gly Phe Ile Leu Arg Leu Leu Gly Pro
65              70              75              80
Leu Gly Leu His His Ile Phe Tyr Leu Pro Phe Trp Gln Thr Ala Leu
          85              90              95
Gly Gly Thr Arg
          100

```

(2) INFORMATION FOR SEQ ID NO:370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

```

Met Leu Ala Xaa Met Cys Gly Phe Leu Phe Leu Ala Ser Asp Pro Ala
 1              5              10              15
Lys Asp Gly Gly Phe Leu Ser Ala Phe Met Gly Thr Lys Gly Leu Leu
          20              25              30
Thr Ala Phe Leu Ser Ala Phe Val Thr Val Ile Val Tyr Asn Phe Cys
          35              40              45
Val Lys Arg Asn Ile Thr Ile Lys Met Pro Lys Glu Val Pro Pro Asn
          50              55              60
Ile Ser Gln Val Phe Lys Asp Leu Ile Pro Phe Ser Ala Val Ile Ile
65              70              75              80
Ile Leu Tyr Ala Leu Asp Leu Val Ile Arg Asn Ser Phe Lys Ser Asn
          85              90              95
Val Ala Glu Gly Ile Leu Lys Leu Phe Glu Pro Leu Phe Thr Ala Ala
          100              105              110
Asp Gly Trp Ile Gly Val Thr Ile Ile Phe Gly Ala Phe Ala Leu Phe
          115              120              125
Trp Phe Val Gly Ile His Gly Pro Ser Ile Val Glu Pro Ala Ile Ala
          130              135              140
Ala Ile Thr Tyr Ala Asn Ile Glu Ala Asn Phe Lys Leu Leu Gln Ala
145              150              155              160
Gly Glu His Ala Asp Lys Ile Ile Thr Ser Gly Thr Gln Met Phe Ile

```

	165	170	175
Val Thr Phe Gly Gly Thr Gly Ala Thr Leu Val Xaa Pro Phe Met Phe			
180	185	190	
Met Leu Asp Asp Glu Ile			
195			

(2) INFORMATION FOR SEQ ID NO:371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

Met Asn Arg Asn Gly Ile Xaa Ser Arg Xaa Pro Asp Gln Pro Gln Ser			
1	5	10	15
Ala Pro Lys Glu Gln Asn Ser Asp Ser Asn Asp Glu Glu Thr Val Thr			
20	25	30	
Xaa Lys Glu Arg Lys Ser Lys Val Thr Gln Leu Lys Pro Leu Thr Leu			
35	40	45	
Glu Xaa Lys Arg Lys Leu Arg Arg Lys Arg Gln Lys Arg Ile Gln Tyr			
50	55	60	
Ser Val Ile Thr Ile Leu Val Leu Leu Ile Ala Val Ile Leu Ile Tyr			
65	70	75	80
Met Phe Ser Pro Leu Ser Lys Ile Ala Ala Cys Lys Tyr Lys Trp Lys			
85	90	95	

(2) INFORMATION FOR SEQ ID NO:372:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

```

Met Tyr Thr Phe Ser Lys Xaa Asn Ala Ile Xaa Asp Leu Glu Glu Asp
 1           5           10           15
Pro Leu Leu Xaa Ser Val Glu Ile His Lys Gln Leu Pro Xaa Thr Leu
          20           25           30
Asn Val Asp Ile Thr Glu Asn Glu Ile Ile Ala Leu Ser Glu Lys Ile
          35           40           45
Xaa Val Asn Ile Tyr Leu Tyr
          50           55

```

(2) INFORMATION FOR SEQ ID NO:373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

```

Met Asp Gly Phe Lys Gly Thr Gln Glu Asp Asp Met Ile Lys Ala Leu
 1           5           10           15
Ser Glu Met Thr Pro Glu Val Xaa Arg Tyr Ile Ala Glu Val Thr Tyr
          20           25           30
Ala Pro Ser Lys Thr Lys His Ser Arg Ile Glu Leu Phe Xaa Thr Asp
          35           40           45
Gly Leu Gln Val Ile Gly Asp Ile Ser Thr Ile Ser Lys Lys Met Lys
          50           55           60
Tyr Tyr Pro Gln Met Ser Gln Ser Leu Ser Arg Asp Arg Ser Gly Lys
          65           70           75           80
Leu Lys Thr Arg Gly Tyr Ile Asp Leu Ser Val Gly Ala Ser Phe Ile
          85           90           95
Pro Xaa Arg Gly Asn Thr Ser Ser Gln Ser Glu Ser Asp Lys Asn Val
          100          105          110
Thr Lys Ser Ser Gln Glu Glu Asn Gln Xaa Xaa Glu Glu Xaa Gln Ser
          115          120          125
Val Leu Xaa Lys Xaa Xaa Lys Gln Ser Ser Lys Asn Asn
          130          135          140

```

(2) INFORMATION FOR SEQ ID NO:374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

```

Met Ser Thr Leu Val Gly Thr Val Leu Ser Gly Phe Glu Tyr Arg Ala
 1           5           10           15
His Lys Glu Glu Leu Asp Asn Leu Thr Glu Val Leu Lys Glu Tyr Lys
      20           25           30
Ser Lys Tyr Lys Tyr Thr Gly Tyr Thr Glu Asn Ala Ile Met Lys Thr
      35           40           45
Gln Asn Ser Gly Phe Arg Asn Glu Tyr Tyr Tyr Leu Thr Ala Ile Pro
      50           55           60
Tyr Thr Leu Asp Glu Tyr Lys Arg Tyr Phe Gln Pro Leu Ile Lys Glu
      65           70           75           80
Asp Asp Lys Ser Phe Arg Asp Gly Met Arg Asn Ser Lys Lys Gln Leu
      85           90           95
Lys Asp Lys Ser Arg Pro Tyr Val Val Thr Thr Leu Phe Ser Thr Lys
      100          105          110
Asp Asn Phe Thr Lys Asp Asn Thr Ile Asp Glu Met Ile Asp Phe Ser
      115          120          125
Glu Val Ser Cys Leu Lys Lys Lys Lys Asn Ile Pro His Asp Val
      130          135          140

```

(2) INFORMATION FOR SEQ ID NO:375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

```

Met Ser Thr Leu Val Gly Thr Val Leu Ser Gly Phe Glu Tyr Arg Ala
 1           5           10           15
Gln Lys Glu Lys Tyr Asp Asn Leu Tyr Lys Phe Leu Lys Glu Asn Glu
                        469

```

(2) INFORMATION FOR SEQ ID NO:376:

(A) LENGTH: 99 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

(2) INFORMATION FOR SEO ID NO:377:

(A) LENGTH: 79 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

```

Met Lys Tyr Gln Pro Leu Ser Tyr Lys Glu Ile Glu Ala Val Val His
 1           5           10           15
Lys Gly Glu Thr Val Pro Ala Gly Val Thr Arg Phe Asn Ile Ser Gly
          20           25           30
Arg Cys Leu Asn Leu Gln Val Pro Leu Ala Leu Leu Lys Gln Asp Asp
          35           40           45
Asp Val Glu Gln Leu Arg Asn Trp Lys Gln Phe Leu Ala Asp Lys Phe
          50           55           60
Ala Asn Met Arg Cys Tyr Thr Glu Lys Val Tyr Leu Val Glu Gln
65           70           75

```

(2) INFORMATION FOR SEQ ID NO:378:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

```

Met Lys Glu His Gly Arg His Tyr Leu Asp Asn His Asn Tyr Lys Asp
 1           5           10           15
Ile His Met Pro Asn Asn Thr Pro Val Gly Phe Trp Ile Gly Ile Phe
          20           25           30
Met Thr Ile Gly Gly Phe Phe Leu Ile Phe Glu Thr Val Ile Pro Ala
          35           40           45
Leu Ile Cys Leu Phe Gly Ile Phe Gly Thr Met Ile Tyr Arg Lys Xaa
          50           55           60
Pro Lys Ser Asp Xaa Gly Ile Ser Tyr Pro Ser Cys
65           70           75

```

(2) INFORMATION FOR SEQ ID NO:379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

```

Met Ser His Asp Thr Asn Thr Ile Asp Ser Arg Thr His Glu Gly Glu
 1           5           10           15
Leu Asn Lys Leu Gly Phe Trp Ile Phe Ile Thr Ala Glu Phe Ala Leu
          20           25           30
Phe Gly Thr Leu Phe Ala Thr Leu Leu Thr Leu Gln His Gly Gly Asp
          35           40           45
Tyr Ala Gly Lys Met Thr Thr Glu Leu Phe Glu Leu Pro Leu Val Leu
          50           55           60
Ile Met Thr Phe Ala Leu Leu Phe Ser Ser Tyr Thr Cys Gly Ile Ala
65           70           75           80
Ile Tyr Tyr Met Arg Gln Glu Lys Gln Lys Leu Met Met Phe Trp Met
          85           90           95
Ile Ile Thr Leu Leu Leu Gly Leu Val Phe Val Gly Phe Glu Ile Tyr
          100          105          110
Glu Phe Ala His Leu Cys Ile Arg Arg Arg
          115          120

```

(2) INFORMATION FOR SEQ ID NO:380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

```

Met Ala Glu Asn Lys Asn Asn Leu Ser Ile Asn Asp Asp His Ser Asn
 1           5           10           15
Ala Ala Met Thr His Thr Ser Asp Ala Ile Ala Ser Ser Asp Phe Ile
          20           25           30
Ile Arg Glu Leu Asp Leu Asn Gln Glu Pro Glu Met Gln Arg Glu Ser
          472

```

```

          35              40              45
Lys Asn Phe Gly Gln Asp Ala Trp Ala Gln Leu Lys Arg Asn Lys Leu
          50              55              60
Ala Val Val Gly Met Ile Gly Leu Ile Ile Ile Val Ile Phe Ala Phe
65              70              75              80
Ile Gly Pro Val Ile Asn Lys His Asp Tyr Ala Glu Gln Asn Val Glu
          85              90              95
His Arg Asn Leu Pro Ala Lys Ile Pro Val Phe Arg Gln Ser Ser Ile
          100             105             110
Phe Thr Phe Trp Met Val Lys Met Gln Asp Gly Lys Asp Cys Leu Leu
          115             120             125
Lys Gln Gln Met Leu Lys Lys Ile Ile Gly Leu Gly Tyr
          130             135             140

```

(2) INFORMATION FOR SEQ ID NO:381:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

```

Met Leu Asp Ile Phe Ile Gly Val Val Tyr Gly Ala Ile Ser Gly Phe
 1              5              10              15
Phe Gly Gly Arg Val Asp Thr Ile Met Gln Arg Ile Leu Glu Val Ile
          20              25              30
Ala Ser Ile Pro Asn Leu Ile Val Val Ile Leu Phe Val Leu Ile Phe
          35              40              45
Glu Pro Ser Ile Trp Thr Ile Ile Leu Ala Met Ser Ile Thr Gly Trp
          50              55              60
Leu Gly Met Ser Arg Val Val Arg Gly Glu Phe Leu Lys Leu Lys Asn
65              70              75              80
Gln Glu Phe Val Met Ala Ser Lys Thr Leu Gly Ala Ser Lys Phe Lys
          85              90              95
Leu Ile Phe Lys His Ile Leu Pro Asn Thr Leu Gly Ala Ile Val Val
          100             105             110
Thr Ser Met Phe Thr Val Ser Cys His Phe Leu Arg Ser Ile Phe Lys
          115             120             125
Phe His Trp Tyr Arg Xaa Thr Cys Thr Ser Asn Ile Val Arg Val Ile

```

130 135 140
 Ser Lys
 145

(2) INFORMATION FOR SEQ ID NO:382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

Met Asn Asn Ser Gly Phe Phe Lys Gln Lys Ser Arg Leu Phe Trp Thr
 1 5 10 15
 Gln Met Asn Gln Ala Pro Ser Leu Ala Lys Glu Asp Glu Lys Glu Gly
 20 25 30
 Ala Lys Ala Gly Ile Glu Met Met Lys Asn Asn Tyr Lys Glu Ile Met
 35 40 45
 Thr Val Ala Pro Tyr
 50

(2) INFORMATION FOR SEQ ID NO:383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

Met Gln Ala Phe Trp Pro Gly Pro Ile Ser Phe Ile Leu Pro Leu Lys
 1 5 10 15
 Pro Gly Tyr Leu Cys Arg Lys Val Ser Gly Gly Leu Ser Ser Val Ala
 20 25 30
 Val Arg Met Pro Ser His Ser Val Gly Arg Gln Leu Leu Gln Ile Ile
 35 40 45

```

Asn Glu Pro Leu Ala Ala Pro Ser Ala Asn Leu Ser Gly Arg Pro Ser
50          55          60
Pro Thr Thr Phe Asn His Val Tyr Gln Asp Leu Asn Ala Arg Ile Asp
65          70          75          80
Gly Ile Val Gln Ala Glu Gln Ser Glu Glu Gly Leu Glu Ser Thr Val
          85          90          95
Leu Asp Cys Thr Ser Phe Pro Tyr Lys Ile Ala Arg Pro Gly Ser Ile
          100         105         110
Thr Ala Ala Met Ile Thr Glu Ile Leu Pro Asn Ser Ile Ala His Ala
          115         120         125
Asp Tyr Asn Asp Thr Glu Gln Ala Ile Ala Pro Gly Met Lys Tyr
          130         135         140

```

(2) INFORMATION FOR SEQ ID NO:384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

```

Met Pro Thr Pro Asp Glu Val His Ile Thr Val Gly Thr Val Arg Tyr
1          5          10          15
Gln Ala His Gly Arg Glu Arg Lys Gly Val Cys Ser Val His Phe Ala
          20          25          30
Glu Arg Ile Lys Pro Gly Asp Ile Val Pro Ile Tyr Leu Xaa Lys Asn
          35          40          45
Pro Asn Phe Lys Phe Pro Met Lys Gln Asp Ile Pro Val Ile Met Ile
          50          55          60
Gly Pro Gly Thr Gly Ile Ala Pro Phe Arg Ala Tyr Leu Gln Glu Arg
65          70          75          80
Glu Glu Leu Gly Met Thr Gly Lys Thr Trp Leu Phe Phe Gly Asp Gln
          85          90          95
His Arg Ser Ser Asp Phe Leu Tyr Glu Glu Glu Ile Glu Glu Trp Leu
          100         105         110
Glu Asn Gly Asn Leu Thr Arg Ser Cys Leu
          115         120

```

(2) INFORMATION FOR SEQ ID NO:385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

```

Met Asn Xaa Leu Arg Arg Gln Leu Ser Met Asn Ser Leu Leu Ile Asp
 1             5             10             15
Thr Ser Asn Gln Pro Leu Ser Val Ala Leu Met Gln Asn Asp Glu Val
          20             25             30
Leu Ala Glu Ile Thr Thr Asp Ser Lys Gln Asn His Ser Val Gln Leu
          35             40             45
Met Pro Ala Ile Ser Gln Leu Phe Glu Gln Ser Lys Ile Ala Lys Gln
          50             55             60
Gln Leu Asp Ala Ile Ile Val Ala Glu Gly Pro Gly Ser Tyr Thr Gly
65             70             75             80
Leu Arg Ile Gly Val Thr Val Ala Lys Thr Leu Ala Tyr Ala Leu Asp
          85             90             95
Val Lys Leu Tyr Gly Val Ser Ser Leu Lys Ala Leu Ala Ala Thr Ile
          100            105            110
Asp His Thr Asp Lys Leu Leu Gly Ser Cys Val Trp Met Gln Arg Arg
          115            120            125
Gln Ala Gly Leu Phe Arg His Ile Pro Gly Gly Lys Met Gly Asn
          130            135            140

```

(2) INFORMATION FOR SEQ ID NO:386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

```

Met Ala Ile Lys Ala Glu Glu Ile Ser Ala Leu Leu Arg Ser Gln Ile

```

```

      1             5             10             15
Glu Asn Tyr Glu Ser Glu Met Ser Val Thr Asp Val Gly Thr Val Leu
      20             25             30
Gln Ile Gly Asp Gly Ile Ala Leu Ile His Gly Leu Asn Asp Val Met
      35             40             45
Ala Gly Glu Leu Val Thr Phe His Asn Gly Val Leu Gly Leu Ala Gln
      50             55             60
Asn Leu Glu Glu Ser Asn Val Gly Val Val Ile Leu Gly Pro Tyr Thr
      65             70             75             80
Gly Ile Thr Glu Gly Asp Glu Leu Xaa Thr Tyr Trp Val Val Ser Trp
      85             90             95
Glu Val Pro Val Gly Glu Glu Leu Ile Arg Lys Ser Cys Xaa Ser Ile
      100            105            110
Arg Thr Thr Tyr
      115

```

(2) INFORMATION FOR SEQ ID NO:387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

```

Met Lys Ser Ala Glu Gln Trp Ile Asp Glu Leu Gln Leu Glu Ser His
  1             5             10             15
Pro Glu Gly Gly Phe Tyr Arg Glu Thr Ile Arg Glu Val Leu Lys Asp
      20             25             30
Gly Arg Arg Ala Pro Phe Xaa Ser Ile Tyr Phe Leu Leu Thr Asp Asp
      35             40             45
Asn Ile Ser His Phe His Arg Ile Asp Ala Asp Glu Val Trp Tyr Tyr
      50             55             60
His Ala Gly Asp Ser Leu Thr Ile His Met Ile Asn Pro Asp Gly Glu
      65             70             75             80
Tyr Thr Thr Ala Thr Leu Gly Thr Asp Ile Gln Asn Gly Asp Val Leu
      85             90             95
Gln Tyr Val Val Pro Lys Gly Thr Ile Phe Ala Ser Ser Ile Glu Ile
      100            105            110
Ser Asn Thr Tyr Ser Leu Val Gly Cys Met Cys Gln Pro Ala Xaa Glu

```

115	120	125
Phe Lys Gln Phe Glu Leu	Phe Lys Gln Ser Glu Leu	Ile Thr Gln Tyr
130	135	140
Pro His Leu Lys Ser Val	Ile Xaa Lys Tyr Ala Leu	Lys
145	150	155

(2) INFORMATION FOR SEQ ID NO:388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

Met Tyr Glu Arg Lys Leu Val Met Gln Lys Ser Ala Leu Phe Ala Pro			
1	5	10	15
Glu Lys Tyr Asn Ile Ile Ser Glu Ile Glu Lys Tyr Ser His Ile Pro			
20	25	30	
Asp Lys Lys Ala Ile Leu Tyr His Asn Thr Glu Gly Glu Asp Ile Ser			
35	40	45	
Val Thr Tyr Gln Gln Leu Ile Glu Gln Ser Asn Lys Val Gly Asn Val			
50	55	60	
Leu Ala Ser His Gly Leu Ser Lys Gly Asp Lys Val Leu Ile Met Met			
65	70	75	80
Pro Arg Ser Ile Ala Thr Tyr Glu Leu Tyr Ile Ala Ala Leu Lys Leu			
85	90	95	
Gly Val Ala Ile Ile Pro Cys Ser Glu Met Leu Arg Thr Lys Asp Leu			
100	105	110	
Gln Tyr Arg Ile Thr His Gly Glu Ile Asn Ala Val Ile Ala Leu Glu			
115	120	125	
Pro Phe Thr Val Glu Phe Glu Lys Ile Lys Glu Tyr Asp Ala Leu Xaa			
130	135	140	
Lys Phe Val Ile Ala Gly Gln Lys Asp Gly Trp Ile Ser Leu Glu Ala			
145	150	155	160
Glu Lys Glu Asn Ala Ser Asn Lys Leu Glu Met Ala Asp Thr Thr Arg			
165	170	175	
Asp Asp Met Ala Xaa Leu Ser Tyr Thr Ser Gly Thr Thr Gly Asn Pro			
180	185	190	
Lys Ala Arg Tyr Thr Leu Ser Trp Met Gly Ile Cys Thr Phe Thr Lys			

(2) INFORMATION FOR SEQ ID NO:389:

(A) LENGTH: 58 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

(2) INFORMATION FOR SEQ ID NO:390:

(A) LENGTH: 123 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

Met	Ile	Gly	Asp	Ser	Ala	Met	Asp	Gly	Phe	Lys	Ile	Ala	Val	Val	Val
1				5					10					15	
Ala	Val	Met	Leu	Leu	Ala	Phe	Ile	Ser	Leu	Met	Glu	Ala	Ile	Asn	Ile
			20					25					30		
								479							

Met Phe Gly Ser Val Gly Leu Xaa Xaa Lys Gln Leu Ile Gly Tyr Val
 35 40 45
 Phe Ala Pro Ile Ala Phe Leu Met Gly Ile Pro Trp Ser Glu Ala Val
 50 55 60
 Pro Ala Gly Ser Leu Met Ala Thr Lys Leu Ile Thr Asn Glu Phe Val
 65 70 75 80
 Ala Met Leu Asp Phe Lys Asn Val Leu Gly Asp Val Ser Ala Arg Thr
 85 90 95
 Gln Gly Ile Ile Ser Val Tyr Leu Val Ser Phe Ala Asn Val Gly Thr
 100 105 110
 Val Gly Ile Ile Val Gly Ser Xaa Gln Gly Thr
 115 120

(2) INFORMATION FOR SEQ ID NO:391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

Met Ser Leu Ala Ile Val Ile Gly Ser Glu Gly Gln Gly Met Ser Arg
 1 5 10 15
 Leu Val Ser Asp Lys Cys Asp Phe Tyr Ile Lys Ile Pro Met Val Gly
 20 25 30
 His Val Asn Ser Leu Asn Ala Ser Val Ala Ala Ser Leu Met Met Tyr
 35 40 45
 Glu Val Phe Arg Lys Arg His
 50 55

(2) INFORMATION FOR SEQ ID NO:392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

```

Met Phe Leu Leu Ser Met Ser Leu Ala Pro Asn Phe Lys Thr Tyr Gly
 1             5             10             15
Phe Trp Asn Arg Val Gly Leu Gly Thr Leu Val Thr Asp Glu Thr Phe
          20             25             30
Gly Val Ala Ile Thr Pro Tyr Leu Lys Gly Glu Ala Ile Asn Asp Arg
      35             40             45
Trp Met His Gly Leu Asn Ile Thr Ala Tyr Leu Phe Gly Asp Asn Phe
      50             55             60
Met Cys Ser Trp Gly Phe Ile Leu Ala Asn Ile Ser Gln Ile Arg Lys
65             70             75             80
Arg

```

(2) INFORMATION FOR SEQ ID NO:393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

```

Met Arg Arg Ser Val Lys Gln Ile Thr Glu Ile Thr Ala Ala Gln Arg
 1             5             10             15
Val Ile Asp Asn Gly Asp Ala Thr Ala Gln Gln Ile Ser Asp Glu Lys
          20             25             30
His Arg Val Asp Asn Ala Leu Thr Ala Leu Asn Gln Ala Lys His Asp
      35             40             45
Leu Thr Ala Asp Thr His Ala Leu Glu Gln Ala Val Gln Gln Leu Asn
      50             55             60
Arg Thr Gly Thr Thr Thr Gly Lys Lys Pro Ala Ser Ile Thr Ala Tyr
65             70             75             80
Asn Asn Ser Ile Arg Ala Leu Gln Ser Asp Leu Thr Ser Xaa Lys Asn
          85             90             95
Ser Ala Asn Ala Ile Ile Gln Lys Pro Ile Arg Thr Val Gln Glu Val
      100             105             110
His Leu Arg

```

115

(2) INFORMATION FOR SEQ ID NO:394:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

```

Met Thr Gln Ser Ser Ile Gln Ala Tyr Glu Asn Ala Lys Arg Ala Gly
 1             5             10             15
Gln Xaa Glu Xaa Thr Asn Ala Gln Asn Val Ile Asn Asn Gly Ala Arg
      20             25             30
Ala Thr Asp Gln Gln Ile Ala Ala Glu Lys Thr Lys Val Glu Glu Lys
      35             40             45
Tyr Asn Ser Leu Lys Gln Ala Ile Ala Gly Leu Thr Pro Asp Leu Ala
      50             55             60
Pro Leu Gln Thr Ala Lys Thr Gln Leu Gln Asn Asp Ile Asp Gln Pro
65             70             75             80
Thr Ser Thr Thr Gly Met Thr Ser Ala Ser Val Ala Ala Phe Asn Asp
      85             90             95
Lys Leu Ser Ala Ala Arg Thr Lys Ile Gln Glu Ile Asp Arg Val Leu
      100            105            110
Ala Ser His Pro Asp Val Ala Thr Ile Arg Gln Asn Val Thr Ala Ala
      115            120            125
Asn Ala Ala Lys Thr Ala Leu Gly Ser Ser Ala Gln Met Pro
      130            135            140

```

(2) INFORMATION FOR SEQ ID NO:395:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

Met Thr Gln Leu Asp Asn His Trp Met Ala Met Phe Xaa Asp Met Asn
 1 5 10 15
 Phe Asp Leu Gly Ile Met Ala Leu Tyr Ala Ile Glu Ser Asp Pro Leu
 20 25 30
 Ala Asn Xaa Pro Arg Asn Ser Asp Ala Glu Ile Ala Val Xaa Asp Glu
 35 40 45
 Ser His Ile Asp Ala Tyr
 50

(2) INFORMATION FOR SEQ ID NO:396:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

Met Val Arg Glu His Tyr Gln Lys Asp Val Ile Lys Arg Leu Val Ala
 1 5 10 15
 Tyr Leu Asn Asn Glu Pro Ile Gly Val Val Asp Val Ile Glu Ser Glu
 20 25 30
 Asn Tyr Ile Glu Leu Asp Gly Phe Gly Val Leu Glu Gln Phe Arg His
 35 40 45
 Gln Gly Ile Gly Ser Thr Ile Gln Ser Val Asp Arg
 50 55 60

(2) INFORMATION FOR SEQ ID NO:397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

Met Tyr Ala Lys Gln Gly Tyr Val Tyr Gln Ser Xaa Leu Leu Ser Xaa
 1 5 10 15
 Ile Lys Arg Arg Tyr Trp Lys Leu Xaa Ile Asp Asp Arg Phe Val Leu
 20 25 30
 Glu

(2) INFORMATION FOR SEQ ID NO:398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

Met Ala Tyr Ile Ser Leu Xaa Tyr His Ser Pro Thr Ile Gly Met His
 1 5 10 15
 Gln Asn Leu Xaa Val Ile Leu Pro Glu Asp Gln Ser Phe Phe Asn Asn
 20 25 30
 Asp Ile Xaa Ala Lys Pro Leu Lys Thr Leu Met Leu Leu His Gly Leu
 35 40 45
 Ser Ser Asp Glu Thr Thr Tyr Met Arg Tyr Thr Ser Ile Glu Arg Tyr
 50 55 60
 Ala Asn Glu His Lys Leu Ala Val Ile Met Pro Asn Val Asp His Ser
 65 70 75 80
 Ala Tyr Ala Asn Met Ala Tyr Gly His Ser Tyr Tyr Asp Tyr Ile Leu
 85 90 95
 Glu Val Tyr Asp Tyr Val His Gln Ile Phe Pro Leu Ser Lys Lys Arg
 100 105 110
 Asp Asp Asn Phe Ile Ala Gly His Ser Met Gly Gly Tyr Gly Thr Ile
 115 120 125
 Lys Phe Ala Leu Thr Gln Gly Asp Lys Phe Ala Lys Ala Val Pro Leu
 130 135 140
 Ser Ala Val Phe Glu Ala Gln Asn Leu Met Asp Leu Glu Trp Asn Asp
 145 150 155 160
 Phe Ser Lys Glu Ala Ile Ile Gly Asn Leu Ser Ser Cys
 165 170

(2) INFORMATION FOR SEQ ID NO:399:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

```

Met Leu Val Leu Ser Gly Cys Gly Met Lys Asp Asn Asp Lys Gln Gly
 1             5             10             15
Ser Asp Asp Asn Gly Ser Ser Lys Ser Pro Tyr His Arg Xaa Val Ser
          20             25             30
Leu Met Pro Ser Asn Thr Glu Ile Leu Tyr Glu Leu Gly Leu Gly Lys
          35             40             45
Tyr Ile Val Gly Val Phe Asn Gly
          50             55

```

(2) INFORMATION FOR SEQ ID NO:400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

```

Met Lys Trp Phe Lys Xaa Trp Asp Glu Asn Gly Asn Val Val Asn Glu
 1             5             10             15
Asp Leu Val Pro Asp Leu Thr Asp Glu Gln Leu Val Glu Leu Met Glu
          20             25             30
Arg Met Val Trp Thr Arg Ile Leu Asp Gln Arg Ser Ile Ser Leu Asn
          35             40             45
Arg Gln Gly Arg Leu Gly Phe Tyr Ala Pro Thr Ala Gly Gln Glu Ala
          50             55             60
Ser Gln Leu Ala Ser Gln Tyr Ala Leu Glu Lys Glu Asp Tyr Ile Leu
          65             70             75             80

```

Pro Gly Tyr Arg Asp Val Pro Gln Ile Ile Trp Ala Trp Phe Thr Ile
 85 90 95
 Asn

(2) INFORMATION FOR SEQ ID NO:401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

Met Thr Tyr Arg Tyr Gly Pro His Thr Met Ala Gly Asp Asp Pro Thr
 1 5 10 15
 Arg Tyr Arg Thr Ser Asp Glu Asp Ala Glu Trp Glu Lys Lys Asp Pro
 20 25 30
 Leu Val Arg Phe Arg Lys Phe Leu Glu Asn Lys Gly Leu Trp Asn Glu
 35 40 45
 Asp Lys Glu Asn Glu Val Ile Glu Arg Ala Lys Ala Asp Ile Lys Ala
 50 55 60
 Ala Ile Lys Glu Ala Asp Asn Thr Glu Lys Gln Thr Val Thr Ser Leu
 65 70 75 80
 Met Glu Ile Met Tyr Glu Asp Met Pro Gln Asn Leu Ala Glu Gln Tyr
 85 90 95
 Glu Ile Tyr Lys Glu Lys Glu Ser Lys
 100 105

(2) INFORMATION FOR SEQ ID NO:402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

Met Leu Leu His Ser Gln Ser Phe Val Val Ile Val Ile Gly Ile Phe
 1 5 10 15
 Ile Leu Gly Phe Phe Leu Ser Thr Tyr Glu Ala Thr Met Pro Gly Ser
 20 25 30
 Leu Pro Thr Met Phe Tyr Ser His Ile Arg Tyr Arg Thr Leu Ser Val
 35 40 45
 Thr Phe Asn Ile Ser Val Ser Ile Phe Gly Gly Thr Thr Pro Leu Val
 50 55 60
 Ala Thr Trp Leu Val Thr Lys Thr Gly Asp Pro Leu Ala Pro Ala Tyr
 65 70 75 80
 Tyr Leu Thr Ala Ile Ser Val Ile Gly Phe Leu Val Ile Thr Phe Leu
 85 90 95
 His Leu Ser Thr Ala Gly Lys Ser Leu Lys Gly Ser Tyr Pro Asn Val
 100 105 110
 Asp Asn Glu Gln Asp Arg Ala Tyr Tyr Ala Glu His Pro Lys Glu Ala
 115 120 125
 Leu Trp Trp Val Lys Glu Arg Lys Asn
 130 135

(2) INFORMATION FOR SEQ ID NO:403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

Met Ala Lys Gln Asp Val Ile Glu Leu Glu Gly Thr Val Leu Asp Thr
 1 5 10 15
 Leu Pro Asn Ala Met Phe Lys Val Glu Leu Glu Asn Xaa His Glu Ile
 20 25 30
 Leu Ala His Val Ser Gly Xaa Ile Arg Asn Glu Leu Gln Phe Val Phe
 35 40 45
 Tyr Pro Xaa Asp Lys Val Thr Val Glu Met Ser Pro Tyr Asp Leu Thr
 50 55 60
 Xaa Gly Thr Ser Tyr Leu Ser Leu
 65 70

(2) INFORMATION FOR SEQ ID NO:404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

```

Met Glu Val Thr Val Gly Ile Val Lys Gly Lys Glu Phe Leu Xaa Gly
 1             5             10             15
Arg Met Xaa Xaa Gln Gly Phe Leu Leu Asp Gly Phe Pro Arg Thr Ile
      20             25             30
Glu Gln Ala Glu Ala Leu Asn Asn Ile Met Ser Glu Leu Asp Arg Asn
      35             40             45
Ile Asp Ala Val Ile Asn Ile Glu Val Pro Glu Glu Glu Leu Met Asn
      50             55             60
Arg Leu Thr Gly Arg Arg Ile Cys Glu Ser Cys Gly Thr Thr Tyr His
65             70             75             80
Leu Val Phe Asn Pro Pro Lys Val Glu Gly Ile Cys Asp Ile Asp Gly
      85             90             95
Val Xaa Xaa Tyr Gln Arg Glu Asp Asp Asn Pro Glu Xaa Val Ala Arg
      100            105            110
Ala Val

```

(2) INFORMATION FOR SEQ ID NO:405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

```

Met Arg Thr Leu Ile Thr Ile Ala Ser Thr Ile Ile Gly Thr Phe Leu
 1             5             10             15

```

Ser Ile Gly Leu Thr Glu Leu Ile Ile Tyr Met Thr Asp Gly Lys Gly
 20 25 30
 Ile Lys Tyr Glu Thr Met Asn Phe Leu Ser Leu Pro Pro Lys Asp Ile
 35 40 45
 Phe Leu Ala Ser Val Leu Ile Gly Ser Leu Gly Ala Ile Met Asp Val
 50 55 60
 Ala Ile Thr Ile Ala Ser Gly Met His Glu Ile Xaa Gln Arg Thr Xaa
 65 70 75 80
 His Ile Ser Met Arg Arg Trp Ala Leu Ala Trp Ala Lys His Pro Thr
 85 90 95
 Arg Tyr Tyr Gly Asn Asn Asp
 100

(2) INFORMATION FOR SEQ ID NO:406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

Met Gln Ala Leu Arg Leu Met Phe Glu Ala Thr Glu Glu Thr Lys Gln
 1 5 10 15
 Glu Ile Lys Asn Val Lys Asp Asp Val Asp Xaa Phe Glu Arg Lys Ser
 20 25 30
 Lys Thr Gly Cys Gly Arg Leu Gln Phe Leu Asn
 35 40

(2) INFORMATION FOR SEQ ID NO:407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

Met Ser Arg Gln His His Arg Phe Leu Phe Phe Ile Asn Lys Leu Pro
 1 5 10 15
 Gly Ile Thr Ile Lys Ser Leu Leu Glu Ile Leu Glu Ile Ser Lys Gln
 20 25 30
 Gly Ser His Ala Thr Leu Gln Lys Leu Lys Glu Gln Gly Leu Ile Ile
 35 40 45
 Glu Lys Val Leu Glu Thr Asp Arg Arg Val Lys Lys Leu Tyr Ser Thr
 50 55 60
 Asp Lys Gly Asp Gln Leu Ile Ala Glu Leu Asn Lys Ala Gln Asp Glu
 65 70 75 80
 Leu Leu Gln Asn Ile Tyr Gln Gln Val Gly Ser Asp Trp Tyr Asp Val
 85 90 95
 Met Glu Ala Leu Ala Lys Arg Arg Pro Gly Phe Asp Phe Ile Lys His
 100 105 110
 Leu Lys Asp Glu Lys Glu Ser
 115

(2) INFORMATION FOR SEQ ID NO:408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

Met Ile His His Ser Asn Glu Tyr Asn Ile Asp Ile Thr Ala Gln Asn
 1 5 10 15
 Ile Asn Lys Tyr Thr Ala Leu Gln Tyr Ile Phe Asp Ala Asp Val Lys
 20 25 30
 Tyr Ile Ala Phe Gly
 35

(2) INFORMATION FOR SEQ ID NO:409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

```

Met Leu Val Gly Gly Tyr Ile Ile Gly Pro Ser Glu Ala Tyr Thr His
 1             5             10             15
Ala Ile Leu Lys Leu Asp Lys Ile Lys Tyr Ile Asn Asn Asn Thr Gln
      20             25             30
Ala Ile Cys Lys Val Leu Lys Ser Tyr Lys
      35             40

```

(2) INFORMATION FOR SEQ ID NO:410:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

```

Met Gly Gly Ser Ile Thr Ile Met Ser Lys Phe Asp Asp Asn Gln Ser
 1             5             10             15
Asp Phe Ile Pro Ala Trp Phe Ala Gly Asn Ile Trp Gly Asp Glu Cys
      20             25             30
Pro Phe Val Ile Ala Phe Leu Pro Trp Val Leu Ile Ile Ile Pro Tyr
      35             40             45
Leu Leu Phe Lys Ser Asn Thr Leu Asn Ile Ile His Thr Gly Asp Asn
      50             55             60
Ile Ala Arg Gly Leu Gly Val Arg Leu Ser Arg Glu Arg Leu Ile Leu
      65             70             75             80
Phe Phe Ile Ala Val Met Leu Ser Ser Ala Ala Val Ala Val Ala Gly
      85             90             95
Ser Ile Ser Phe Ile Gly Leu Met Gly Pro His Ile Ala Lys Arg Ile
      100            105            110
Val Gly Pro Arg His Gln Leu Phe Leu Pro Ile Ala Ile Leu Val Gly
      115            120            125
Ala Cys Leu Leu Val Ile Ala Arg Ala Ile Gly Gln Asn Leu Tyr Tyr
      130            135            140

```

Asn Gln Val Gly Phe Gln Gln Val Leu Ser
145 150

(2) INFORMATION FOR SEQ ID NO:411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

Met	Asp	Xaa	Ser	Lys	Thr	Ser	Xaa	Ala	Ser	Gly	Gly	Asp	Cys	Xaa	Ile
1				5				10					15		
Thr	Ile	Ile	Asn	Xaa	Asp	Val	Asp	Lys	Glu	Xaa	Ile	Tyr	Asp	Glu	Trp
			20					25					30		
Thr	Lys	His	Gly	Ile	Lys	Pro	Leu	Lys	Phe	Asn	Ile	Tyr	His	Gly	Gln
			35				40						45		

(2) INFORMATION FOR SEQ ID NO:412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

Met	Val	Lys	Ile	Ala	Ile	Phe	Ala	Ser	Gly	Ser	Gly	Ser	Asn	Phe	Glu
1				5				10					15		
Asn	Ile	Val	Glu	His	Val	Glu	Ser	Gly	Lys	Leu	Glu	Asn	Ile	Glu	Val
			20					25					30		
Thr	Xaa	Leu	Tyr	Thr	Asp	His	Gln	Asn	Ala	Phe	Cys	Ile	Asp	Arg	Ala
			35				40					45			
Asn	Lys	His	Asp	Ile	Pro	Val	Tyr	Ile	Asn	Glu	Pro	Lys	Gln	Phe	Asp
			50				55					60			
Ser	Lys	Ala	Ala	Tyr	Glu	Gln	His	Leu	Val	Thr	Leu	Leu	Thr	Lys	Asp

65	70	75	80
Lys Val Glu Trp Ile Leu Ala Trp Leu His Ala Ser Tyr Ser Gly			
	85	90	95
Pro Gly Leu His			
100			

(2) INFORMATION FOR SEQ ID NO:413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

Met Lys Trp His Glu Arg Arg Ile Ile Val Asp Ile Arg Asp Lys Gln			
1	5	10	15
Leu Arg Tyr Gln Asp Ile Ala Ile Leu Tyr Arg Asp Glu Ser Tyr Ala			
	20	25	30
Tyr Leu Phe Asp Ser Ile Leu Pro Leu Tyr Asn Ile Pro Tyr Asn Ile			
	35	40	45
Asp Thr Lys Arg Ser Met Thr His His Pro Val Met Glu Met Ile Arg			
	50	55	60
Ser Leu Ile Glu Val Ile Gln Ser Asn Trp Gln Val Asn Pro Met Leu			
65	70	75	80
Arg Leu Leu Lys Thr Asp Val Leu Thr Ala Ser Tyr Leu Lys Ser Ala			
	85	90	95
Tyr Leu Val Asp Leu Leu Glu Asn Phe Val Leu Glu Arg Gly Ile Tyr			
	100	105	110
Gly Lys Arg Trp Leu Asp Asp Glu Leu Phe Asn Val Glu His Phe Ser			
	115	120	125
Lys Met Gly Arg Lys Ala His Lys Leu His Arg Arg			
	130	135	140

(2) INFORMATION FOR SEQ ID NO:414:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

```

Met Ser Ile Glu Ile Gln Ala Asp Ile Glu Phe Lys Leu Asp Glu Met
 1             5             10             15
Val Asp Cys Ala Ala Ala Lys Met Ala Ala Ile Ser Asn Pro Ala Thr
      20             25             30
Asn Gly Gly Ile Ser Val Lys Met Lys Tyr Gly Thr Thr Asp Asp Val
      35             40             45
Leu Lys Pro Phe Gly Lys Thr Ala Ser Cys Val
 50             55

```

(2) INFORMATION FOR SEQ ID NO:415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

```

Met Thr His Leu Leu Glu Thr Phe Glu Met Ser Ile Asp His Gln Glu
 1             5             10             15
Asp Gly Leu Val Val Ile Ser Met Pro Val Thr Asp Lys Val Lys Gln
      20             25             30
Pro Phe Gly Tyr Leu His Gly Gly Ala Ser Ile Ala Leu Gly Glu Thr
      35             40             45
Ala Cys Ser Leu Gly Ser Ala Asn Leu Ile Asp Thr Thr Lys Phe Ile
      50             55             60
Pro Leu Gly Leu Glu Met Asn Ala Asn His Ile His Ser Ala Lys Asp
      65             70             75             80
Gly Arg Val Thr Ala Thr Ala Glu Ile Ile His Arg Gly Lys Ser Thr
      85             90             95
His Val Trp Asp Ile Lys Ile Lys Asn Asp Xaa Glu Gln Leu Ile Thr
      100             105             110
Val Met Arg Gly Tyr Xaa Leu Leu Phe Lys Pro Leu Lys
      115             120             125

```

(2) INFORMATION FOR SEQ ID NO:416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

Met	Leu	Ala	Tyr	Gly	Thr	Gly	Thr	Phe	Thr	Gly	Lys	Asp	Phe	Leu	Lys
1				5				10						15	
Ala	Gly	Ile	Pro	Leu	Thr	Ile	Val	Gly	Tyr	Ile	Leu	Val	Ile	Val	Phe
				20				25						30	
Ser	Met	Thr	Tyr	Trp	Lys	Trp	Leu	Gly	Leu	Leu					
				35				40							

(2) INFORMATION FOR SEQ ID NO:417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

Met	Ser	Arg	Gly	Ile	Ser	Gln	Arg	Glu	Ala	Glu	Arg	Leu	Val	Ile	Gln
1				5				10						15	
Gly	Phe	Leu	Asp	Pro	Val	Val	Arg	Glu	Leu	Pro	Ile	Glu	Asp	Val	Lys
				20				25						30	
Arg	Gln	Leu	Arg	Glu	Val	Ile	Glu	Arg	Lys	Val	Ser	Lys			
				35				40						45	

(2) INFORMATION FOR SEQ ID NO:418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids

495

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:

```

Met Asn His Asn Val Ile Ile Val Ile Ala Leu Ile Ile Val Val Ile
 1             5             10             15
Ser Met Leu Ala Met Leu Ile Arg Val Val Leu Gly Pro Ser Leu Ala
      20             25             30
Asp Arg Val Val Ala Leu Asp Ala Ile Gly Leu Gln Leu Met Ala Val
      35             40             45
Arg Ala Leu Phe Ser Ile Leu Leu Asn Ile Lys Tyr Met Ile Val Val
      50             55             60
Ile Met Met Ile Gly Ile Leu Ala Phe Leu Gly Thr Ala Val Phe Ser
65             70             75             80
Lys Phe Met Asp Lys Gly Lys Val Ile Glu His Asp Gln Asn His Thr
      85             90             95
Asp

```

(2) INFORMATION FOR SEQ ID NO:419:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

```

Met Thr Ile Ala Met Thr Ile Trp Asn Ala Ile Trp Thr Phe Xaa Gln
 1             5             10             15
Thr Leu Trp Asn Thr Ile Val Thr Val Ala Thr Lys Val Trp Asn Ala
      20             25             30
Ile Thr Thr Ala Ile Ser Thr Ala Leu Gln Ala Ala Trp Ser Phe Ile
      35             40             45
Ser Asn Ile Trp Asn Thr Ile Trp Ser Phe Leu Ser Ser Ile Leu Thr
      50             55             60

```

(2) INFORMATION FOR SEO ID NO:420:

(A) LENGTH: 79 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEO ID NO:420:

(2) INFORMATION FOR SEQ ID NO:421:

(A) LENGTH: 148 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEO ID NO:421:

```

Met Leu Thr Thr Glu Lys Leu Val Glu Thr Leu Lys Leu Asp Leu Ile
 1              5              10              15
Ala Gly Glu Glu Gly Leu Ser Lys Pro Ile Lys Asn Ala Asp Ile Ser
      20              25              30
Arg Pro Gly Leu Glu Met Ala Gly Tyr Xaa Xaa His Tyr Ala Ser Asp
      35              40              45
Arg Ile Gln Leu Leu Gly Thr Thr Glu Leu Ser Phe Tyr Asn Leu Leu
      50              55              60
Pro Asp Lys Asp Arg Ala Gly Arg Met Arg Lys Leu Cys Arg Pro Glu
65              70              75              80
Thr Pro Ala Ile Ile Val Thr Arg Gly Leu Gln Pro Pro Glu Glu Leu
      85              90              95
Val Glu Ala Ala Lys Glu Leu Asn Thr Pro Leu Ile Val Ala Lys Asp
      100              105              110
Ala Thr Thr Ser Leu Met Ser Arg Leu Thr Thr Phe Leu Glu His Ala
      115              120              125
Leu Ala Lys Thr Thr Ser Leu His Gly Val Leu Val Asp Val Tyr Gly
      130              135              140
Val Gly Cys Thr
145

```

(2) INFORMATION FOR SEQ ID NO:422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

```

Met Ile His Gly Xaa Xaa Val Leu Gly Trp Gly Val Gly Gly Ile Glu
 1              5              10              15
Xaa Glu Ala Gly Met Leu Gly Gln Pro Ser Tyr Phe Pro Ile Pro Glu
      20              25              30
Val Ile Gly Val Arg Leu Val Xaa Ser Leu Pro Gln Gly Ala Thr Ala
      35              40              45
Thr Asp Leu Cys Val Lys Ser Asn Ser Arg Ala Thr
      50              55              60

```

(2) INFORMATION FOR SEQ ID NO:423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

```

Met His Asn Gln Val Thr Xaa Thr Leu Lys Leu Phe Gln Ala Pro Thr
 1           5           10           15
Tyr His Asn Tyr Ser Thr Ser Thr Thr Ser Ser Ser Val Arg Leu Ser
          20           25           30
Asn Gly Asn Thr Ala Gly Ala Thr Gly Ser Ser Ala Ala Gln Ile Met
          35           40           45
Ala Gln Arg Thr Gly Val Ser Ala Ser Thr Trp Ala Ala Ile Ile Ala
          50           55           60
Arg Glu Ser Asn Gly Gln Val Asn Ala Tyr Asn Pro Ser Gly Ala Ser
65           70           75           80
Gly Leu Phe Gln Thr Met Pro Gly Trp Gly Pro Thr Asn Thr Gly Asp
          85           90           95
Gln Gln Ile Asn Ala Xaa Val Lys Ala Tyr Lys Ala Gln Gly Leu Gly
          100          105          110
Ala Trp Gly Phe
          115

```

(2) INFORMATION FOR SEQ ID NO:424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

```

Met Lys Tyr Ile His Arg Arg His Ile Thr Met Lys Pro Gln Leu Ser
 1           5           10           15

```

Trp Lys Val Gly Gly Gln Gln Gly Glu Gly Ile Glu Ser Thr Gly Glu
 20 25 30
 Xaa Phe Ala Thr Ala Met Asn Arg Lys Gly Tyr Tyr Leu Tyr Gly Tyr
 35 40 45
 Arg His Phe Ser Ser Arg Ile Lys Gly Gly His Thr Asn Asn Lys Ile
 50 55 60
 Arg Val Ser Thr Thr Pro Val His Ala Ile Ser Asp Asp Leu Asp Ile
 65 70 75 80
 Leu Ile Ala Phe Asp Gln Glu Thr Ile Asp Val Asn His His Glu Met
 85 90 95
 Arg Glu Asp Ser Ile Ile Leu Ala Asp Ala Lys Ala Lys Pro Val Lys
 100 105 110
 Pro Glu Gly Cys His Ala Gln Leu Ile Glu Leu Pro Phe Thr Ala Thr
 115 120 125
 Ala Lys Glu Leu Gly Thr Ser Ile Arg Ala Lys His Gly Cys Asn Arg
 130 135 140
 Cys Tyr
 145

(2) INFORMATION FOR SEQ ID NO:425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

Met Gly Ser Arg Gly Leu Arg Lys Lys Gly Leu Arg Pro Phe Arg Asn
 1 5 10 15
 Lys Gly Gly His Ala Glu Ala Phe Phe Pro Ser Lys Leu Pro Leu Ile
 20 25 30
 Asn Leu Arg Met Asn Asn Arg Asn His Arg Lys Ile Val Val Ile Asp
 35 40 45
 Gly Gln Ile Gly Tyr Val Gly Gly Phe Asn Val Gly Asp Glu Tyr Leu
 50 55 60
 Gly Lys Ser Lys Lys Phe Gly Tyr Trp Arg Asp Thr His Leu Arg Ile
 65 70 75 80
 Val Gly Asp Ala Val Asn Ala Leu Gln Leu Arg Phe Ile Leu Asp Trp
 85 90 95

Asn Ser Thr Ser His Thr
100

(2) INFORMATION FOR SEQ ID NO:426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

Met	Gly	Ile	Gly	Arg	Val	Thr	Gln	Val	Met	Gly	Pro	Val	Ile	Ala	Val
1				5				10					15		
Arg	Xaa	Glu	His	Asn	Glu	Val	Pro	Lys	Ile	Asn	Asn	Ala	Leu	Val	Ile
			20					25					30		
Asp	Val	Pro	Lys	Glu	Glu	Gly	Thr	Ile	Gln	Leu	Thr	Leu	Glu	Val	Ala
			35					40					45		
Leu	Gln	Leu	Gly	Asp	Asp	Xaa	Xaa	Arg	Thr	Ile	Ala	Met	Asp	Ser	Xaa
			50					55					60		
Asp	Gly	Val	Gln	Arg	Gly	Met	Asp	Val	Lys	Asp	Thr	Gly	Lys	Glu	Ile
65						70				75					80
Ser	Val	Pro	Val	Gly	Asp	Glu	Thr	Leu	Gly	Arg	Val	Phe	Asn	Val	Leu
						85				90					95
Gly	Glu	Thr	Ile	Asp	Leu	Lys	Glu	Glu	Ile	Ser	Asp	Ser	Val	Arg	Arg
						100				105				110	
Asp	Pro	Ile	His	Arg	Gln	Ala	Pro	Ala	Phe	Asp	Glu	Leu	Ser	Thr	Glu
						115				120				125	
Val	Gln	Ile	Leu	Glu	Thr	Gly	Ile	Lys	Val	Val	Asp	Leu	Leu	Ala	Pro
						130				135				140	
Tyr	Ile	Lys	Gly	Gly	Lys	Ile	Gly	Leu	Phe	Gly	Gly	Ala	Gly	Val	Gly
145						150				155					160
Lys	Thr	Val	Leu	Ile	Gln	Glu	Leu	Ile	Asn	Asn	Ile	Ala	Gln	Arg	Ala
						165				170				175	
Arg	Trp	Val	Phe	Leu	Val	Phe	Arg	Arg	Cys	Arg	Leu	Asn	Gly	Thr	Pro
						180				185				190	

(2) INFORMATION FOR SEQ ID NO:427:

(i) SEQUENCE CHARACTERISTICS:

501

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

```

Met Leu Asn Pro Pro Leu Xaa Gln Leu Thr Ser Gln Ile Lys Ser Lys
 1             5             10             15
Tyr Leu Ile Ala Thr Thr Ala Ala Lys Arg Ala Arg Glu Ile Asp Glu
          20             25             30
Gln Pro Glu Thr Glu Leu Leu Ser Glu Tyr His Ser Phe Xaa Pro Val
          35             40             45
Gly Arg Ala Leu Glu Glu Ile Ala Asp Gly Lys Ile Arg Pro Val Ile
          50             55             60
Ser Ser Asp Tyr Tyr Gly Lys Glu
65             70

```

(2) INFORMATION FOR SEQ ID NO:428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

```

Met His Pro Gln Leu Val Ser Gln Tyr Asp Leu Ala Lys Gly Asn Ile
 1             5             10             15
Pro Thr Trp Asn Leu Phe Gly Leu Glu Ile Lys Gln Leu Asn Tyr Gln
          20             25             30
Gly Gln Val Leu Pro Val Leu Ile Ala Ala Tyr Val Leu Ala Lys Ile
          35             40             45

```

(2) INFORMATION FOR SEQ ID NO:429:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:

```

Met Ile Ala Ser Ser Leu Val Asn Lys Lys Ser Tyr His Gln Asp Lys
 1             5             10             15
Asn Thr Ile Ala Ile Asp Lys Pro Tyr Phe Gly Val Ser Leu Ile Val
          20             25             30
Phe Ile Val Leu Leu Ser Gly Leu Thr Phe Ile Pro Val Leu Leu Leu
          35             40             45
Gly Pro Ile Gly Glu Phe Leu Thr Leu Lys
 50             55

```

(2) INFORMATION FOR SEQ ID NO:430:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

```

Met Asn Ile Ile Glu Gln Lys Phe Tyr Asp Ser Lys Ala Phe Phe Asn
 1             5             10             15
Thr Gln Gln Thr Lys Val Ile Ser Phe Arg Lys Asp Gln Leu Lys Lys
          20             25             30
Leu Ser Lys Ala Ile Lys Ser Tyr Glu Ser Asp Ile Leu Glu Ala Leu
          35             40             45
Tyr Thr Asp Leu Gly Lys Asn Lys Gly Thr Lys Leu Met Leu Leu Lys
 50             55             60
Leu Ala
65

```

(2) INFORMATION FOR SEQ ID NO:431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

```

Met Xaa Leu Ile Gly Lys Ile Xaa Gly Ser Val Asp Cys Ala Lys Glu
 1             5             10             15
Trp Thr Xaa Trp Gly Ile Lys Tyr Gly Leu Phe Ile Gln Ser Val Ile
          20             25             30
Asp Phe Ile Ile Ile Ala Cys Ala Leu Phe Ile Cys Val Lys Ile Ala
          35             40             45
Asn Thr Leu Met Lys Lys Glu Glu Ala Glu Glu Glu Ala Val Val Glu
          50             55             60
Glu Asn Val Val Leu Leu Thr Glu Ile Arg Asp Leu Leu Arg Glu Lys
65             70             75             80
Lys

```

(2) INFORMATION FOR SEQ ID NO:432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

```

Met Asn Leu Leu Thr Phe Asp Glu Met Ala Arg Ile Ala Lys Val Tyr
 1             5             10             15
Ala Glu Leu Gly Val Lys Lys Ile Arg Ile Thr Gly Gly Glu Pro Leu
          20             25             30
Met Arg Arg Asp Leu Glu Pro Cys Thr Tyr Ser
          35             40

```

(2) INFORMATION FOR SEQ ID NO:433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

```

Met Phe Asn Pro Phe Asp Glu Phe Pro His Thr Ile Glu Ile Gly Glu
 1           5           10           15
Val Glu Val Ala Gly Thr Phe Pro Lys Glu Tyr Glu Arg Phe Lys Ser
          20           25           30
Asn Glu Thr Ile Lys Gly Phe Met Asp Thr Pro Thr Ser Ser Glu Thr
          35           40           45
Leu Lys Phe His Gln Met Ser Lys Asp Phe Asp Arg Asn Leu Tyr Thr
          50           55           60
Pro Tyr His Ile Pro Ile Thr Asn Lys Thr Leu Phe Asn Tyr Glu Gly
65           70           75           80
Lys Thr Tyr Glu Val Val Val Arg Thr Gly Arg Pro Arg Arg Thr Thr
          85           90           95

```

(2) INFORMATION FOR SEQ ID NO:434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

```

Met Thr Lys His Glu Gln Ile Leu Asp Tyr Ile Glu Ser Leu Ser Ile
 1           5           10           15
Gly Ser Lys Ile Ser Val Arg Lys Ile Ala Lys Phe Leu Asn Val Ser
          20           25           30
Glu Gly Thr Ala Tyr Arg Ala Ile Lys Asp Ala Asp Lys Met Gly Met
          35           40           45
Val Ala Thr Ile Asp Arg Val Gly Thr Val Arg Ile Glu Lys Arg Asn
          50           55           60

```

```

Arg Tyr Glu Ile Glu His Leu Thr Phe Asn Glu Ile Phe Asn Ile Ile
65              70              75              80
Asp Gly Gln Val Leu Gly Cys His Xaa Gly Ile Thr Lys Met Val Ser
              85              90              95
Lys Phe Ala Ile Gly Ala Met Glu Leu Lys Asp Ile Leu Lys Tyr Ile
              100             105             110
Gly Pro Lys Thr Leu Leu Ile Val Gly Asn Arg Glu Asp Val Pro Gly
              115             120             125
Xaa Ser Xaa Xaa Lys Glu Val Arg Pro Ile Leu Ile Thr Trp Trp Ile
              130             135             140

```

(2) INFORMATION FOR SEQ ID NO:435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

```

Met Ser Phe Gln Arg Val Pro Cys Glu Ile Ser Ala Val Pro Val Ile
1              5              10              15
His Val Asp Pro Phe Ile Asn Gln Gln Xaa Arg Gln Lys Leu Asn Gln
              20              25              30
Ile Ile Asn Asp Ser Arg Glu Xaa Arg Val Met Lys Met Ala Thr Asp
              35              40              45
Gly Lys Ser Leu Ala Asp Leu Leu Ser
              50              55

```

(2) INFORMATION FOR SEQ ID NO:436:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

```

Met Trp Ser Phe Lys Ser Met Phe Asn Thr Pro Glu Asp Pro Glu Lys
 1              5              10              15
Asp Ala Tyr Glu Phe Tyr Gly Lys Val Gln Pro Gly Ile Thr Thr Pro
      20              25              30
Thr Gln Lys Thr Cys Asn Phe Val Ala Leu Asp Leu Lys Ser Lys Asp
      35              40              45
Arg Asp Ala Ile Lys Ala Met Phe Lys Lys Trp Thr Val Met Ala Asp
      50              55              60
Arg Met Met Asp Gly Asp Thr Val Gly Lys Thr Ser Asn Asn Pro Leu
65              70              75              80
Met Pro Pro Val Asp Thr Gly Glu Ser Ile Gly Leu Gly Ala Ser Lys
      85              90              95
Leu Thr Ile Thr Phe Gly Ile Ser Lys Ser Leu Met Lys Lys Asn Gly
      100              105              110
Leu Ser Lys
      115

```

(2) INFORMATION FOR SEQ ID NO:437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

```

Met Leu Thr His Phe Tyr Ala Xaa His Ile Glu His Arg Arg Trp Gly
 1              5              10              15
Ala Pro Xaa Pro Xaa Ile Glu Ile Val Lys Leu Gly Ile Asn Lys Ala
      20              25              30
Arg Gly Ile Glu Gln Val Arg Gln Phe Leu Xaa Ile Asp Arg Asn Asn
      35              40              45
Ile Ile Ala Phe Gly Asp Glu Asp Asn Asp Ile Glu Met Ile Glu Tyr
      50              55              60
Ala Arg His Gly Val Ala Met Glu Asn Gly Val Gln Glu Leu Lys Asp
65              70              75              80
Val Ala Asn Asn Ile Thr Phe Asn Asn Asn Glu Asp Gly Ile Gly Ser
      85              90              95
Ile Phe Glu

```

(2) INFORMATION FOR SEQ ID NO:438:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

```

Met Ile Glu Arg Phe Val His Glu His Asp Val Ile Met Phe Thr Ile
 1             5             10             15
Cys Met Asp Val Ile Asp Ser Ala Phe Ala Pro Gly Val Ser Ala Pro
      20             25             30
Xaa Val Leu Gly Leu Tyr Pro His Thr Val Leu Glu Leu Ala Lys Arg
      35             40             45
Ile Ile Pro Ser Asp Lys Val Ser Ser Val Ser Ile Ala Glu Met Asn
      50             55             60
Pro Thr Tyr Asp Ala Asp Asn Arg Xaa Xaa Lys Leu Val Pro Asn Leu
65             70             75             80
Xaa His His Phe Leu Lys
      85

```

(2) INFORMATION FOR SEQ ID NO:439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

```

Met Met Ser Phe Thr Met Asn Gln Gln Met Arg Gln Leu Leu Gln Lys
 1             5             10             15
Tyr Val Glu Lys His Gln Ile Thr Asp Phe Met Phe Phe Met Ser Val
      20             25             30
                        508

```

Val Met Thr Leu Leu Ser Arg Tyr Ala Arg Lys Asp Asp Val Val Val
 35 40 45
 Gly Ser Val Met Ser Ala Arg Met His Lys Gly Thr Glu Gln Met Leu
 50 55 60
 Gly Met Phe Ala Asn Thr Leu Val Tyr Ser Gly Gln Pro Ser Pro Asp
 65 70 75 80
 Lys Met Trp Thr Gln Phe Leu Gln Glu Val
 85 90

(2) INFORMATION FOR SEQ ID NO:440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

Met Val Ser Tyr Ala Gly Thr Ser Ser Met Glu Val Val Xaa His Ile
 1 5 10 15
 Arg Xaa Val Asp Val Phe Asn Asn Lys His Asp Leu Ala Pro Leu Ser
 20 25 30
 Tyr Leu Thr Phe Val Ala Leu Asp Asp Glu Gly Thr Pro Lys His Val
 35 40 45
 Pro Gly Val Tyr Pro Glu Asp Asp Val Val Lys Trp Phe Tyr Asp Thr
 50 55 60
 Ala Pro Gln Arg Val Glu Arg Arg Lys Ala Arg Arg Ile Glu Ser Lys
 65 70 75 80
 Gln Thr Xaa Glu Tyr Leu Ala Gln Val Gln His Ile Arg Asp
 85 90

(2) INFORMATION FOR SEQ ID NO:441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

```

Met Ala Asn Ala His Asp Phe Ile Met Asn Leu Pro Gln Gly Tyr Asp
 1             5             10             15
Thr Glu Val Gly Glu Arg Gly Val Lys Leu Ser Gly Gly Gln Lys Gln
      20             25             30
Arg Leu Ser Ile Ala Arg Ile Phe Leu Asn Asn Pro Pro Ile Leu Ile
      35             40             45
Leu Asp Glu Ala Thr Ser Ala Leu Asp Leu Glu Ser Glu Ser Xaa Asn
      50             55             60
Ser Arg Ser Ile Arg Cys Val Asp
65             70

```

(2) INFORMATION FOR SEQ ID NO:442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

```

Met Ala Ser Ser Leu Gly Gly Ala Phe Gly Val Ala Ile Ser Gly Ala
 1             5             10             15
Val Tyr Val Gly Ala Val Ala Ala Thr Ser Ile His Thr Gly Ala Met
      20             25             30
Ile Ala Leu Trp Val Asn Val Leu Met Gly Ile Met Ala Phe Ile Ala
      35             40             45
Ile Leu Phe Gly Ala Xaa Ser
50             55

```

(2) INFORMATION FOR SEQ ID NO:443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

```

Met Ile Tyr Phe Asn Ile Gly Gln Ile Ile Ala Asn Ile Ile Cys Trp
 1             5             10             15
Ala Leu Ile Ala Pro Thr Leu Asp Ile Leu Ile Tyr Asn Glu Pro Ala
             20             25             30
Asn Lys Val Tyr Thr Gln Gly Val Ile Ser Ala Val Leu Asn Ile Ile
             35             40             45
Ser Val Gly Ile Ile Gly Thr Ile Leu Leu Lys Ala Tyr Ala Ser Ser
             50             55             60
Gln Ile Lys Lys Gly Ser Leu Arg Lys Glu
65             70

```

(2) INFORMATION FOR SEQ ID NO:444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

```

Met Lys Met Lys Lys Xaa Asp Ile Ser Val Lys Thr Val Val Ala Ile
 1             5             10             15
Gly Ile Gly Ala Ala Val Phe Val Ile Leu Gly Arg Phe Val Val Ile
             20             25             30
Pro Thr Gly Phe Pro Asn Thr Asn Ile Glu Thr Ser Tyr Ala Phe Leu
             35             40             45
Ala Leu Ile Ser Ala Ile Phe Gly Pro Phe Ala Gly Leu Met Pro Gly
             50             55             60
Leu Val Gly His Ala Ile Lys Asp Phe Pro Asp Ile Arg Val Val Leu
65             70             75             80
Gly Gly Val Gly Leu Phe Val Gln Glu Leu Ser Pro Val
             85             90

```

(2) INFORMATION FOR SEQ ID NO:445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

```

Met Leu Asn Ala Asp Leu Lys Gln Gln Leu Lys Gln Leu Leu Glu Leu
 1             5             10             15
Met Glu Gly Asn Val Glu Phe Val Gly Ser Leu Gly Ser Asp Glu Lys
             20             25             30
Ser Lys Glu Leu Lys Glu Leu Leu Thr Gly Asn Phe
             35             40

```

(2) INFORMATION FOR SEQ ID NO:446:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

```

Met Ser Leu Arg Asp Glu Ala Leu Glu Met His Lys Arg Asn Gln Gly
 1             5             10             15
Lys Leu Glu Val Lys Pro Asn Val Lys Val Thr Asn Lys Glu Glu Leu
             20             25             30
Ser Leu Ala Tyr Ser Pro Gly Val Val Glu Pro Cys Lys Asp Ile Tyr
             35             40             45
Glu Asp Lys Arg Lys Val Tyr Asp Tyr Thr Ile Lys Gly Asn Thr Val
             50             55             60
Ala Val Ile Thr Asp Gly Thr Ala Val Leu Gly Leu Gly Asn Ile Gly
             65             70             75             80
Pro Glu Ala Ser Ile Pro Val Met Glu Gly Lys Ala Val Leu Phe Lys
             85             90             95
Ser Phe Ala Gly Ile Asn Gly Val Pro Ile Ala Leu Asn Thr Thr Asp
             100            105            110
Thr Glu Glu Ile Ile Lys Thr Val Lys Ser Leu Glu Pro Asn Tyr Gly

```

115 120 125
 Gly Ile Asn Leu Glu Asp Ile Ser Ala Pro Arg Cys Ser Glu Ile Glu
 130 135 140
 Val Pro Ile Glu Lys Arg Asn
 145 150

(2) INFORMATION FOR SEQ ID NO:447:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:

Met Asp Ile Val Asn Ile Glu Ser Leu Ala Glu Gly Leu Asn Lys Trp
 1 5 10 15
 Met Lys Glu Leu Ser Lys Thr Thr Ser Leu Asp Pro Val Lys Pro Val
 20 25 30
 Asp Val Leu Leu Thr Glu Asn Asp Ile Thr Ile Lys Asn Ile Arg Asp
 35 40 45
 Ile Glu Ser Phe Lys Thr Leu Arg Xaa Lys Ile Phe Leu Arg Pro Ile
 50 55 60
 Phe Glu Met Asp Asp Leu Ser Asp Phe Phe Ser
 65 70 75

(2) INFORMATION FOR SEQ ID NO:448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

Met Thr Gln Tyr Pro Leu Trp Gln Gln Leu Asn Thr Leu Lys Gln Ala
 1 5 10 15

Thr Trp Val Asp Leu Thr His Thr Phe Asp Pro Glu Ile Pro Arg Phe
 20 25 30
 Ser Glu Phe Glu Lys Gly Glu Val Ser Thr Leu Phe Thr Val Lys Asp
 35 40 45
 His Gly Phe Tyr Val Gln Arg Trp Asn Ile Val Thr Gln Tyr Gly Thr
 50 55 60
 His Ile Gly Cys Asn Gln Ser Thr Leu Val Gly Glu Gln Thr Val Ile
 65 70 75 80

(2) INFORMATION FOR SEQ ID NO:449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

Met Gln Leu Phe Glu Thr Met Xaa Ile Asp Asn Gly His Ile Pro Arg
 1 5 10 15
 Leu Thr Tyr His Thr Asn Arg Ile Lys Cys Ser Ser Glu Arg Leu Asn
 20 25 30
 Phe Lys Phe Asp Glu His Ala Trp Arg Asn Glu Leu Asn Asp Val Thr
 35 40 45
 Thr Lys Tyr His Ser Gly Gln Tyr Arg Leu Lys Ile Val Leu Asn Ala
 50 55 60
 Glu Ser Lys Phe Glu Thr Ile Val Ser Pro Leu Pro Glu Lys Ser Ser
 65 70 75 80
 Phe Thr Ala Lys Phe Gln Val Leu Pro Gln Ser
 85 90

(2) INFORMATION FOR SEQ ID NO:450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

```

Met Met Ile Thr Ile Leu Ala Gly Ala Ala Leu Ser Ile Ser Gly Ala
 1             5             10             15
Ile Val Gln Ser Val Thr Lys Asn Pro Ile Ala Glu Pro Gly Ile Leu
          20             25             30
Gly Ile Asn Ala Gly Gly Gly Phe Ala Ile Ala Leu Phe Ile Ala Ile
          35             40             45
Gly Lys Ile Asn Ala Asp Asn Phe Val
 50             55

```

(2) INFORMATION FOR SEQ ID NO:451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

```

Met Pro Leu Asp Thr Cys Gly Ala Met Ser Pro Gly Met Ile Gly Tyr
 1             5             10             15
Trp Leu Glu Thr Glu Ile Asn Arg Ile Leu Thr Glu Met Asn Ser Asp
          20             25             30
Arg Thr Val Gly Thr Ile Val Thr Thr Cys Gly Ser Arg
          35             40             45

```

(2) INFORMATION FOR SEQ ID NO:452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

```

Met Gln Ser Met Glu Leu Leu Tyr Asn Gln Gln Phe Glu Val Xaa Lys
 1             5             10             15
Ala Ile Ile Leu Ala Ala Thr Ser Arg Thr Ser Ser Tyr Ser Arg Ala
      20             25             30
Phe Asn Glu Ile Ala Arg Gln Ala Ile His Leu Gly Gly Lys Glu Gly
      35             40             45
Leu Ser Ile Ala Arg Gln Leu Gly Phe Leu Thr Tyr Arg Ser Ser Lys
      50             55             60
Ser Tyr Asp Glu Arg Phe Thr Pro Asp Glu Xaa Val Ala Tyr Gln Gln
65             70             75             80
His Gln Gly Asn Lys Phe Lys Glu His Phe Asp Leu Asn Xaa Tyr Leu
      85             90             95
Thr Leu Leu Asp Val Leu Asp Ser His Asn Ile Asp Arg Gly Arg Thr
      100            105            110
Asp Val Thr His Ile Phe Lys Asn Leu Glu Thr Lys Val Leu Xaa Met
      115            120            125
Gly Phe Ile Asp Asp Leu Leu Tyr Pro Asp Asp Gln Val Arg Ala Leu
      130            135            140
Gly Glu Arg Phe Lys Tyr His Arg His Phe Phe Val Pro Asp Asn Val
145            150            155            160
Gly His Asp Gly Phe Leu Leu Asn Phe Ser Thr Trp Ala Pro Asn Leu
      165            170            175
Tyr His Phe Leu Asn Leu Lys His Phe Lys Arg Lys
      180            185

```

(2) INFORMATION FOR SEQ ID NO:453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

```

Met Thr Asn Leu Asn Asp Tyr Phe Ser Glu Glu Thr Val Glu Met Met
 1             5             10             15
Leu Ser Asn Ile Glu Val Ile Val Gly Asp Phe Glu Cys Met Asp Asp
      20             25             30
Val Val Leu Pro Glu Asn Met Asp Thr Ile Ile His Ala Xaa Ala Arg
      35             40             45

```

```

Thr Asp His Phe Gly Asp Asp Asp Glu Phe Glu Lys Val Asn Val Gln
 50                      55                      60
Gly Thr Val Asp Val Ile Xaa Val Ala Gln Gln His His Ala Arg Leu
 65                      70                      75                      80
Ile Tyr Val Ser Thr Ile Ser Val Gly Thr Tyr Phe Asp Ile Asp Thr
                      85                      90                      95
Glu Asp Val Thr Phe Ser Glu Ala Asp Val Tyr Lys Gly Gln Leu Leu
          100                      105                      110
Thr Ser Pro Tyr Thr Arg Ser Lys Phe Tyr Ser Glu Leu Asn Ile Arg
          115                      120                      125
Ser Cys Lys
          130

```

(2) INFORMATION FOR SEQ ID NO:454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

```

Met His Xaa Ile Lys Ala Ala Ile Glu Glu Ala His Lys Xaa Asn Lys
 1                      5                      10                      15
Gln Leu Leu Val Asp Met Ile Ala Val Gln Asp Leu Arg Lys Thr Cys
          20                      25                      30
Lys Thr Thr Arg
          35

```

(2) INFORMATION FOR SEQ ID NO:455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

Met Ile Thr Ile Asp Asp Leu Ile Glu Tyr Arg Lys Lys Leu Glu Pro
 1 5 10 15
 Glu Ile Glu Phe Lys Pro Lys Ser Glu Asn Ala Tyr Arg Phe Arg Asn
 20 25 30
 Ile

(2) INFORMATION FOR SEQ ID NO:456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:

Met Ala Pro Ile Ala Ala Trp Gly Ile Thr Thr Thr Ala Phe Ile Asn
 1 5 10 15
 Phe Gly Tyr Leu Lys Gly Phe Glu Gly Val Phe Ile Tyr Pro Ala Leu
 20 25 30
 Leu Ser Leu Ile Ile Gly Ala Ile Ser Tyr Val Leu Ile Arg Asp Thr
 35 40 45
 Pro Gln Ser Gln Gly Leu Pro Pro Ile Glu Ile Tyr Lys Asn Asp Phe
 50 55 60
 Ala Thr Ser Asp Lys Lys His
 65 70

(2) INFORMATION FOR SEQ ID NO:457:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

Met Thr Tyr Gln Ser Cys Gln Asn Phe His Cys Ser Lys Ser Asp Thr
 1 5 10 15
 Ser Ile Leu Lys Thr Lys Val Lys Ser Asp Lys Asn Asp Thr Asn Tyr
 20 25 30
 Arg Pro Val Leu Asn Gln Tyr Tyr Gly Glu Leu Leu Phe Leu Leu Asn
 35 40 45
 Ser Glu Pro Asn Asn Gln Lys Tyr Lys Xaa Asn Ser Asn Val
 50 55 60

(2) INFORMATION FOR SEQ ID NO:458:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

Met Glu Thr Ile Glu Lys Gly Met Gly Xaa Thr Leu Gly His Ile Ala
 1 5 10 15
 Leu Ile Phe Gly Leu Gly Ala Ile Leu Gly Lys Leu Leu Ala Asp Gly
 20 25 30
 Gly Gly Ala Thr Arg Ile Ala Asp Thr Leu Xaa Gln Lys Phe Gly Gln
 35 40 45
 Lys His Val Gln Trp Ala Met Leu Gly Cys Ser Ile Tyr Arg Arg Tyr
 50 55 60
 Cys Ile Val Leu
 65

(2) INFORMATION FOR SEQ ID NO:459:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:

Met Leu Gly Val Val Pro Val Ile Arg Ala Leu Arg Val Lys Ala Met
 1 5 10 15
 Ala Ile Gln Ala Glu Thr Met Asp Ser Ile Asp Arg Lys Leu Pro Gly
 20 25 30
 Leu Ser Glu Arg Glu Arg Lys Ile Ile Ser Lys His Thr Gln Ser Ile
 35 40 45
 Ile Asn His Met Leu
 50

(2) INFORMATION FOR SEQ ID NO:460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:

Met Val Val Ile Phe Ile Pro Val Leu Ala Xaa Trp Arg Gly Ile Phe
 1 5 10 15
 His Gly Tyr Lys Ser Xaa Gly Xaa Ala Ala Val Ser Xaa Val Thr Glu
 20 25 30
 Gln Ile Ala Arg Ser Xaa Phe Thr Tyr
 35 40

(2) INFORMATION FOR SEQ ID NO:461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:

Met Pro Thr Gly Thr Asn Ile Tyr Ala Val Lys Gly Gly Ile Ala Asp
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:462:

(A) LENGTH: 44 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:

(2) INFORMATION FOR SEQ ID NO:463:

(A) LENGTH: 106 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

```

Met Gln Ile Lys Leu Pro Lys Pro Phe Phe Phe Glu Glu Gly Lys Arg
  1                      5                      10                      15
Ala Val Leu Leu Leu His Gly Phe Thr Gly Asn Ser Ser Asp Val Arg
      20                      25                      30
Gln Leu Gly Arg Phe Leu Gln Lys Lys Gly Tyr Thr Ser Tyr Ala Pro
      35                      40                      45
Gln Tyr Glu Gly His Ala Ala Pro Pro Glu Glu Ile Leu Lys Ser Ser
                        521

```

```

      50              55              60
Pro Phe Xaa Trp Phe Lys Asp Ala Leu Asp Gly Tyr Asp Tyr Leu Val
65              70              75              80
Glu Gln Gly Tyr Asp Glu Ile Val Gly Cys Trp Ser Ile Ile Xaa Arg
      85              90              95
Val Gly Ile Leu Arg Phe Lys Ile Lys Ala
      100             105

```

(2) INFORMATION FOR SEQ ID NO:464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

```

Met Lys Gln Tyr Pro Met Thr Leu Ser Gly Gly Glu Ala Gln Arg Val
 1              5              10              15
Ala Leu Ala Arg Ala Leu Ser Thr Lys Pro Asp Leu Ile Leu Leu Asp
      20              25              30
Glu Pro Phe Ser Ser Leu Asp Asp Thr Thr Gln Asp Glu Ser Ile Thr
      35              40              45
Leu Val Lys Arg Ile Phe Xaa Xaa Trp Xaa Ile Pro Ile Ile Phe Val
      50              55              60
Thr His Ser Xaa Tyr Glu Ala Xaa His Met Ala His Glu Ile Ile Thr
65              70              75              80
Ile Gly

```

(2) INFORMATION FOR SEQ ID NO:465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

```

Met Arg Tyr His Ser Leu Ile Ala Asp Gly Ala Thr Phe Pro Asn Cys
 1           5           10           15
Leu Lys Ile Thr Ala Lys Asn Asp Glu Ala Ile Ile Met Ala Phe Glu
          20           25           30
His Ile Arg Phe Pro Val Phe Gly Val Gln Tyr His Pro Glu Ser Ile
          35           40           45
Leu Ser Glu Tyr Gly Tyr Arg Gln Val
          50           55

```

(2) INFORMATION FOR SEQ ID NO:466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

```

Met Gly Val Asp Thr Glu Asp Asn Ser Asp Pro Lys Tyr Ile Thr Ile
 1           5           10           15
Arg Gly Lys Gly Pro Val Val Lys Glu Leu Lys Lys His Ala Lys Lys
          20           25           30
Ala Lys Asn Val Phe Leu Ala Ser Asp Pro Asp Arg Glu Gly Glu Ala
          35           40           45
Ile Ala Trp His Leu Ser Lys Ile Leu Glu Leu Glu Asp Ser Lys Glu
          50           55           60
Asn Arg His Ala Cys Phe Gln Arg Asn Asn
          65           70

```

(2) INFORMATION FOR SEQ ID NO:467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

```

Met Val Leu His Asp Ile Xaa Gln Ala Ile Arg Phe Ser Asp His Leu
 1             5             10             15
Ile Ala Met Lys Glu Gly Asp Ile Ile Ala Thr Gly Ser Thr Glu Asp
      20             25             30
Val Leu Thr Gln Glu Ile Leu Glu Lys Val Phe Asn Ile Asp Val Val
      35             40             45
Leu Arg Lys Asp Pro Lys Thr Gly Lys Pro Leu Leu Val Thr Tyr Asp
      50             55             60
Leu Cys Arg Thr Ser Leu Phe Leu Ile Lys
65             70

```

(2) INFORMATION FOR SEQ ID NO:468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

```

Met Tyr Gly Arg Leu Met Asn Thr Pro Ala Val Asn Xaa Ile Phe Glu
 1             5             10             15
Ala Thr Pro Glu Gln Ile Leu Val Asn Gly Glu Leu Ile Val His Arg
      20             25             30
Asp Asp Ile Ile Thr Glu Gln Asp Ile Leu Ala His Ile Asn Leu Ile
      35             40             45
Asp Gln Leu Ser Ala Glu Val Ile Asp Thr Pro Ser Thr Ala Thr Ile
      50             55             60
Ser Asp Ser Leu Thr Ala Lys Val Glu Val Thr Leu Leu Glu Gly Ser
65             70             75             80
Lys

```

(2) INFORMATION FOR SEQ ID NO:469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

```

Met Val Met Gly Val Glu Val Phe Pro His His Asp Val Lys Gln Xaa
 1             5             10             15
Pro His Ile Pro Ala Thr Glu Ile Met Arg His Xaa Pro Thr His Pro
      20             25             30
Asn Asn Gln His Lys Gly Tyr Ala Gly His His Leu Phe Ile Lys Leu
      35             40             45
Xaa Asn Tyr His Gln Thr Asp Ile Ser Arg Ser Ile Cys Thr Ile Phe
      50             55             60
Thr Lys Ile Thr Ile Leu Ile Phe Val Asp Gly Thr Gly Lys Ser Leu
      65             70             75             80
Glu Asp Leu Lys Gly Ile Ile Asp Gln Gly Gln Pro Val Leu Ile Tyr
      85             90             95
His Thr Asn Leu Gly Ser Lys Pro Leu Leu Arg Val Phe Arg Phe Asp
      100            105            110
Asn Lys Pro Ala Lys Gln Val Ser Asn Ile His Val Thr Val Leu Ile
      115            120            125
Gly Tyr Asp Asp Tyr Tyr Tyr Tyr Tyr Ile Asp Pro Leu Trp Ser His
      130            135            140
Ile Arg Arg Gly Leu Val Leu Pro Ala Ile Ile Pro Asn Arg Lys Gln
      145            150            155            160
Ile Ile Lys Ile Arg Lys Glu Lys Met Glu Tyr Ser Phe Asn Ser Pro
      165            170            175
Gly Arg Lys Cys Ile Tyr Val Gln Pro His Ser Tyr Thr Ile Glu Asn
      180            185            190
Gln Gln Gln Asn Lys His Thr
      195

```

(2) INFORMATION FOR SEQ ID NO:470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

```

Met Thr Asn Tyr Lys Val Val Val Leu Asp Met Asp Asp Thr Leu Leu
 1             5             10             15
Asn Ser Asp Asn Val Ile Ser Glu Glu Thr Ala Asn Tyr Leu Thr Ala
          20             25             30
Ile Gln Asp Glu Gly Tyr Tyr Val Val Leu Ala Ser Gly Arg Pro Thr
          35             40             45
Glu Gly Met Ile Pro Thr Ala Arg Asp Leu Lys Leu Pro Glu His His
          50             55             60
Ser
65

```

(2) INFORMATION FOR SEQ ID NO:471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

```

Met Ala Val Lys His Ala Ser Ala Pro Lys Ala Tyr Ile Asn Ile Thr
 1             5             10             15
Gly Leu Gly Phe Ala Lys Leu Thr Lys Glu Gly Ala Glu Leu Lys Tyr
          20             25             30
Ser Asp Ile Thr Lys Thr Arg Gly Leu Gln Lys Ile Gly Val Glu Thr
          35             40             45
Gly Gly Glu Leu Lys Thr Ala Tyr Ala Asp Gly Gly Pro Ile Glu Ser
          50             55             60
Gly Asn Thr Asp Gly Glu Gly Lys Ile Ser Leu Pro Met His Ala Phe
65             70             75             80
Pro Lys Glu Ile Arg Lys Ile Val Phe Asn Glu Asp Tyr Asp Glu Gly
          85             90             95
Trp Arg Leu Arg Thr Arg Lys Pro Gly Lys Pro His Gln Leu Arg Xaa
          100             105             110
Leu Tyr Gly Ser Asp Lys Glu Arg Xaa Xaa Thr Gly Thr Ile
          115             120             125

```

(2) INFORMATION FOR SEQ ID NO:472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

```

Met Tyr Thr Thr Gly Cys Leu Glu Ile Glu His Gly Asp Ala Asn Glu
 1             5             10             15
Gly Val Leu Leu Leu Lys Gln Ala Leu Glu Val Asp Asn Ala Tyr Pro
          20             25             30
Arg Thr Phe Ile Asp Phe Lys Ala Asp Leu Tyr Ser
      35             40

```

(2) INFORMATION FOR SEQ ID NO:473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

```

Met Lys Glu Asp Leu Asp Pro Thr Phe Met Trp His Leu Ala Phe Ala
 1             5             10             15
Tyr Gly Gln Glu Glu Arg Asp Lys Glu Ala Gln His Phe Phe Glu Leu
          20             25             30
Ala Tyr Pro Thr Met Lys Thr Asn Ile Asp Phe Met Ser Asp Tyr Tyr
      35             40             45
Phe Tyr Leu Ile Glu Ile Gly Gln Lys Glu Gln Ala Ile Thr Ile Leu
      50             55             60
Asn Gln Leu Leu Glu Leu Glu Pro Ser Asn Glu Asn Trp His Asp Glu
65             70             75             80
Leu Ser Arg Leu Gln Ser

```


85

(2) INFORMATION FOR SEQ ID NO:474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

```

Met Asn Ser Gln Glu Leu Leu Ala Ile Ala Val Asp Xaa Ile Xaa Asn
 1             5             10             15
Lys Lys Gly Glu Asp Thr Ile Ser Leu Glu Met Lys Gly Ile Ser Asp
          20             25             30
Met Thr Asp Tyr Phe Val Val Thr His Gly Asn Asn Glu Arg Xaa Val
          35             40             45
Gln Ala Ile Ala Arg Ala Val Lys Glu Val Ala Asn Glu Gln Asn Ile
          50             55             60
Glu Val Lys Arg Met Glu Gly Tyr Asn Glu Ala Arg Trp Ile Leu Ile
65             70             75             80
Asp Leu Ala Arg Cys Cys Gly Thr Cys Phe Pro
          85             90

```

(2) INFORMATION FOR SEQ ID NO:475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

```

Met Ile Asp Ile Pro Leu Asp Glu Ser Ser Phe Met Tyr Asp Thr Pro
 1             5             10             15
Gly Ile Ile Gln Asp His His Met Thr His Leu Val Ser Val Lys Glu
          20             25             30

```

528

Leu Xaa Ile Ile Met Pro Lys Lys Glu Xaa Lys Gln Arg Val Tyr Gln
35 40 45
Leu Asn Glu Ala Gln Thr Leu Phe Phe Gly Gly Leu Arg Ala His Arg
50 55 60
Leu Cys Ile Arg Trp
65

(2) INFORMATION FOR SEQ ID NO:476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

```
Met Ile Ser Gly Leu Gly Phe Ile Thr Ile Gly Pro Gly Ala Lys Val  
1           5              10          15  
Ile Val Arg Val Pro Lys Asn Val Asp Val Val Leu Arg Asn Ser Ile  
                20             25            30  
Leu
```

(2) INFORMATION FOR SEQ ID NO:477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

Met Ala Ile His Tyr Glu Thr Lys Ala Thr Asn Val Gly Gly Arg Lys
1 5 10 15
Gly His Val Tyr Thr Asp Asp Arg Ala Leu Asp Ile Asp Ile Val Pro
20 25 30
Pro Ala Gln Ala Asp Gly Lys Ala Thr Asn Pro Glu Gln Leu Phe Ala
529

35	40	45
Ala Gly Tyr Ala Ser Cys Phe Asn Gly Ala Phe Asp Leu Ile Leu Lys		
50	55	60
Gln Asn Lys Cys Val Met Leu Ile Gln Lys Val Thr Leu Thr Val Arg		
65	70	75
Leu Glu Asp Asp Gln Thr Gln Lys Val Leu Ile Xaa Trp Phe Asn		80
85	90	95

(2) INFORMATION FOR SEQ ID NO:478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:

Met Arg Asn Val Lys Gln Ile Ala Thr Lys Ser Ile Ile Ala Ile Ile		
1	5	10
Ser Leu Cys Ile Leu Thr Tyr Thr Thr Met Ile Gly Ser Val Leu Ala		15
20	25	30
Asp Glu Ile Lys Tyr Pro Ser Ala Lys Phe Asn Gln Pro Glu Ala Lys		
35	40	45
Asp Lys Thr Glu Leu Thr Thr Ser Ile Phe Asp Glu Lys Ile Lys Glu		
50	55	60
Asn Lys Ala Leu Glu Leu Leu Ile Phe Asn Gln Glu Asn Lys Asn Val		
65	70	75
Thr Glu Glu Gln Gln Leu Val Asp Glu Lys Ala Gln Leu Ile Ser Asp		80
85	90	95
Met Thr Gly Lys Ile Tyr Leu Gln Val Lys Leu Lys Gly Gln Ile Asp		
100	105	110
Lys Glu Gln Leu Val Phe Gln Asn Asp Lys Asn Glu Glu Phe Pro Phe		
115	120	125
Val Ile Lys Asp Glu Lys Asp Asp Pro		
130	135	

(2) INFORMATION FOR SEQ ID NO:479:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids

- (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:

```

Met Ser Arg Thr Lys Leu Gln Asp Phe Pro Ser Lys Glu Asn Thr Val
 1           5           10           15
Thr Glu Pro Lys Gln Val Val Val Asn Pro Leu Phe Ala Lys Pro Asn
          20           25           30
Ala Leu Ala Gly Ile Phe Gly Ile Ser Tyr Ser Ser Val Asn Arg Ile
          35           40           45
Leu Lys Glu Trp Glu Lys Asp Ser Lys Gly Val Asp Asp Leu Tyr Tyr
          50           55           60
Ser Leu Ser Ser Thr Leu Ile Val Ile Ser Ile Pro Arg Phe Xaa Glu
65           70           75           80
Tyr Met Lys Val Arg Pro Lys Lys Trp Met Phe Glu Val Lys Gln
          85           90           95

```

(2) INFORMATION FOR SEQ ID NO:480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:

```

Met Leu Glu Pro Thr Ile Lys Pro Ile Glu Ala Val Asp Glu Cys Leu
 1           5           10           15
Gly Glu Val Val Asp Lys Ile Leu Asp Met Asp Gly Tyr Ala Ile Ile
          20           25           30
Thr Ala Asp His Gly Asn Ser Asp Gln Val Leu Thr Asp Asp Asp Gln
          35           40           45
Pro Met Thr Thr His Thr Thr Asn Pro Val Pro Val Ile Val Thr Lys
          50           55           60
Glu Gly Val Thr Leu Arg Glu Thr Gly Arg Leu Gly Asp Leu Ala Pro
65           70           75           80

```

Thr Leu Leu Asp Leu Leu Asn Val Glu Gln Pro Val Asp Met Thr Gly
85 90 95
Glu Ser Leu Ile Lys His
100

(2) INFORMATION FOR SEQ ID NO:481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:

Met	Thr	Xaa	Arg	Ile	Ser	Xaa	Ile	Gly	Gly	Xaa	Xaa	Leu	Gly	Phe	Gly
1				5				10					15		
Ala	Ser	Xaa	Ala	Gly	Gly	Cys	Ser	Ile	Gly	Asn	Gly	Leu	Val	Glu	Thr
			20					25				30			
Ala	Thr	Met	Thr	Trp	Gln	Gly	Trp	Ile	Ala	Leu	Ala	Ser	Met	Ile	Xaa
			35					40				45			
Gly	Val	Trp	Thr	Met	Ser	His	Phe	Xaa	Xaa	Val	Arg	Pro	Met	Lys	Xaa
			50				55				60				
Val	Gln	Gln	Xaa	Ser	Ala	Ile	Gly								
65						70									

(2) INFORMATION FOR SEQ ID NO:482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:482:

Met Ile Gln Thr His Ile Asn Val Val Gly Leu Ser Ile Asn Thr Gly
1 5 10 15
Val Phe Ala Ala Gly Ala Asn Asp Asn His Glu Pro Lys Lys Gly Ile
532

20 25 30
 Lys Phe Ala Thr Pro Ala Asn Arg Thr Asn Lys Gly Ile Tyr Gly Lys
 35 40 45
 Ser Ile Ile Glu
 50

(2) INFORMATION FOR SEQ ID NO:483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:

Met Leu Glu Thr Gln Glu Val Asp Ser Tyr Arg Thr Ala Thr Asn His
 1 5 10 15
 Ile Phe Lys Arg Lys Asn Gly Ala Ser Lys Asn Ile Ile Asp Glu Lys
 20 25 30
 Leu Ile Pro Lys Asp Tyr Trp Leu Ser Gln Ala Pro Lys Leu Asn Ser
 35 40 45
 Lys Gln Leu Ile Asp Asp Leu Lys Ala Gly Lys Asp Ile Pro Gly Val
 50 55 60
 Glu Leu Lys Val Thr Glu Ser Leu Val Ile Lys
 65 70 75

(2) INFORMATION FOR SEQ ID NO:484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:

Met Ser Glu Ile Ile Val Tyr Thr Gln Asn Asp Cys Pro Pro Cys Thr
 1 5 10 15

Phe Val Lys Asn Tyr Leu Asn Glu His Gln Ile Asp Phe Glu Glu Arg
 20 25 30
 Asn Ile Asn Asn Gln Gln Tyr Arg Asn Glu Met Ile Asp Phe Asp Ala
 35 40 45
 Phe Ser Thr Pro Phe Ile Leu Leu Asn Gly Asn Pro Met Tyr His Val
 50 55 60
 Asp Leu Asp Glu Ile Asn Lys Val Leu Asn Ile Gln Asp
 65 70 75

(2) INFORMATION FOR SEQ ID NO:485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:

Met Lys Tyr Ala Asp Lys Lys Gly Val Asp Ile Tyr Tyr Ile Ser Asp
 1 5 10 15
 Arg Asp Lys Glu Lys Asp Leu Lys Ala Thr Gln Lys Asn Leu Lys Gln
 20 25 30
 Gln Gly Ile Pro Gln Ala Lys Lys Ser His Ile Leu Leu Lys Gly Lys
 35 40 45
 Asp Asp Lys Ser Lys Glu Ser Arg Arg Gln Met Val Gln Lys Asp His
 50 55 60
 Lys Leu Val Met Leu Phe Gly Asp Asn Leu Leu Asp Phe Thr Asp Pro
 65 70 75 80
 Lys Glu Ala Thr Ala Glu Ser Arg Glu Ala Leu Ile Glu Lys His Lys
 85 90 95
 Asp Asp Phe Gly Lys Lys Tyr Ile Ile Phe Pro Asn Pro Met Tyr Gly
 100 105 110
 Ser Trp Glu Ala Thr Ile Tyr Asn Asn Asn Tyr Lys Ala Ser Asp Lys
 115 120 125
 Ala Lys Asp Lys Leu Arg Lys Asn Ala Ile Lys Gln Ser Asp Pro Lys
 130 135 140
 Thr Gly Glu Val Lys
 145

(2) INFORMATION FOR SEQ ID NO:486:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:486:

```

Met Ser Leu Gln Asp Pro Thr Arg Lys Met Ser Lys Ser Asp Asp Asn
 1             5             10             15
Ala Lys Asn Phe Ile Ser Leu Leu Asp Glu Pro Asn Val Ala Ala Lys
      20             25             30
Lys Ile Lys Ser Ala Val Thr Asp Ser Asp Gly Ile Ile Lys Phe Asp
      35             40             45
Arg Asp Asn Lys Pro Gly Ile Thr Asn Leu Ile Ser Ile Tyr Ala Gly
      50             55             60
Leu Thr Asp Met Pro Ile Lys Asp Ile Glu Ala Lys Tyr Glu Gly Glu
      65             70             75             80
Gly Tyr Gly Lys Phe Lys Gly Asp Leu Ala Glu Ile Val Lys Ala Phe
      85             90             95
Leu Val Glu Phe Gln Xaa Lys Ile Arg Lys Phe Leu
      100             105

```

(2) INFORMATION FOR SEQ ID NO:487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:487:

```

Met Leu Ser Asp Ala Gln Glu Gly Asp Val Ile Ser Gly Lys Pro Trp
 1             5             10             15
Ile Trp Met Pro Pro Ala Ile Met Ile Thr Leu Thr Ile Leu Ser Ile
      20             25             30
Asn Phe Val Gly Gly Gly Leu Lys Asp Ala Phe Asn Pro Arg Gly Arg
                        35

```


35 40 45
Arg

(2) INFORMATION FOR SEQ ID NO:488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:488:

```

Met Gly Arg Asp Asn Val Leu Ile Thr Pro His Ile Gly Ser Ala Ser
 1             5             10             15
Val Thr Thr Arg Asp Asn Met Ile Gln Leu Cys Ile Asn Asn Ile Glu
          20             25             30
Ala Val Met Thr Asn Gln Val Pro His Thr Pro Val Asn
      35             40             45

```

(2) INFORMATION FOR SEQ ID NO:489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489:

```

Met Lys Ser Lys Ser Lys Gln Pro Pro Asn Lys Tyr Val Glu Ala Phe
 1             5             10             15
Lys Pro Tyr Leu Leu Thr Leu Leu Tyr Leu Ala Ile Phe Ile Thr Leu
          20             25             30
Tyr Leu Ile Tyr Gly Ser Gly Asp Thr His Asn Asn Phe Ile Tyr Asn
      35             40             45
Glu Phe
      50

```

(2) INFORMATION FOR SEQ ID NO:490:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:490:

```

Met Thr Asp Ile Ile Asn Lys Leu Gln Ala Phe Ala Asp Ala Asn Pro
 1             5             10             15
Gln Ser Ile Ala Val Arg His Thr Thr Asp Glu Leu Thr Tyr Gln Gln
          20             25             30
Leu Met Asp Glu Ser Ser Lys Leu Ala His Arg Leu Gln Gly Ser Lys
      35             40             45
Lys Pro Met Ile Leu Phe Gly His Met Ser Pro Tyr Met Ile Val Gly
      50             55             60
Met Ile Gly Ala Ile Lys Ala Gly Cys Gly Tyr Val Pro Val Asp Thr
65             70             75             80
Ser Asn Ser Trp Lys Thr Val Leu Lys
          85

```

(2) INFORMATION FOR SEQ ID NO:491:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:491:

```

Met Leu Ile Ala Asn Glu Thr Val Ala Glu His Phe Ser Lys Leu Asn
 1             5             10             15
Val Pro Phe Ile Tyr Arg Val His Glu Gln Pro Lys Ser Asp Arg Leu
          20             25             30
Arg Gln Phe Phe Asp Phe Ile Thr Asn Phe Gly Ile Met Ile Lys Gly
          537

```

```

      35              40              45
Thr Gly Glu Asp Ile His Pro Thr Thr Leu Gln Lys Val Gln Glu Glu
      50              55              60
Val Glu Gly Arg Pro Glu Gln Met Val Ile Ser Thr Met Met Leu Arg
      65              70              75              80
Ser Met Gln Gln Ala His Tyr Asp Asp Val Asn Leu Gly His Cys Gly
      85              90              95
Leu Ser Ala Glu Tyr Tyr Thr His Xaa Thr Ser Pro Ile Arg Arg Tyr
      100             105             110
Pro Asp Leu Thr Xaa His Arg Leu Ile Arg Lys Tyr Leu Ile Glu Lys
      115             120             125
Ser Met Asp Asn Lys Glu Val Lys Arg Trp Glu Asp Lys Leu Pro Glu
      130             135             140
Leu Ala Glu His Thr Ser Lys Arg Glu Arg Arg Ala Ile Glu Ala Glu
      145             150             155             160
Arg Asp Thr Asp Glu Leu Lys Lys Ala Glu Tyr Met Ile Gln His Ile
      165             170             175
Gly Asp Glu Phe Glu Gly Ile Val Ser Ser Val Ala Asn Phe Gly Xaa
      180             185             190
Phe Ile Glu Leu Xaa Asn Thr Ile Glu Gly Met Xaa His Ile Ala Asn
      195             200             205
Met Thr Asp Asp Tyr Tyr Arg Val Glu Glu Arg Gln Met Ala Leu Ile
      210             215             220
Gly
      225

```

(2) INFORMATION FOR SEQ ID NO:492:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:

```

Met His Thr Leu Ser His Asn Lys Ile Lys Ser Gln Leu Arg Met Thr
  1              5              10              15
Leu Pro Glu Tyr Met Ile Pro Val Asn Phe Met His Ile Glu Gln Ile
      20              25              30
Pro Ile Thr Ile Asn Gly Lys Leu Asp Lys Lys Ala Leu Pro Ile Met
      538

```

```

          35              40              45
Asp Tyr Val Asp Thr Asp Ala Tyr Val Ala Pro Ser Thr Asp Thr Glu
    50              55              60
His Leu Leu Cys Gln Ile Cys Ala Asp Ile Leu His Val Asn Gln Val
    65              70              75              80
Gly Ile His Asp Asn Phe Phe Glu Leu Gly Gly His Ser Leu Lys Ala
          85              90              95
Thr Leu Val Val Asn Arg Ile Glu Ala Ser Thr Gly Lys Arg Leu Gln
          100              105              110
Ile Gly Asp Leu Leu Xaa Lys Pro Thr Val Phe Glu Leu Ala Arg Ala
          115              120              125
Ile Ala Lys Val Gln Glu Gln Asn Tyr Glu Val Ile Pro Arg Xaa Tyr
          130              135              140
Lys Xaa Lys Val Asp Tyr Val Ala Trp Ser Ser Cys Pro Lys Ser Val
          145              150              155              160
Leu Tyr Leu Leu Trp Lys Ser Xaa Pro Ile Lys Ile Arg Leu Tyr Asn
          165              170              175
Arg Thr Phe Phe Met Ala Val Ile Ile Arg Thr
          180              185

```

(2) INFORMATION FOR SEQ ID NO:493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:

```

Met Lys Asn Leu Asn Ser Phe Asn Tyr Val Arg Lys Gly Leu Glu Tyr
  1              5              10              15
Glu Glu Lys Arg Gln Glu Glu Glu Leu Leu Asn Gly Gly Glu Ile Gly
          20              25              30
Gln Glu Thr Arg Arg Phe Asp Glu Ser Thr Gly Lys Thr Ile Leu Met
          35              40              45
Arg Val Lys Glu Gly Ser Asp Asp Tyr Arg Tyr Phe Pro Glu Pro Asp
          50              55              60
Ile Val Pro Leu Tyr Ile Asp Asp Ala Trp Lys Glu Arg Val Arg Gln
          65              70              75              80
Thr Ile Pro Glu Leu Pro Asp Glu Arg Lys Ala Lys Tyr Val Asn Glu

```

85 90 95
 Leu Gly Leu Leu His Thr Met Xaa Xaa Tyr
 100 105

(2) INFORMATION FOR SEQ ID NO:494:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:494:

Met Val Lys Ala Lys Leu Trp Gly Phe Leu Val Gly Gln Ile Met Lys
 1 5 10 15
 Ala Ser Lys Gly Gln Ala Asn Pro Gln Leu Val Asn Gln Leu Leu Lys
 20 25 30
 Gln Glu Leu Asp Lys Arg
 35

(2) INFORMATION FOR SEQ ID NO:495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495:

Met His Glu Asn Tyr Asp Val Leu Ile Ala Ala Gly Gly Asp Gly Thr
 1 5 10 15
 Leu Asn Glu Val Val Asn Gly Ile Ala Glu Lys Pro Asn Arg Pro Lys
 20 25 30
 Leu Gly Val Ile Pro Met Gly Thr Val Asn Asp Phe Gly Arg Ala Leu
 35 40 45
 His Ile Pro Asn Asp Ile Met Gly Ala Leu Asp Val Ile Ile Glu Gly
 50 55 60

His	Ser	Thr	Lys	Val	Asp	Ile	Gly	Lys	Met	Asn	Asn	Arg	Tyr	Phe	Ile	
65					70					75					80	
Asn	Leu	Ala	Ala	Gly	Gly	Gln	Leu	Thr	Gln	Val	Ser	Tyr	Glu	Thr	Pro	
				85					90						95	
Ser	Lys	Leu	Lys	Ser	Ile	Val	Gly	Pro	Phe	Ala	Tyr	Tyr	Ile	Lys	Gly	
			100					105					110			
Phe	Glu	Met	Leu	Pro	Gln	Met	Lys	Ala	Val	Asp	Leu	Arg	Ile	Glu	Tyr	
		115					120					125				
Asp	Gly	Asn	Val	Xaa	Gln	Gly	Glu	Ala	Leu	Leu	Phe	Phe	Xaa	Gly	Leu	
	130					135					140					
Thr	Asn	Pro	Met	Ala	Gly	Phe	Glu	Lys	Leu	Val	Pro	Gly	Arg			
145					150					155						

(2) INFORMATION FOR SEQ ID NO:496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:

```

Met Asp Xaa Gly Asn Pro Val Xaa Xaa Ile Tyr Phe Xaa Glu Pro Asp
 1                               5                               10                               15
Leu His Phe Thr Ile Ile Asp Phe Asn Gln Glu Leu Leu Cys Ile Tyr
      20                               25                               30
Ile Asp Phe Asp Ser Gly Leu Arg His Ser Asn Met Ala Thr Glu Ser
      35                               40                               45
Gly Ile Ser Leu Arg Ile Asn Ile Ala Lys Ser Asp Phe Thr Lys Phe
      50                               55                               60
Ile Asn Glu Leu Ala Ser Leu Tyr
65                               70

```

(2) INFORMATION FOR SEQ ID NO:497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497:

```

Met Gln Ile Glu Leu Thr Asp Ala Ala Val Thr Trp Phe Lys Asn Glu
 1             5             10             15
Leu Glu Leu Pro Glu Asn Asn Lys Val Leu Val Phe Phe Val Arg Tyr
      20             25             30
Gly Gly Glu Phe Gln Leu Lys Gln Gly Phe Ser Pro Ala Phe Thr Val
      35             40             45
Glu Pro Lys Glu Asp Val Asp Ile Gly Tyr Glu Gln Gln Tyr Asp Asp
      50             55             60
Leu Asn Val Val Val Ala Glu Lys Asp Leu Trp Tyr Phe Glu Asp Asp
      65             70             75             80
His Ile Ile Val Asn Val Xaa Asp His Glu Asp Glu Ile Ser Tyr Ser
      85             90             95
Thr Lys

```

(2) INFORMATION FOR SEQ ID NO:498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498:

```

Met Thr Lys Ile Ser Lys Ile Ile Asp Glu Leu Asn Asn Gln Gln Ala
 1             5             10             15
Asp Ala Ala Trp Ile Thr Thr Pro Leu Asn Val Tyr Tyr Phe Thr Gly
      20             25             30
Tyr Arg Ser Glu Pro Met Lys Asp Tyr Leu His Tyr
      35             40

```

(2) INFORMATION FOR SEQ ID NO:499:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499:

```

Met Val Ile Thr Ile Glu Pro Gly Ile Tyr Val Pro Gly Val Ala Gly
 1             5             10             15
Val Arg Ile Glu Asp Asp Ile Leu Val Thr Asn Glu Gly Tyr Glu Val
          20             25             30
Leu Thr His Tyr Glu Lys
          35

```

(2) INFORMATION FOR SEQ ID NO:500:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500:

```

Met Leu Arg Arg Xaa Gly Asn Pro Gly Ile Ser Thr Cys Ala Ile Val
 1             5             10             15
Ile Lys Glu Asp Lys Gln His Xaa Thr Tyr Thr His Glu Leu Gly Glu
          20             25             30
Met Asp Asn His Thr Ala Glu Trp Ala Ala Cys Ile Tyr Ala Leu Glu
          35             40             45
His Ala Arg Glu Leu Asn Val Gln Asn Ala Leu Leu Tyr Thr Asp Ser
          50             55             60
Lys Leu Ile Ala Arg
          65

```

(2) INFORMATION FOR SEQ ID NO:501:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:

```

Met His Pro Arg Thr Ile Xaa Ile Asp Val Ile Ser Lys Leu His Gln
 1             5             10             15
Asn Lys Asp Ile Gln Trp His Gln Ile Lys Ser Ser Ile Ile Glu Thr
      20             25             30
Leu Gln Pro Tyr Leu Phe Glu Lys Thr Ala Arg Lys Pro Met Ile Leu
      35             40             45
Pro Val Ile Met Lys Val Asn Glu Gln Lys Glu Ser Asn Asn Lys
 50             55             60

```

(2) INFORMATION FOR SEQ ID NO:502:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502:

```

Met Ala Arg Leu Arg Thr Ile Xaa Gly Val Met Ser His Asp Leu Gln
 1             5             10             15
Leu Pro Ile Gly Ile Leu Pro Gly Gly Thr Phe Asn Asp Phe Thr Xaa
      20             25             30
Thr Leu Asn Ile Ala Pro Asn His Lys Gln Ala Ser Glu Gln Met Ile
      35             40             45
Ser Ala Gln Val Gly Thr Tyr Asp Val Ile Lys Ile Asn Asn Gln Tyr
      50             55             60
Ala Leu Asn Phe Val Gly Leu Gly Leu Ile Val Gln Asn Ala Glu Asn
      65             70             75             80
Val Gln Asp Gly Ser Lys Asp Ile Phe Gly Lys Leu Ser Tyr Ile Gly
      85             90             95
Ser Thr Val Lys Thr Leu Leu Asn Pro Thr Gln Phe Asn Tyr Gln Leu
      100             105             110
Ser Ile Asp Asp Lys Thr Tyr Ser Gly Glu Thr Thr Met Ile Leu Thr

```

115 120 125
 Ala Asn Gly Pro Phe Ile Gly Gly Ser Arg Xaa Pro Leu Thr Asp Leu
 130 135 140
 Ser Pro Gln Asp Gly
 145

(2) INFORMATION FOR SEQ ID NO:503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503:

Met Lys Phe Asn Glu Ile Trp Ile Asn Glu Tyr Leu Ala Leu Val Asn
 1 5 10 15
 Asp Asp Asn Pro Ile His Asn Glu Ile Val Pro Gly Gln Leu Val Ser
 20 25 30
 Gln Met Met Leu Met Ala Met Ser Leu Glu Thr Asn Gln Cys Gln Ile
 35 40 45
 Asn Tyr Val Lys Pro Ile Leu Ile Asn Glu Asn Ile Glu Phe Ile Glu
 50 55 60
 Gln His Glu His Glu Ile Ile Ala Ile Asn Asp Asp Gly Glu Ile Lys
 65 70 75 80
 Ile Lys Ile Ser Leu Ser Thr Lys Lys
 85

(2) INFORMATION FOR SEQ ID NO:504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:504:

Met Phe Gln Gln Ser Tyr Asn His Gly Ala Gly Cys Thr Phe Ala Ala
 1 5 10 15
 Ala Thr Pro Ala Tyr Leu Ala Asn Gly Lys Ser Pro Lys Glu Ala Val
 20 25 30
 Ile Ser Thr Ser Glu Ser Phe Arg Arg Phe Cys Tyr
 35 40

(2) INFORMATION FOR SEQ ID NO:505:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:505:

Met His Ser Leu His Glu Leu Val Lys Leu Phe Thr Val His Gln Arg
 1 5 10 15
 Ile Phe Ile Glu Gln Ile Arg Glu Gly Ala His Leu Thr Ala Gly Lys
 20 25 30
 Phe Met Gln Gly Glu Phe Pro Val Met Met Phe Gly Leu Pro Gly Ala
 35 40 45
 Ala Leu Ala Ile Tyr His Thr Ala Asn Pro Glu Asn Lys Lys Val Val
 50 55 60
 Ala Gly Leu Met Gly Ser Ala Ala Leu Thr Ser Xaa Leu Xaa Gly Ile
 65 70 75 80
 Thr Glu Pro Leu Glu Phe Ser Phe Leu Phe Val Ala Pro Leu Leu Phe
 85 90 95
 Phe Ile His Ala Val Leu Asp Gly Leu Ser Phe Leu Thr Leu Tyr Leu
 100 105 110
 Leu Asp Val His Leu Gly Tyr Thr Phe Ser Gly Gly Phe Ile Asp Tyr
 115 120 125
 Val Leu Leu Gly Val Leu Pro Asn Lys Thr Gln Trp Trp Leu Val Ile
 130 135 140
 Pro Val Gly Leu Val Tyr Ala Val Ile Tyr Tyr Phe Val Phe Arg Phe
 145 150 155 160
 Leu Ile Val Lys Leu Lys Tyr Lys Thr Pro Gly Arg Glu Asp Lys Gln
 165 170 175
 Ser Gln Ala Val Thr Ala Ser Ala Thr Glu Leu Pro Tyr Ala Val Leu
 180 185 190

Glu Ala Met Gly Gly Lys Ala Asn Ile Lys His Leu Asp Ala Cys Ile
 195 200 205
 Thr Arg Leu Arg Val Glu Val Asn Asp Lys Ser Lys Val Asp Val Pro
 210 215 220
 Gly Val Lys Asp Leu Gly Ala Ser Gly Val Leu Glu Val Gly Asn Asn
 225 230 235 240
 Met Gln Ala Ile Cys Gly Ser
 245

(2) INFORMATION FOR SEQ ID NO:506:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506:

Met Phe Arg Pro Ile Ser Asp Ala Gly Ala Ala Ile Phe Glu Leu Xaa
 1 5 10 15
 Asp Asp Gln Ile Glu Lys Ala Lys Gln Asn Ile Ser Ala Ala Gly Tyr
 20 25 30
 Gln Pro Gly Glu Glu Glu Ser Gln Pro Ser Glu Asn Ser Val Asp Phe
 35 40 45
 Asn Arg Asp Gly Asp Tyr Asp Leu Leu Ile Ile Gly Ser Gly Gly Ala
 50 55 60
 Ala Phe Ser Ala Ala Ile Lys Ala Asn Glu Asn Gly Ala Lys Val Ser
 65 70 75 80
 Met Val Glu Arg Gly Thr Val Gly Gly Thr Cys Val Asn Ile Gly Cys
 85 90 95
 Val Pro Ser Lys Thr Met Leu Arg Ala Gly Glu Ile Asn Gly Leu Ala
 100 105 110
 Gln Asn Asn Pro Phe Thr Gly Leu Gln Thr Ser Thr Gly Ala Ala Asp
 115 120 125
 Leu Ala Gln Leu Thr Glu Gln Lys Asp Gly Leu Val Ser Gln Met Arg
 130 135 140
 Gln Glu Lys Tyr Ile Asp Leu Ile Glu Glu Tyr Gly Phe Asp Leu Ile
 145 150 155 160
 Arg Gly Glu Ala Ser Phe Ile Asp Asp Lys Thr Ile Gln Val Asn Gly
 165 170 175

```

His Asn Ile Thr Ser Lys Ser Phe Leu Ile Ala Thr Gly Ala Ser Pro
      180                      185                      190
Ala Val Pro Glu Ile Pro Gly Met Asn Glu Val Asp Tyr Leu Thr Ser
      195                      200                      205
Thr Ser Ala Leu Glu Leu Lys Glu Val Pro Gln Arg Leu Ala Val Ile
      210                      215                      220
Gly Ser Gly Tyr Ile Ala Ala Glu Leu Gly Gln Met Phe His Asn Leu
225                      230                      235                      240
Gly Thr Glu Val Thr Leu Met Gln Arg Ser Glu Arg Leu Phe Lys Thr
      245                      250                      255
Tyr Asp Pro Glu Ile Ser Glu Ala Ile Asp Glu Ser Leu Thr Glu Gln
      260                      265                      270
Gly Leu Asn Leu Ile Thr Gly Val Thr Tyr Gln Lys Val Glu Gln Asn
      275                      280                      285
Gly Lys Ser Thr Ser Ile Tyr Ile Glu Val Asn Gly Gln Glu Gln Val
      290                      295                      300
Ile Glu Ala Asp Gln Val Leu Val Ala Thr Gly Arg Lys Pro Asn Thr
305                      310                      315                      320
Glu Thr Leu Asn Leu Glu Ser Ala Gly Val Lys Thr Gly Lys Lys Gly
      325                      330                      335
Glu Val Leu Thr Asn Glu Tyr Leu Gln Thr Ser Asn Asn Arg Ile Tyr
      340                      345                      350
Ala Ala Gly Asp Val Thr Leu Gly Pro Gln Phe Val Tyr Val Ala Ala
      355                      360                      365
Tyr Glu Gly Gly Ile Val Ala Asn Asn Ala Leu Gly Leu Ala Lys Arg
      370                      375                      380
Lys Ile Asp Leu Arg Phe Val Pro Gly Val Thr Phe Thr Asn Pro Ser
385                      390                      395                      400
Ile Ala Thr Val Gly Leu Thr Glu Gln Gln Ala Lys Glu Lys Gly Tyr
      405                      410                      415
Asp Val Lys Thr Ser Val Leu Pro Leu Asp Ala Val Pro Arg Ala Leu
      420                      425                      430
Val Asn His Glu Thr Thr Gly Val Tyr
      435                      440

```

(2) INFORMATION FOR SEQ ID NO:507:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:507:

```

Met Lys Asn Leu Lys Ser Phe Phe Ile Lys Asn Thr Leu Val Leu Thr
 1           5           10           15
Ser Thr Ala Leu Leu Phe Ser Ser Phe Glu Pro Val Val His Ala Ala
      20           25           30
Glu Asn Lys Glu Val Val Lys Thr Val Glu Asn Asp Asn Val Glu Phe
      35           40           45
Asn Glu Leu Leu Glu Gly Gln Glu Tyr Ile Trp Glu Val Leu Ser Arg
      50           55           60
Asp Asp Glu Gly Phe Lys Met Phe Leu Asp Glu Gln Arg Ala Phe Asn
      65           70           75           80
Pro Asn Phe Asp Asn Asp Val Leu Leu Ala Lys Gln Glu Gly Ala Leu
      85           90           95
Asn Ser Ser Val Phe Ala Asn Asn Ser Met Thr Leu Asn Ser Asn Lys
      100          105          110
Pro Thr Pro Arg Gly Pro Ile Gly Ala Thr Leu Lys Ala Ile Lys Ala
      115          120          125
Leu Ser Pro Ser Leu Arg His Gly Gly Asn Cys Tyr Ile Leu Asp His
      130          135          140

```

(2) INFORMATION FOR SEQ ID NO:508:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:508:

```

Met Ile Asn Thr Gly Ser Ala Ala Ser Ile Val Tyr Gln Gln Gly Ala
 1           5           10           15
Ile Tyr Ala Asn Ala Glu Phe Ile Gln Ile His Pro Thr Ala Ile Pro
      20           25           30
Gly Asp Asp Lys Leu Arg Leu Met Ser Asp Gln His Xaa Cys
      35           40           45

```

(2) INFORMATION FOR SEQ ID NO:509:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:509:

```

Met Xaa Lys Thr Trp Xaa Ile Leu Ile Cys His Ile Lys Ile Gln His
 1             5             10             15
Glu Leu Asp Val Lys Leu Gly Gly Ile Ile Glu Ile Tyr Xaa Lys Phe
      20             25             30
Thr Gly Asp Asp Pro Arg Lys Val Pro Met Lys Ile Phe Pro Ala Val
      35             40             45
His Tyr Ser Met Gly Gly Leu Tyr Val Asp Tyr Asp Gln Met Thr Asn
 50             55             60
Ile Lys Gly Leu Phe Ala Ala Gly Glu Cys Asp Phe Ser Gln His Gly
65             70             75             80
Gly Asn Arg Leu Gly Ala Asn Ser Leu Leu Ser Ala Ile Tyr Gly Gly
      85             90             95
Thr Val Ala Gly Pro Asn Ala Ile Asp
      100             105

```

(2) INFORMATION FOR SEQ ID NO:510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510:

```

Met Thr Pro Asn Val Thr Val Val Arg Glu Asn Glu Lys Leu Leu Glu
 1             5             10             15
Thr Asp Xaa Lys Ile Val Glu Leu Met Lys Arg Tyr Glu Asp Ile Asp
      20             25             30
Met Glu Asp Thr Gln Thr Trp Ser Asn Gln Ala Val Phe Phe Thr Arg
      550

```

```

          35          40          45
Gln Leu Trp Asn Met Leu Val Leu Ala Arg Val Ile Thr Ile Gly Ala
    50          55          60
Tyr Asn Arg Asn Glu Ser Arg Gly Ala His Tyr Lys Pro Glu Phe Leu
    65          70          75          80
Ile Ser Ile Phe Val Arg Ser Thr
          85

```

(2) INFORMATION FOR SEQ ID NO:511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511:

```

Met Gly Leu Thr Asp Leu Arg Lys His Ile Ile Tyr Glu Asp Val Trp
 1          5          10          15
Thr Pro Glu Asp Ile Glu Lys Asn Tyr Arg Ser Asn Arg Gly Ala Ile
    20          25          30
Tyr Gly Val Val Ala Asp Lys Lys Lys Asn Lys Gly Phe Thr Phe Pro
    35          40          45
Lys Glu Ser Gln Tyr Phe Glu Asn Leu Tyr Phe Val Gly Gly Ser Xaa
    50          55          60
Asn Pro Gly Gly Gly Met Pro Met Val Thr Leu Ser Gly Gln Gln Xaa
    65          70          75          80
Ala Asp Lys Xaa Asn Ala Arg Arg Ser Glu Xaa Ile Gly Xaa
          85          90

```

(2) INFORMATION FOR SEQ ID NO:512:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512:

```

Met Glu Tyr Ile Asp Ala Ser His Ile Val Ile Ala Leu Leu Ile Ile
 1           5           10           15
Leu Val Ile Ile Thr Leu Phe Ile Leu Leu Phe Ile Glu Leu Val Glu
           20           25           30
Val Arg Ile Pro Tyr Ile Asp Leu Met Asn Val Ser Ala Thr Asn Met
           35           40           45
Lys Ser Tyr Leu Ser Trp Lys Val Asn Pro Ala Gly Ser Ile Thr Leu
           50           55           60
Met Met Ser Ile Ser Ala Phe Val Phe Leu Lys Ser Gly Ile His Phe
65           70           75           80
Ile Leu Ser Met Phe Asn Lys Ser Ile Ser Asp Asp Met Pro Met Leu
           85           90           95
Thr Phe Asp Ser Pro Val Gly Ile Ser Val Tyr Leu Val Ile Gln Met
           100          105          110
Leu Leu Gly Tyr Phe Leu Ser Arg Phe Leu Ile Asn Thr Lys Gln Lys
           115          120          125
Ser Lys Asp Phe Leu Lys Ser Gly Asn Tyr Phe Ser Gly Val Lys Pro
           130          135          140
Gly Lys Asp Thr Glu Arg Tyr Leu Asn Tyr Gln Ala Arg Arg Val Cys
145          150          155          160
Trp Phe Gly Ser Ala Leu Val Thr Val Ile Ile Gly Ile Pro Leu Tyr
           165          170          175
Phe Thr Leu Phe Val Pro His Leu Ser Thr Glu Ile Tyr Phe Ser Val
           180          185          190
Gln Leu Ile Val Leu Val Tyr Ile Ser Ile Asn Ile Ala Glu Thr Ile
           195          200          205
Arg Thr Tyr Leu Tyr Phe Asp Lys Tyr Lys Pro Phe Leu Asn Gln Tyr
           210          215          220
Trp
225

```

(2) INFORMATION FOR SEQ ID NO:513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513:

```

Met Lys Tyr Phe Ile Pro Ala Trp Tyr Asp Asp Gln Arg Trp Trp Gln
 1             5             10             15
Asp Thr Thr Val Pro Tyr Tyr Gln Leu Gln Asn Lys Thr Glu Phe Asp
      20             25             30
Asp Met Ile Ser Leu Met Gly Met His Leu Glu Asn Asp Leu Asp Tyr
      35             40             45
Gln Leu Ile Val Leu Asn His Ala Pro Asn Leu Arg Thr Phe Leu His
      50             55             60
Arg Tyr Asp Leu Tyr Glu Thr Lys Tyr Ser Ser Val Phe Asp Glu Ile
      65             70             75             80
Gln Gly Phe Ser His His Ala Pro Gln Ala Ile Asn Tyr His His Leu
      85             90             95
Lys Trp Xaa Asp Asp Val Gly Val Trp Val His Ala Arg Ile Tyr
      100             105             110

```

(2) INFORMATION FOR SEQ ID NO:514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514:

```

Met Ile Ala Gln Gln Ile His Glu Asp Asp His Val Ile Val Ala Ser
 1             5             10             15
Asp Ala Arg His Asn Arg Gln Ile Ala Asn His Ile Pro Ala Lys Leu
      20             25             30
Leu Ser Tyr Ser Phe Phe Lys Asn Arg Asn Glu Xaa Val Ser Asp Glu
      35             40             45
Glu Tyr Gln Ser Ile Val Lys Asn Ala His Leu Ile Val Asp Ser Val
      50             55             60
Gln Leu Glu Arg Asp Leu Ile Ser His Gln Glu Lys Tyr Gln Arg Glu
      65             70             75             80
Asn Thr Met Ile Arg Ile Thr Pro Phe Glu Thr Arg Gln Ser Pro Asn
      85             90             95
Ile Ser Ser Gln Leu Met Glu Thr Phe Ile Gly Val Trp Ile Asp Gly
      100             105             110

```

```

Met Ser Asp Ala Asp Leu Gln Gln Met Met Gln Arg Leu Val Asp Tyr
 115                      120                      125
Ile Ala Gln Glu Asp Tyr Tyr Arg Leu Ile Leu Leu Ser Arg His Gln
 130                      135                      140
Asn Asp Ile Pro Met Trp Leu Arg Glu Cys Ile Thr Ser Val Asn Glu
145                      150                      155                      160
Glu Tyr Gln Ala Lys Gln Asn Ala Asp Val Asn Val Ser Ala Leu Met
                      165                      170                      175
Thr Pro Glu Asp Gln Asp Asp Ile Ile Ala Val Lys Thr Ile His Ala
                      180                      185                      190
Glu His Asp Val Val Glu Ala Leu Arg Thr Leu Arg Leu Val Ile Asp
195                      200                      205
Met Ser Lys Glu Pro Asp Leu Tyr Leu Gln Ile Ser Ala Ile Ser Ala
210                      215                      220
Gly Ile Pro Gln Ile Asn Gly Gln Gln Thr Asp Tyr Val Ser Asp Tyr
225                      230                      235                      240
Asp Asn Gly Arg Ile Ile Asn Thr Ala Gly
                      245                      250

```

(2) INFORMATION FOR SEQ ID NO:515:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515:

```

Met Leu Asp Ser Pro Leu Glu Ile Pro Ala Lys Pro Phe Asp Ala Tyr
 1                      5                      10                      15
Ile Ser Val Thr Val Lys Ala Arg Gly Asn Gly Thr Val His Leu Gly
20                      25                      30
Pro Lys His Thr Arg Trp Ser Arg Xaa Xaa Xaa Xaa Gln Phe Leu Xaa
35                      40                      45
Gly Gly Asn Arg Phe Glu Asp Xaa Xaa Arg Xaa Glu Phe Asn Tyr
50                      55                      60

```

(2) INFORMATION FOR SEQ ID NO:516:

(i) SEQUENCE CHARACTERISTICS:

554

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:516:

```

Met Xaa Pro Pro Leu Asn Val Asn Phe Ser Gly Tyr Arg Xaa Pro Glu
 1             5             10             15
Gly Phe Glu Gly Tyr Tyr Met Met Xaa Arg Met Asn Ala Pro Phe Leu
          20             25             30
Leu Ile Ala Asp Pro Arg Val Xaa Gly Gly Ser Phe Tyr Ile Gly Ser
          35             40             45
Ser Glu Tyr Glu Gln Arg Asp Tyr Gln Cys Tyr
 50             55

```

(2) INFORMATION FOR SEQ ID NO:517:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517:

```

Met Ile Glu Xaa Leu Asp Ala Arg Val Asn Val Ile Ile Leu Glu His
 1             5             10             15
Leu Val Gly Pro Ile Asp Phe Lys Gln Asp Ile Leu Ala Val Lys Val
          20             25             30
Leu Ala Gln Leu Phe Ser Lys Ile Lys Pro Asp Val Ile His Leu His
          35             40             45
Ser Ser Lys Ala Gly Thr Val Gly Arg Ile Ala Lys Phe Ile Ser Lys
          50             55             60
Ser Lys Asp Thr Arg Val Val Phe Thr Ala His Gly Trp Ala Phe Thr
          65             70             75             80
Glu Gly Val Lys Pro Ala Lys Lys Phe Leu Tyr Leu Val Ile Glu Lys
          85             90             95
Leu Met Ser Cys Ile Thr Asp Ser Ile Ile Cys Val Ser Asp Phe Asp
                    555

```

```

          100              105              110
Lys Gln Leu Ala Leu Lys Tyr Arg Phe Asn Arg Leu Lys Leu Thr Thr
          115              120              125
Ile His Asn Gly Ile Ala Asp Val Pro Ala Val Xaa Gln Thr Leu Lys
          130              135              140
Ser Gln Ser His Asn Asn Ile Gly Glu Val Val Gly Xaa Leu Pro Asn
          145              150              155              160
Lys Gln Asp Leu Gln Ile Asn Ala Pro Thr Lys His Gln Phe Val Met
          165              170              175
Ile Ala Arg Phe Ala Tyr Pro Lys Leu Pro Gln Asn Leu Ile Ala Ala
          180              185              190
Ile Glu Ile Leu Lys Leu His Asn Ser Asn His Ala His Phe Thr Phe
          195              200              205
Ile Gly Asp Gly Pro Thr Leu Asn Asp Cys Gln Pro Pro Ser Cys Thr
          210              215              220
Ser Trp Val Lys Lys Met Met Ser His Phe Trp Ala Met Ser Leu Met
          225              230              235              240
Arg Val Ile Tyr Tyr His Asn Thr Ile Arg Leu Phe
          245              250

```

(2) INFORMATION FOR SEQ ID NO:518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:518:

```

Met Pro Thr Gly Leu Pro Val Ile Ala Ser His Val Gly Gly Ile Ser
 1              5              10              15
Glu Leu Val Ala Asp Asn Gly Ile Cys Met Met Asn Thr Gln Pro Glu
          20              25              30
Thr Ile Ala Lys Val Leu Glu Lys Tyr Leu Ile Asp Ser Asp Tyr Ile
          35              40              45
Lys Met Ser Asn Gln Ser Arg Lys Arg Tyr Leu Glu Cys Phe Thr Glu
          50              55              60
Glu Lys Met Ile Lys Glu Val Glu Asp Val Tyr Asn Gly Lys Ser Thr
          65              70              75              80
Gln

```

(2) INFORMATION FOR SEQ ID NO:519:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:519:

```

Met Lys Arg Leu Phe Asp Val Val Ser Ser Ile Tyr Gly Leu Val Val
 1             5             10             15
Leu Ser Pro Ile Leu Leu Ile Thr Ala Leu Leu Ile Lys Met Glu Ser
          20             25             30
Pro Gly Pro Ala Ile Phe Lys Gln Lys Arg Pro Thr Ile Asn Asn Glu
      35             40             45
Leu Phe Asn Ile Tyr Lys Phe Arg Ser Met Lys Ile Asp Thr Pro Asn
      50             55             60
Val Ala Thr Asp Leu Met Asp Ser Thr Ser Tyr Ile Thr Lys Thr Gly
65             70             75             80
Lys Val Ile Arg Lys Thr Ser Ile Asp Glu Leu Pro Gln Leu Leu Asn
          85             90             95
Val Leu Lys Gly Glu Met Ser Ile Val Gly Pro Arg Pro Ala Leu Tyr
          100             105             110
Asn Gln Gly Leu Arg Ile Asn Arg Lys Thr Tyr Lys Ser Glu Arg Ala
          115             120             125
Tyr Glu
130

```

(2) INFORMATION FOR SEQ ID NO:520:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:520:

```

Met Gly Phe Ile Asn Pro Asn Xaa Gln Pro Gly Met Thr Val Ala Val
 1             5             10             15
Met Gly Cys Gly Ser Ile Gly Leu Leu Ala Ile Gln Trp Ala Arg Ile
          20             25             30
Phe Gly Ala Ala His Ile Ile Ala Ile Asp Ile Asp Ala His Lys Leu
      35             40             45
Asp Ile Ala Thr Ser Leu Gly Ala His Gln Thr Ile Asn Ser Lys Glu
      50             55             60
Glu Asn Leu Glu Lys Phe Ile Glu Asn His Tyr Ala Asn Gln Ile Asp
65             70             75             80
Leu Ala Ile Glu Ser Ser Gly Ala Lys Val Thr Ile Gly Gln Ile Leu
          85             90             95
Thr Leu Pro Lys Lys Gly Gly Glu Val Val Leu Leu Gly Ile Pro Tyr
          100             105             110
Asp Asp Ile Glu Ile Asp Arg Val His Phe Glu Lys Ile Leu Arg Asn
      115             120             125
Glu Leu Thr Val Cys Gly Ser Trp Asn Cys Leu Ser Ser Asn Phe Pro
      130             135             140
Gly Lys Glu Trp Thr Ala Thr Leu His Tyr Met Lys Thr Lys Asp Ile
145             150             155             160
Asn Val Lys Pro Ile Ile Ser His Phe Leu Pro Leu Arg Lys Arg Pro
          165             170             175
Gly Asp Ile Leu Ile Asn
          180

```

(2) INFORMATION FOR SEQ ID NO:521:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:521:

```

Met Ile Lys Arg Asp Thr Pro Met Ile Pro Leu His Gln Thr Glu Glu
 1             5             10             15
Glu Glu Phe Tyr Thr Phe Ile Gly Gln Phe Tyr Ser Leu Asn Gln His
      20             25             30

```

558

```

Ile Leu Pro Lys Glu Val His Val Pro Arg Asn Leu Asp Lys Glu Met
  35                      40                      45
Ile Gln Ser Val Val Asp Thr Lys Ile Val Gln Pro Ala Arg Gly Pro
  50                      55                      60
Lys Lys Asp Met Val Asp Leu Ala Ala His Asn Ala Lys Val Ser Leu
  65                      70                      75                      80
Asn Asn Lys Phe Glu Leu Ile Ser Arg Asp Glu Ser Arg Thr Ile Lys
                      85                      90                      95
Ala Ile Glu Glu Leu Gly Thr Gln Met Gly Ile Gln Thr Pro Ile Arg
                      100                      105                      110
Ile Glu Ala Phe Asp Asn Ser Asn Ile Gln Gly Val Asp Pro Val Ser
                      115                      120                      125
Ala Met Val Thr Phe Val Asp Gly Lys Pro Asp Lys Lys Asn Tyr Arg
                      130                      135                      140
Lys Tyr Lys Ile Lys Thr Val Lys Gly Pro Asp Asp Tyr Lys Ser Met
                      145                      150                      155                      160
Arg Glu Val Val Arg Arg Arg Tyr Ser Arg Val Leu Asn Glu Gly Leu
                      165                      170                      175
Pro Leu Pro Asp Leu Ile Ile Val Asp Gly Gly Lys Gly His Met Asn
                      180                      185                      190
Gly Val Ile Asp Val Leu Gln Asn Glu Leu Gly Leu Asp Ile Pro Val
                      195                      200                      205
Ala Gly Leu Gln Lys Asn Asp Lys His Gln Thr Ser Glu Leu Leu Leu
                      210                      215                      220
Trp Arg
225

```

(2) INFORMATION FOR SEQ ID NO:522:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:522:

```

Met Tyr Arg Glu Arg Trp Ser His Asp Lys Glu Val Arg Thr Thr His
  1                      5                      10                      15
Gly Val Asn Cys Thr Gly Ser Cys Ser Trp Lys Val Phe Val Lys Asn
                      20                      25                      30
559

```


Gly Val Ile Thr Trp Glu Asn Gln Gln Thr Asp Tyr Pro Ser Cys Gly
 35 40 45
 Pro Asp Met Pro Glu Tyr Glu Pro Arg Gly Cys Pro Arg Gly Ala Ser
 50 55 60
 Phe Ser Trp Tyr Glu Tyr Ser Pro Leu Arg Ile Lys Tyr Pro Tyr Ile
 65 70 75 80
 Arg Gly Lys Leu Trp Asp Leu Trp Thr Glu Ala Leu Glu Glu Asn Tyr
 85 90 95
 Gly Asn Arg Val Ala Ala Trp Ala Ser Ile Val Glu Asn Glu Asp Lys
 100 105 110
 Ala Lys Gln Tyr Lys Gln Ala Arg Gly Met Gly Gly His Val Arg Ser
 115 120 125
 Asn Trp Lys Asp Val Thr Glu Ile Ile Ala Ala Gln Leu Leu Tyr Thr
 130 135 140
 Ile Lys Lys Tyr Gly Pro Asp Arg Ile Ala Gly Phe Thr Pro Ile Pro
 145 150 155 160
 Ala Met Ser Met Ile Ser Tyr Ala Ala Gly Ala Arg Phe Ile Asn Leu
 165 170 175
 Leu Gly Gly Glu Met Leu Ser Phe Tyr Asp Trp Tyr Ala Asp Leu Pro
 180 185 190
 Pro Ala Ser Pro Gln Ile Trp Gly Glu Gln Thr Asp Val Pro Glu Ser
 195 200 205
 Ser Asp Trp Tyr Asn Ala Ser Tyr Ile Ile Met Trp Gly Ser Asn Val
 210 215 220
 Pro Leu Thr Arg Thr Pro Asp Ala His Phe Met Thr Glu Val Arg Tyr
 225 230 235 240

(2) INFORMATION FOR SEQ ID NO:523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:523:

Met Gln Thr Gly Leu Xaa Xaa Arg Ala Val Ala Lys Ser Xaa Thr Phe
 1 5 10 15
 Ser Thr Gly His Xaa Xaa Asp Ser Glu Glu Asn Asp Val Asp Val Asn
 20 25 30
 560

```

Xaa Leu Val Asn Gly Gly Thr Leu Ala Ile Tyr Met Gly Val Lys Arg
   35                               40                               45
Leu Gly Lys Ile Ile Ala Gln Ile Gln Gln Tyr Thr Asp Ile Asp Tyr
   50                               55                               60
Pro Ile Ala Ile Val Phe Gln Ala Ser Cys Phe Asn Glu Phe Val Val
   65                               70                               75                               80
Lys Gly Arg Leu Ser Asn Ile Val Gly Lys Leu Glu His Tyr Ala Ile
                               85                               90                               95
Glu Ala Lys Pro Gly Ile Cys Ile Ile Gly Glu Val Val Gly Tyr Thr
                               100                               105                               110
Glu Asn Val Ser Thr Thr Ser Asn Pro Thr Gln Gln Phe Tyr Val Val
                               115                               120                               125
Ser Gly Ser Arg His Asp Ala Leu Met Leu Cys Glu His Leu Tyr Asp
                               130                               135                               140
Glu Gly Tyr Gly Cys Leu Leu Asn Pro Asn Asp Thr Ser Asn Gly Thr
   145                               150                               155                               160
Tyr His Ser Gly Arg Gln Tyr Asp Tyr Tyr Asp Ala Phe Ile Lys Gln
                               165                               170                               175
Gln Glu Asn Val Thr Tyr Ile Ser Thr Asp Arg Ala Asp Ala Asn Thr
                               180                               185                               190
Val Leu Cys His
                               195

```

(2) INFORMATION FOR SEQ ID NO:524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524:

```

Met Ser Val Asp Lys Tyr Gly Lys Val Tyr Leu Ile Gly Ala Gly Pro
  1                               5                               10                               15
Gly Asn Pro Asn Tyr Leu Thr Lys Lys Ala Glu Arg Leu Ile Arg Glu
                               20                               25                               30
Ala Asp Val Ile Leu Tyr Asp Arg Leu Val Asn Pro Leu Ile Leu Gln
                               35                               40                               45
Tyr Ala Asn Leu Thr Thr Glu Ile Ile Asp Val Gly Lys Lys Pro Tyr
   50                               55                               60

```

(2) INFORMATION FOR SEQ ID NO:525:

(A) LENGTH: 77 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:525:

(2) INFORMATION FOR SEQ ID NO:526:

(A) LENGTH: 70 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:526:

562

```

                20                25                30
Asp Val Asp Glu Ser Ser Thr Lys Gln Lys His Ile Lys Asn Lys Thr
                35                40                45
Thr Ile Asp His Asn Asp Asp Leu Phe Lys His Val Lys Asp Ile Leu
                50                55                60
Arg Lys Gln Gly Gln Ile
                65                70

```

(2) INFORMATION FOR SEQ ID NO:527:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:527:

```

Met Asn Tyr Val Arg Ser Ser Asn Lys Ser His Gly Asn Gln Asn Gln
 1                5                10                15
Ile Glu Gly Ala Lys Ser Glu Gly Lys Lys Val Val Val Ile Glu Asp
                20                25                30
Leu Ile Ser Thr Gly Gly Ser Ser Val Thr Ala Val Glu Ala Leu Lys
                35                40                45
Gln Ala Gly Ala Glu Val Leu Gly Val Val Ala Ile Phe Thr Tyr Gly
                50                55                60
Leu Lys Lys Ala Asp Asp Thr Phe Ser Asn Ile Gln Leu Pro Phe Tyr
65                70                75                80
Thr Leu Ser Asp Tyr Asn Glu Leu Ile Glu Val Ala Glu Asn Glu Gly
                85                90                95
Lys Ile Ser Ser Glu Asp Ile Gln Thr Leu Val Glu Trp Arg Asp Asn
                100                105                110
Leu Ala

```

(2) INFORMATION FOR SEQ ID NO:528:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:528:

```

Met Lys Ala Cys Arg Val Leu Val Asn Thr Pro Ser Ala Val Gly Gly
 1           5           10           15
Ile Gly Asp Met Tyr Asn Glu Leu Ile Pro Ser Leu Thr Leu Gly Cys
      20           25           30
Gly Ser Tyr Gly Arg Asn Ser Ile Ser His Asn Val Ser Ala Thr Asp
      35           40           45
Leu Leu Asn Ile Lys Thr Ile Ala Lys Arg Arg Asn Asn Thr Gln Ile
 50           55           60
Phe Lys Val Pro Ala Gln Ile Tyr Phe Glu Glu Asn Ala Ile Met Ser
65           70           75           80
Leu Thr Thr Met Asp Lys Ile Glu Lys Val Met Ile Val Cys Asp Pro
      85           90           95
Gly Met Val Glu Phe Gly Tyr Thr Lys Thr Val Glu Asn Val Leu Arg
      100           105           110
Gln Arg Thr Glu Gln Pro Gln Ile Lys Ile Phe Ser Glu Val Glu Pro
      115           120           125
Asn Pro Ser Thr Asn Thr Val Tyr Lys Gly Leu Glu Met Met Val Asp
      130           135           140
Phe Gln Pro Asp Thr Ile Ile Ala Leu Gly Gly Gly Ser Ala Met Asp
145           150           155           160
Ala Ala Lys Ala Met Trp Met Phe Phe Glu His Pro Glu Thr Ser Phe
      165           170           175
Phe Gly Ala Lys Gln Lys Phe Leu Asp Ile Gly Lys Arg Thr Tyr Lys
      180           185           190
Ile Gly Met Pro Glu Asn Ala Thr Phe Ile Cys Ile Pro Thr Thr Ser
      195           200           205
Gly Thr Gly Ser Glu Val Thr Pro Phe Ala Gly Ile Thr Asp Ser Glu
      210           215           220
Thr Asn Val Lys Tyr Pro Xaa Ala Asp Phe Gly Leu Thr Thr Asp Val
225           230           235           240
Gly Ile Ile Asp Leu Asn Leu Val Met Ser Val Pro Xaa Ser Val Thr
      245           250           255
Ala Gly Thr Gly Met Val Val Leu Thr His Ala Met Glu Ser Tyr Val
      260           265           270
Ser Cys Asn Gly Phe Arg Leu Ser Arg Gly Trp Gly Leu Gln Ala Ile
      275           280           285
Asn

```

(2) INFORMATION FOR SEQ ID NO:529:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:529:

```

Met Xaa Asn Leu Lys Asn Ser Leu Asn Asp Lys Asp Thr Thr Leu Ala
 1             5             10             15
Ser Pro Xaa Leu Cys Lys Met Gln Asp Pro Glu Lys Xaa Asn Ala Tyr
          20             25             30
Asn Glu Ala Val Arg Asn Ala Glu Asn Ile Leu Asn Lys Ser Thr Gly
          35             40             45
Thr Asn Val Pro Lys Asp Gln Val Glu Ala Ala Met Asn Gln Val Asn
          50             55             60
Thr Thr Lys Ala Ala Leu Asn Gly Thr Gln Asn Leu Glu Lys Ala Lys
          65             70             75             80
Gln His Ala Asn Thr Ala Ile Asp Gly Leu Ser His Leu Thr Asn Ala
          85             90             95
Gln Lys Glu Ala Leu Lys Gln Leu Val Gln Gln Ser Thr Thr Val Ala
          100            105            110
Glu Ala Gln Gly Asn Glu Gln Lys Ala Asn Asn Val Asp Ala Ala Met
          115            120            125
Asp Lys Leu Arg Gln Ser Ile Ala Asp Asn Ala Thr Thr Lys Gln Asn
          130            135            140
Gln Asn Tyr Thr Asp Ala Ser Pro Asn Lys Lys Asp Ala Tyr Asn Asn
          145            150            155            160
Ala Val Thr Thr Ala Gln Gly Ile Ile Asp Gln Thr Thr Asn Pro Ser
          165            170            175
Leu Asp Pro Thr Val Ile Asn Gln Ala Ala Gly Gln Val Ser Thr Ser
          180            185            190
Lys Asn Ala Leu Asn Gly Asn Glu Asn Leu Glu Ala Ala Lys Gln Leu
          195            200            205
Ala Thr Gln Ser Leu Gly Ser Leu Asp Xaa Leu Asn Asn Ala Gln Lys
          210            215            220
Gln Ala Val Thr Asn Gln Ile Asn Gly Ala His Thr Gly Asp Glu Ala
          565

```

Leu

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:530:

Met	Lys	His	Leu	Leu	Gly	Thr	Lys	Ser	Gly	Leu	Leu	Ala	Thr	Pro	Asn
1				5					10					15	
Glu	Asp	Glu	Lys	Pro	Glu	Glu	Ile	Thr	Trp	Arg	Glu	Glu	Thr	Thr	Gly
			20					25					30		
Lys	Leu	Asp	Leu	Val	Val	Ser	Leu	Asp	Phe	Arg	Met	Thr	Ala	Thr	Pro
		35					40				45				
Leu	Tyr	Ser	Asp	Ile	Val	Leu	Pro	Ala	Ala	Thr	Trp	Tyr	Glu	Lys	His
	50					55					60				
Asp	Leu	Ser	Ser	Thr	Asp	Met	His	Pro	Tyr	Val	His	Pro	Phe	Asn	Pro
65				70						75				80	
Ala	Ile	Asp	Pro	Leu	Trp	Glu	Ser	Arg	Ser	Asp	Trp	Asp	Ile	Tyr	Lys
			85					90					95		
Thr	Leu	Ala	Lys	Ala	Phe	Ser	Glu	Met	Ala	Lys	Asp	Tyr	Leu	Pro	Gly
		100						105				110			
Thr	Phe	Lys	Asp	Val	Val	Thr	Thr	Pro	Leu	Ser	His	Asp	Thr	Lys	Gln
	115					120					125				
Glu	Ile	Ser	Thr	Pro	Tyr	Gly	Val	Val	Lys	Asp	Trp	Ser	Lys	Gly	Glu
	130					135				140					
Ile	Glu	Ala	Val	Pro	Gly	Arg	Thr	Met	Pro	Asn	Phe	Ala	Ile	Val	Glu
145				150						155				160	
Arg	Asp	Tyr	Thr	Lys	Ile	Tyr	Asp	Lys	Tyr	Val	Thr	Leu	Gly	Pro	Val
			165					170				175			
Leu	Glu	Lys	Gly	Lys	Val	Gly	Ala	His	Gly	Val	Ser	Phe	Gly	Val	Ser
		180				185					190				
Glu	Gln	Tyr	Glu	Glu	Leu	Lys	Ser	Met	Leu	Gly	Thr	Trp	Ser	Asp	Thr
								566							

195	200	205
Asn Asp Asp Ser Val Arg Ala Asn Arg Pro Arg Ile Asp Thr Ala Arg		
210	215	220
Asn Val Ala Asp Ala Ile Leu Ser Ile Ser Ser Ala Thr Asn Gly Lys		
225	230	235
Leu Ser Gln Lys Ser Tyr Glu Asp Leu Glu Glu Gln Thr Gly Met Pro		
245	250	255
Leu Lys Asp Ile Ser Ser Glu Arg Ala Ala Glu Lys Ile Arg Phe		
260	265	270

(2) INFORMATION FOR SEQ ID NO:531:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:531:

Met	Ala	Ala	Ile	Lys	Pro	Ile	Thr	Thr	Tyr	Lys	Gly	Lys	Ile	Val	Pro
1				5					10					15	
Leu	Phe	Asn	Asp	Asn	Ile	Asp	Thr	Asp	Gln	Ile	Ile	Pro	Lys	Val	His
			20					25					30		
Leu	Lys	Arg	Ile	Ser	Lys	Ser	Gly	Phe	Gly	Pro	Phe	Ala	Phe	Asp	Glu
		35					40					45			
Trp	Arg	Tyr	Leu	Pro	Asp	Gly	Ser	Asp	Asn	Pro	Asp	Phe	Asn	Pro	Asn
		50				55					60				
Lys	Pro	Gln	Tyr	Lys	Gly	Ala	Ser	Ile	Leu	Ile	Thr	Gly	Asp	Asn	Phe
65				70					75					80	
Gly	Cys	Gly	Ser	Ser	Arg	Glu	His	Ala	Ala	Trp	Ala	Leu	Lys	Asp	Tyr
			85					90					95		
Gly	Xaa	His	Ile	Ile	Ile	Ala	Gly	Ser	Phe	Ser	Asp	Ile	Phe	Tyr	Met
		100					105					110			
Asn	Cys	Thr	Lys	Asn	Ala	Met	Leu	Pro	Ile	Xaa	Leu	Glu	Lys	Ser	Ala
		115				120						125			
Arg	Glu	His	Leu	Ala	Gln	Tyr	Glu	Glu	Ile	Glu	Ile	Asp	Leu	Pro	Asn
		130			135						140				
Gln	Thr	Val	Ser	Ser	Pro	Asp	Lys	Arg	Phe	His	Phe	Glu	Ile	Asp	Glu
145				150					155					160	
Thr	Leu	Glu	Lys												

(2) INFORMATION FOR SEQ ID NO:532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:532:

```

Met Trp His Arg Gln Ala Leu Ser Cys Leu Leu Val Ile Leu Ile Leu
 1             5             10             15
Met Ser Gly Val Ala Ile Ile Leu Arg Glu Gln Xaa Xaa Val Lys Xaa
      20             25             30
Ser Asn Leu Asn Asn Gln Ser His Leu Ser Ile Xaa Lys Gly Val Leu
      35             40             45
Xaa Met Ala Gln Thr Leu Ala Gln Xaa Lys Xaa Ile Ser Gln Ser His
      50             55             60
Thr Xaa Asp Val Ser Gln Ser His His Lys Thr Pro Ala Asp Thr Xaa
65             70             75             80
Leu Thr Val Leu Ile Cys Pro His Lys Tyr
      85             90

```

(2) INFORMATION FOR SEQ ID NO:533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein .

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:533:

```

Met Met Ala Arg Arg Lys Val Ile Arg Val Arg Ile Lys Gly Lys Leu
 1             5             10             15
Met Thr Leu Arg Glu Val Ser Glu Lys Tyr His Ile Ser Pro Glu Leu
      20             25             30

```

568

Leu Arg Tyr Arg Tyr Lys His Lys Met Arg Gly Asp Glu Leu Leu Cys
 35 40 45
 Gly Arg Lys Asp Ser Lys Ser Lys Glu Glu Val Gly Ile Tyr Glu Glu
 50 55 60
 Ser Asn Lys Arg
 65

(2) INFORMATION FOR SEQ ID NO:534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:534:

Met Ile Cys Xaa Leu Gln Glu Ile Gly Ile Ser Ser Asn Tyr Xaa Pro
 1 5 10 15
 Thr Gly Cys Xaa Ser Gly Ile Tyr Val Phe Ser Glu Ser Xaa Val Pro
 20 25 30
 Gly Thr Asp Ala Leu Gln Ala Xaa Tyr Leu Asp Asp Xaa Val Met Glu
 35 40 45
 Cys Asp Xaa Thr Pro Thr Arg Ala Asp Ala Leu Arg Met Ile Gly Thr
 50 55 60
 Ala Tyr Glu Val Ala Ala Leu Tyr Asn Thr Xaa Leu Thr Thr Pro Glu
 65 70 75 80
 Thr Thr Ser Asn Glu Leu Xaa Leu Ser Ala Asn Asp Xaa Leu Thr Val
 85 90 95
 Thr Xaa Xaa Asn Glu Asp Thr Ser Thr Ile Leu
 100 105

(2) INFORMATION FOR SEQ ID NO:535:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:535:

```

Met Asp Trp Met Glu Gln Glu Xaa Arg Pro Trp Tyr Tyr Tyr His Asn
 1           5           10           15
Leu Leu Gln Gln Gln Ala Ala Trp Glu Gly His Arg Val Asn Ile Ile
      20           25           30
Asp Thr Pro Gly His Val Asp Phe Thr Val Glu Val Glu Arg Ser Leu
      35           40           45
Arg Val Leu Asp Gly Ala Val Thr Val Leu Asp Ala Gln Ser Gly Val
      50           55           60
Glu Pro Gln Thr Glu Thr Xaa Trp Arg Gln Ala Thr Thr Tyr Gly Val
65           70           75           80
Pro Arg Ile Val Phe Val Asn Lys Met Asp Lys Leu Gly Ala Asn Phe
      85           90           95
Glu Tyr Ser Val Ser Thr Leu His Asp Arg Leu Gln Ala Asn Ala Ala
      100           105           110
Pro Ile Gln Leu Pro Ile Gly Ala Glu Asp Glu Phe Glu Ala Ile Ile
      115           120           125
Asp Leu Val Glu Met Lys Cys Phe Lys Tyr Thr Asn Asp Leu Gly Thr
      130           135           140
Glu Ile Glu Glu Ile Glu Ile Pro Glu Asp His Leu Asp Thr Ser
145           150           155

```

(2) INFORMATION FOR SEQ ID NO:536:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:536:

```

Met Glu Lys Tyr Leu Gly Asp Glu Glu Ile Ser Val Ser Glu Leu Lys
 1           5           10           15
Glu Ala Ile Arg Gln Ala Thr Thr Asn Val Glu Phe Tyr Pro Val Leu
      20           25           30
Cys Gly Thr Ala Phe Lys Asn Lys Gly Val Gln Leu Met Leu Asp Ala
      35           40           45
Val Ile Asp Tyr Leu Pro Ser Pro Leu Asp Val Lys Pro Ile Ile Gly
                        570

```

```

      50              55              60
His Arg Ala Ser Asn Pro Glu Glu Glu Val Ile Ala Lys Ala Asp Asp
65              70              75              80
Ser Ala Glu Phe Ala Ala Leu Ala Phe Lys Val Met Thr Asp Pro Tyr
      85              90              95
Val Gly Lys Leu Thr Phe Phe Arg Val Tyr Ser Gly Thr Met Thr Ser
      100             105             110
Gly Ser Tyr Val Lys Asn Ser Thr Lys Gly Lys Arg Glu Arg Val Val
      115             120             125
Val Tyr
      130

```

(2) INFORMATION FOR SEQ ID NO:537:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:537:

```

Met Asn Met Lys Thr Ile Ala Lys Thr Ser Leu Ala Leu Gly Leu Leu
 1              5              10              15
Thr Thr Gly Ala Ile Thr Val Thr Thr Gln Ser Val Lys Ala Glu Lys
      20              25              30
Ile Gln Ser Thr Lys Val Asp Lys Val Pro Thr Leu Lys Ala Glu Arg
      35              40              45
Leu Ala Met Ile Asn Ile Thr Ala Gly Ala Asn Ser Ala Thr Thr Gln
      50              55              60
Ala Ala Asn Thr Arg Gln Glu Arg Thr Pro Lys Leu Glu Lys Ala Pro
65              70              75              80
Asn Thr Asn Xaa Glu Lys Thr Ser Ala Ser Lys Ile Glu Lys Ile Ser
      85              90              95
Gln Pro Lys Gln Glu Glu Gln Lys Ser Leu Asn Ile Ser Ala Thr Pro
      100             105             110
Ala Pro Lys Gln Xaa Gln Ser Gln Thr Ala Thr Glu Ser Thr Thr Pro
      115             120             125
Lys Thr Lys Val Thr Thr Pro Ser Thr Asn Thr Pro Gln Pro Met
      130             135             140
Gln Ser Thr Lys Ser Asp Thr Pro Gln Ser Pro Thr Ile Lys Gln Ala

```

```

145              150              155              160
Gln Thr Asp Met Thr Pro Lys Tyr Glu Asp Leu Arg Ala Tyr Tyr Thr
              165              170              175
Lys Pro Ser Phe Xaa Phe Glu Lys Gln Phe Gly Phe Leu Leu Lys Pro
              180              185              190
Trp Thr Thr Val Arg Phe Met Xaa Val Ile Pro Asn Arg Phe Ile Tyr
              195              200              205
Lys Ile Ala Leu Val Arg Lys Arg
              210              215

```

(2) INFORMATION FOR SEQ ID NO:538:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:538:

```

Met Lys Asn Lys Ser Val Ser Leu Val Phe Trp Val Ser Leu Val Ile
 1              5              10              15
Cys Thr Ile Phe Val Ala Phe Gly Ala Ile Phe Pro Lys Gln Leu Glu
              20              25              30
Lys Leu Thr Gln Asn Ile Thr Thr Phe Ile Ala Leu His Phe Ser Trp
              35              40              45
Tyr Tyr Leu Leu Leu Val Leu Val Ile Leu Phe Val Cys Val Tyr Ile
              50              55              60
Leu Phe Ser Arg Tyr Ala Asn Ile Thr Leu Gly Glu Glu Gly Glu Asp
65              70              75              80
Pro Glu Phe Ser Leu Pro Ser Trp Phe Ala Met Leu Phe Ser Ala Gly
              85              90              95
Met Gly Ile Gly Leu Val Phe Trp Thr Thr Ala Glu Pro Ile Ser His
              100              105              110
Ala Phe Lys Leu Thr Pro Ile His Lys Ala Gly Thr Gln Ser Ala Ile
              115              120              125
Asn Asp Ala Met Gln Phe Ser Phe Phe His Trp Gly Ile His Ala Trp
              130              135              140
Ala Val Tyr Gly Ile Val Ala Leu Val Phe Ala Tyr Phe Ser Phe His
145              150              155              160
Lys Gly Tyr Pro Gly Leu Val Ser Ala Thr Leu Thr Pro Leu Leu Gly

```

	165	170	175
Glu Lys Ala Met Arg Gly Pro Leu Gly Gly Ala Ile Asp Val Leu Ala			
	180	185	190
Val Ile Ala Thr Val Thr Gly Val Ala Ala His			
	195	200	

(2) INFORMATION FOR SEQ ID NO:539:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:539:

Met Val Leu Val Arg Asn Ile Asn Leu Ala Leu Arg Ala Gln Tyr Leu			
1	5	10	15
Xaa Xaa Ser Xaa Val Asp Tyr Phe Val Tyr Xaa Gly Asp Ile Val Leu			
	20	25	30
Thr Asp Xaa Ile Thr Gly Arg Xaa Leu Pro Xaa Thr Lys Leu Gln Ala			
	35	40	45
Gly Leu His Xaa Ala Ile Glu Ala Lys Glu Gly Met Glu Val Ser Thr			
	50	55	60
Asp Lys Ser Val Met Pro Thr Asn Tyr Pro Ser Arg Ile Tyr Leu Asn			
65	70	75	80
Phe Leu Asn Gln Phe Ser Gly Met Thr Ser Tyr Arg Lys Ile Arg Arg			
	85	90	95
Ile Arg Val Leu			
	100		

(2) INFORMATION FOR SEQ ID NO:540:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:540:

```

Met Asp Ile Pro Asn Asn Leu Leu Ile Ala Gln Asn Val Pro Lys Glu
 1             5             10             15
Ala Gln Met Ile Ala Glu Ala Gly Gln Ile Gly Ser Met Thr Val Ala
          20             25             30
Thr Ser Met Ala Gly Arg Gly Thr Asp Ile Lys Leu Gly Glu Gly Val
      35             40             45
Glu Ala Leu Ala Gly Leu Ala Val Ile Ile His Glu His Met Glu Asn
      50             55             60
Ser Arg Val Asp Arg Gln Leu Arg Gly Arg Ser Gly Arg Gln Gly Asp
65             70             75             80
Pro Gly Ser Ser Cys Ile Tyr Ile Ser Leu Asp Asp Tyr Leu Xaa Lys
          85             90             95
Arg Trp Ser Asp Ser Asn Leu Ala Glu Asn Asn Gln Leu Tyr Ser Xaa
          100             105             110
Asp Ala Gln Arg Leu Ser Gln Ser Asn Leu Phe Asn Arg Lys Val Lys
          115             120             125
Gln Ile Val Val Lys Ala Gln Arg Ile Ser Glu Arg Thr Arg Gly
      130             135             140

```

(2) INFORMATION FOR SEQ ID NO:541:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:541:

```

Met Arg Ala Leu Leu Ile Phe Tyr Met Tyr Phe Ala Val Thr Asp Asn
 1             5             10             15
Gly Leu Gly Ile Asp Lys Thr Thr Ala Met Ser Ile Met Ser Val Tyr
          20             25             30
Gly Ser Leu Ile Tyr Met Thr Ser Asn Thr Arg Arg Asn Gly Leu Leu
          35             40             45
Thr Glu Leu Gln Ala Leu Glu Ala Leu Leu Tyr
      50             55

```

(2) INFORMATION FOR SEQ ID NO:542:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:542:

```

Met Phe Xaa Ile Ile Ile Gly Ser Gly Leu Met Lys Pro Asn Ile Pro
 1             5             10             15
Asn Ile Gly Gly Arg Leu Tyr Pro Glu Asn Asp Arg Arg Met Asp Ala
      20             25             30
Gly Cys Val Ile Phe Tyr Met Ser Val Asn Met Gly Ala Leu Leu Ser
      35             40             45
Pro Ile Ile Val Gln His Cys Val Asn Val Lys Asn Phe His Gly Gly
      50             55             60
Phe Leu Ile Ala Ala Val Gly Met Ala Leu Gly Leu Val Trp Tyr Val
65             70             75             80
Leu Xaa Xaa Arg Lys Asn Leu Gly Ser Gly Gly Ile Glu Thr Xaa
      85             90             95

```

(2) INFORMATION FOR SEQ ID NO:543:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:543:

```

Met Leu Phe Ala Xaa Ile Phe Glu Glu Xaa Ile Gly Lys Leu Glu Arg
 1             5             10             15
Tyr Phe Asn Asp Val Pro Xaa Ala Val Ala His Val Lys Val Lys Thr
      20             25             30
Tyr Ser Xaa Ser Ala Thr Lys Ile Glu Val Thr Ile Pro Leu Lys Asn
      35             40             45
Val Thr Leu Arg Ala Glu Glu Arg Asn Asp Asp Leu Tyr Ala Gly Ile

```


50	55	60	
Asp Leu Ile Asn Asn Lys Leu Glu Arg Gln Val Arg Lys Tyr Lys Thr			
65	70	75	80
Arg Ile Asn Arg Lys Ser Arg Asp Arg Gly Asp Gln Glu Val Phe Val			
	85	90	95
Ala Glu Leu Gln Glu Met Gln Glu Thr Gln Val Asp Asn Asp Ala Tyr			
	100	105	110
Asp Asp Asn Glu Ile Glu Ile Ile Arg Ser Thr Arg Ile Pro Gly			
	115	120	125

(2) INFORMATION FOR SEQ ID NO:544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:544:

Met Leu Leu Ile Met Phe Thr Asn Ile Val Leu Glu Leu Gly Gly Lys		
1	5	10
Asn Pro Asn Ile Ile Phe Asp Asp Ala Asp Xaa Glu Leu Ala Val Asp		
	20	30
Gln Ala Leu Asn Gly Gly Tyr Xaa His Ala Xaa Gln Val Cys Ser Ala		
	35	45
Gly Ser Arg Ile Leu Val Gln Asn Ser Ile Lys Asp Lys Phe Glu Gln		
	50	60
Ala Leu Ile Asp Arg Val Lys Lys Ile Lys Leu Gly Asn Gly Phe Asp		
65	70	80
Ala Asp Thr Glu Met Gly Pro Val Ile Ser Thr Glu His Arg Asn Lys		
	85	95
Ile Glu Ser Tyr Met Asp Val Ala Lys Ala Glu Gly Ala Thr Ile Ala		
	100	110
Val Gly Gly Lys Arg Pro Asp Arg Asp Asp Leu Lys Asp Gly Leu Phe		
	115	125
Phe Glu Pro Thr Val Ile Thr Asn Cys Asp Thr Ser Met Arg Ile Val		
	130	140
Gln Glu Glu Val Phe Gly Pro Val Val Thr Val Glu Gly Phe Glu Thr		
145	150	160
Glu Gln Glu Ala Ile Gln Leu Ala Asn Asp Ser Ile Tyr Gly Leu Ala		

	165		170		175										
Gly	Ala	Val	Phe	Ser	Lys	Asp	Ile	Gly	Lys	Ala	Gln	Arg	Val	Ala	Asn
	180				185				190						
Lys	Leu	Lys	Leu	Gly	Thr	Val	Trp	Ile	Asn	Asp	Phe	His	Pro	Tyr	Phe
	195				200				205						
Ala	Gln	Ala	Pro	Trp	Val	Asp	Thr	Asn	Asn	Gln	Val	Ser	Val	Glu	Asn
	210				215				220						

(2) INFORMATION FOR SEQ ID NO:545:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:545:

Met	Ile	Ala	Asp	Gly	Val	Asn	Asp	Ala	Pro	Ala	Leu	Ala	Ala	Ser	Xaa
1				5				10					15		
Val	Gly	Xaa	Ala	Arg	Leu	Gly	Xaa	Gly	Thr	Asp	Thr	Xaa	Xaa	Glu	Thr
		20				25					30				
Ala	Asp	Ile	Xaa												
		35													

(2) INFORMATION FOR SEQ ID NO:546:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:546:

Met	Asn	Leu	Glu	Lys	Gly	Asn	Ile	Glu	Arg	Lys	Lys	His	Gly	Val	His
1				5				10					15		
Val	Asn	Glu	Tyr	Leu	Gln	Ser	Val	Ser	Asn	Pro	Asn	Val	Tyr	Ala	Ala
		20				25					30				

Gly Asp Ala Ala Ala Thr Asp Gly Leu Pro Leu Thr Pro Val Ala Ser
 35 40 45
 Ala Asp Ser His Val Val Ala Ser Asn Leu Leu Lys Gly Asn Ser Lys
 50 55 60
 Lys Ile Glu Tyr Pro Val Ile Pro Ser Ala Val Phe Thr Val Pro Lys
 65 70 75 80
 Met Ala Ser Val Gly Met Ser Glu Glu Glu Ala Lys Asn Ser Gly Arg
 85 90 95
 Asn Ile Lys Val Lys Gln Lys Asn Ile Ser Asp Trp Phe Thr Tyr
 100 105 110

(2) INFORMATION FOR SEQ ID NO:547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:547:

Met Thr Arg Val Val Leu Ala Ala Ala Tyr Arg Thr Pro Ile Gly Val
 1 5 10 15
 Phe Gly Gly Ala Phe Lys Asp Val Pro Ala Tyr Asp Leu Gly Ala Thr
 20 25 30
 Leu Ile Glu His Ile Ile Lys Glu Thr Gly Leu Asn Pro Ser Glu Ile
 35 40 45
 Asp Glu Val Ile Ile Gly Asn Val Leu Gln Ala Gly Gln Gly Gln Asn
 50 55 60
 Pro Ala Arg Ile Ala Ala Met Lys Gly Gly Leu Pro Glu Thr Ala Pro
 65 70 75 80
 Ala Phe Thr Val Asn Lys Val Cys Gly Leu Trp Val Lys Val Xaa Ser
 85 90 95
 Ile Ser Ile Ser Ile Tyr Xaa
 100

(2) INFORMATION FOR SEQ ID NO:548:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:548:

```

Met Gly Arg Ser Ala Ala Ala Lys Ala Lys Gln Gly Ala Leu Phe His
 1             5             10             15
Glu Arg Pro Asp Asp Val Ala Ala Lys Val Leu Gln Gly Val Leu Lys
      20             25             30
Arg Ile Asp Gly Lys Phe Asn Lys Xaa Met Ile Glu Asp Val Ile Val
      35             40             45
Gly Thr Ala Phe Pro Glu Gly Leu Gln Gly Gln Asn Ile Ala Arg Thr
      50             55             60
Ile Ala Leu Arg Ala Gly Leu Ser Asp Thr Val Pro Gly Gln Thr Val
      65             70             75             80
Asn Arg Tyr Cys Ser Ser Gly Leu Gln Thr Ile Ala Ile Ala Ala Asn
      85             90             95
Gln Ile Met Ala Gly Gln Gly Asp Ile Leu Val Ala Gly Gly Val Glu
      100            105            110
Leu Met Ser Ala Val Pro Met Gly Xaa Asn Glu Pro Thr Asn Asn Pro
      115            120            125
Thr Leu Gln Tyr Asp Asp Ile Gly Ala Ser Tyr Pro Met Gly Leu Thr
      130            135            140
Ala Glu Asn Val Ala Ser Gln Phe Asp Val Ser Arg Ser Lys Met Pro
      145            150            155            160
Arg Cys Leu Cys Cys Gln Lys Ser Ser Thr Cys Leu
      165            170

```

(2) INFORMATION FOR SEQ ID NO:549:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:549:

```

Met Gly Ala Lys Leu Thr Val Asn Ala Asp Ile Thr Lys Leu Asn Gly

```

1	5	10	15												
Leu	Gln	Ser	Ala	Ile	Asp	Lys	Phe	Asn	Asp	Glu	Asp	Leu	Glu	Pro	Met
	20				25					30					
Val	Leu	Phe	Val	Asn	Pro	Leu	Asp	Ala	Gly	Lys	Leu	Arg	Ser	Glu	Met
	35				40					45					
His	Gln	Leu	Thr	Leu	His	Val	Gln	Pro	Asn						
50					55										

(2) INFORMATION FOR SEQ ID NO:550:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:550:

Met	Tyr	Lys	Val	Ile	Glu	Arg	Phe	Glu	Asp	Ala	Gln	Asp	Asn	Gly	His
1			5					10						15	
Glu	Tyr	Gln	Val	Gly	Asp	Ile	Tyr	Pro	Arg	Asp	Gly	Leu	Glu	Val	Ser
		20						25					30		
Glu	Glu	Arg	Phe	Thr	Glu	Leu	Ser	Thr	Thr	Asn	Asn	Arg	Arg	Asn	Leu
		35					40					45			
Ile	Ala	Ile	Lys	Leu	Val	Glu	Asp	Asp	Thr	Thr	Glu	Gln	Ser	Glu	Ala
	50					55					60				
Ser	Ala	Asp	Glu	Gln	Lys	Ser	Leu	Ser	Asp	Met	Lys	Val	Ala	Glu	Leu
65				70					75					80	
Xaa	Glu	Leu	Ala	Lys	Lys	Arg	Glu	Ile	Lys	Gly	Tyr	Ser	Asp	Met	Lys
			85					90					95		
Lys	Asp	Glu	Leu	Ile	Lys	Ala	Leu	Glu	Gly	Val	Lys	Leu	Trp	Thr	Gln
		100					105						110		
Lys	Thr	Ser	Lys												
			115												

(2) INFORMATION FOR SEQ ID NO:551:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551:

```

Met Gly Lys Ser His Ala Cys Tyr Gln Gly Val Thr His Ala Cys Thr
 1             5             10             15
Asn Arg Ile Ala Phe Val Asp Ala Asp Val Thr Phe Leu Arg Lys Asp
          20             25             30
Ala Val Glu Thr Leu Ile Asn Gln Tyr Gln Leu Gln Gly Glu Lys Gly
          35             40             45
Leu Leu Ser Val Gln Pro Tyr His Ile Thr Lys Arg Phe Tyr Glu Gly
          50             55             60
Phe Ser Ala Ile Phe Asn Leu Met Thr Ser Arg Trp Tyr Glu Cys Ile
65             70             75             80
Xaa Tyr Leu Arg Arg Arg Cys Gly Leu Thr Ser Met His Leu Asp Arg
          85             90             95

```

(2) INFORMATION FOR SEQ ID NO:552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:552:

```

Met Arg Leu Phe Ile Asn Leu Lys Gln Ile Ile Ile Arg Lys Ile Ala
 1             5             10             15
Gly Lys Ser Lys Ser Gly Ile Gln Met Val Tyr Gln His Leu Met Asn
          20             25             30
Gly Val Ser Phe Met Xaa Pro Phe Ile Gly Val Gly Gly Leu Leu Ile
          35             40             45
Xaa Ile Ala Leu Thr Leu Gly Gly Glu Thr Thr Ser Lys Gly Leu Val
          50             55             60
Ile Pro Asp Asp Ser Leu Trp Glu Ile His
65             70

```

(2) INFORMATION FOR SEQ ID NO:553:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:553:

```

Met Lys Ile Val Ala Ile Thr Ser Cys Pro Asn Gly Ile Ala His Thr
 1             5             10             15
Tyr Met Ala Gln Glu Lys Leu Glu Gln Val Ala Lys Glu Met Gly Val
      20             25             30
Asp Ile Lys Val Glu Thr Gln Gly Gly Val Gly Ala Glu Asn Val Leu
      35             40             45
Thr Thr Gln Asp Ile Glu Glu Ala Asp Gly Val Ile Ile Ala Ala Asp
      50             55             60
Lys Gln Val Asp Leu Ser Arg Phe Val Gly Lys Arg Leu Ile Asn Glu
65             70             75             80
Asn Val Arg Ser

```

(2) INFORMATION FOR SEQ ID NO:554:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:554:

```

Met Asn Lys Leu Lys Leu Val Gly Ala Asp Val Trp Ala Ser Ile Glu
 1             5             10             15
Ser Ala Phe Ala Pro Val Met Glu Glu Leu Ile Lys Lys Leu Ser Val
      20             25             30
Ala Val Asp Trp Phe Ser Ser Leu Ser Asp Gly Phe Lys Arg Ser Ile
      35             40             45
Val Ile Phe Gly Gly Ile Ala Ala Ala Ile Gly Pro Val Val Phe Gly

```

50	55	60
Ile Arg Cys Ile His Lys His Asn Trp Gln Arg Ser Asn Cys Phe Ser		
65	70	75
Ser Ile Ile Ser		80

(2) INFORMATION FOR SEQ ID NO:555:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:555:

Met	Leu	Tyr	Val	Ile	Asn	Ile	Leu	Asp	Ala	Tyr	Arg	Asn	Ala	Glu	Arg
1				5					10					15	
Phe	Asn	Arg	Asn	Glu	Glu	Ile	Lys	Asp	Arg	Gln	Ala	Arg	Met	Val	Ala
			20					25					30		
Thr	Trp	Asp	Lys	Thr	Phe	Pro	Tyr	Leu	Leu	Ile	Ser	Pro	Gly	Thr	Phe
		35					40				45				
Leu	Leu	Ile	Phe	Val	Val	Val	Phe	Pro	Leu	Ile	Phe	Met	Phe	Gly	Val
	50					55					60				
Ala	Phe	Thr	Asn	Tyr	Asn	Leu	Tyr	Asn	Ala	Pro	Pro	Arg	His	Thr	Leu
65					70					75				80	
Glu	Trp	Val	Gly	Leu	Asp	Asn	Phe	Lys	Thr	Leu	Phe	Thr	Ile	Gly	Val
			85					90					95		
Trp	Arg	Lys	Thr	Phe	Phe	Ser	Val	Ile	Thr	Trp	Thr	Leu	Val	Trp	Thr
		100						105					110		
Leu	Val	Ala	Thr	Thr	Leu	Gln	Ile	Ala	Leu	Gly	Leu	Phe	Leu	Ala	Ile
		115					120					125			
Ile	Val	Asn	His	Pro	Val	Val	Lys	Gly	Lys	Lys	Phe	Ile	Arg	Thr	Val
	130					135					140				
Leu	Ile	Leu	Pro	Trp	Ala	Val	Pro	Ser	Phe	Val	Thr	Ile	Leu	Ile	Phe
145				150						155				160	
Val	Ala	Leu	Phe	Asn	Asp	Glu	Phe	Gly	Ala	Ile	Asn	Asn	Asp	Ile	Leu
			165					170					175		
Gln	Pro	Leu	Leu	Gly	Val	Ala	Pro	Ala	Trp	Leu	Ser	Asp	Pro	Phe	Trp
		180						185					190		
Ala	Lys	Val	Ala	Leu	Ile	Gly	Ile	Gln	Val	Trp	Leu	Gly	Phe	Pro	Phe

195	200	205
Val Phe Ala Leu Phe Thr Gly Val Leu Gln Ser Ile Ser Ser Asp Trp		
210	215	220
Tyr Glu Ala Ala Asp Met Asp Gly Ala Ser Ser Trp Gln Lys Phe Arg		
225	230	235
Asn Ile Thr Phe Pro His Val Ile Tyr Ala Thr Ala Pro Leu Leu Ile		
245	250	255
Met Gln Tyr Ala Gly Tyr Phe Asn Xaa Xaa Xaa Leu Ile Tyr Leu Ile		
260	265	270

(2) INFORMATION FOR SEQ ID NO:556:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:556:

Met Leu Leu Ile Pro Glu Pro Trp Leu Tyr Asn Glu Ala Asn Asp Ala		
1	5	10
Asn Val Arg Ala Phe Tyr Glu Phe Tyr Ser Tyr Leu Met Glu Pro Trp		
20	25	30
Asp Gly Pro Thr Met Ile Ser Xaa Cys Asn Gly Asp Lys Leu Gly Ala		
35	40	45
Leu Thr Asp Arg Asn Gly Leu Arg Pro Gly Arg Tyr Thr Ile Thr Lys		
50	55	60
Asp Asn Phe Ile Val Phe Ser Ser Glu Val Gly Val Val Asp Val Pro		
65	70	75
Glu Ser Asn Val Ala Phe Lys Gly Gln Leu Asn Pro Gly Lys Leu Leu		
85	90	95
Leu Val Asp Phe Lys Gln Asn Lys Val Ile Glu Asn Asn Asp Leu Lys		
100	105	110
Gly Ala Ile Ala Gly Glu Leu Pro Tyr		
115	120	

(2) INFORMATION FOR SEQ ID NO:557:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:557:

```

Met Thr Arg Lys Gly Tyr Gly Glu Ser Thr Gly Lys Ile Ile Leu Ile
 1             5             10             15
Gly Glu His Ala Val Thr Phe Gly Glu Pro Ala Ile Ala Val Pro Phe
             20             25             30
Asn Ala Gly Lys Ile Lys Val Leu Ile Glu Ala Leu Glu Ser Gly Asn
             35             40             45
Tyr Ser Ser Ile Lys Ser Asp Val Tyr Asp Gly Ile Val Ile
 50             55             60

```

(2) INFORMATION FOR SEQ ID NO:558:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:558:

```

Met Ile Glu Leu Lys His Val Thr Phe Gly Tyr Asn Lys Lys Gln Met
 1             5             10             15
Val Leu Gln Asp Ile Asn Ile Thr Ile Pro Asp Gly Glu Asn Val Gly
             20             25             30
Ile Leu Gly Glu Ser Ala Cys Gly Lys Ser Thr Leu Ala Ser Leu Val
             35             40             45
Leu Gly Leu Phe Lys Pro Val Lys Gly Glu Ile Tyr Leu Ser Asp Asn
 50             55             60
Ala Val Leu Thr Ile Phe Gln His Pro Leu Thr Ser Phe Asn Pro Asp
 65             70             75             80
Trp Thr Ile Glu Thr Ser Leu Lys Glu Ala Leu Tyr Tyr Tyr Arg Gly
             85             90             95
Leu Thr Asp Asn Thr Ala Gln Asp Gln Leu Leu Leu Gln His Leu Ser
 100            105            110
585

```

```

Thr Phe Glu Leu Asn Ala Gln Leu Leu Thr Lys Leu Pro Ser Glu Val
      115                      120                      125
Ser Gly Gly Gln Xaa Gln Arg Phe Asn Val Met Arg Ser Leu Leu Ala
      130                      135                      140
Gln Pro Arg Val Leu Ile Cys Asp Glu Ile Thr Ser Asn Leu Asp Val
      145                      150                      155                      160
Ile Ala Xaa Gln Asn Val Ile Asn Ile Xaa Lys Ala Gln Thr Val Xaa
                      165                      170                      175
Glu Leu Lys Ser Phe Tyr Arg Tyr Phe Ser
      180                      185

```

(2) INFORMATION FOR SEQ ID NO:559:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:559:

```

Met Glu Asp Leu Arg Gly Arg Phe Ser Glu Thr Ser Arg Glu Gly Phe
  1                      5                      10                      15
Leu Leu Ala Gln Asp Ile Ser Ser Tyr Ser Leu Thr Ile Val Ala His
      20                      25                      30
Glu Ala Lys Lys Leu Met Pro Glu Gly Gly Ser Ile Val Ala Thr Thr
      35                      40                      45
Tyr Leu Gly Gly Glu Phe Ala Val Gln Asn Tyr Asn Val Met Gly Val
      50                      55                      60
Ala Lys Ala Ser Leu Glu Ala Asn Val Lys Tyr Leu Ala Leu Asp Leu
      65                      70                      75                      80
Gly Pro Asp Asn Ile Arg Val Asn Ala Ile Ser Ala Gly Pro Ile Arg
      85                      90                      95
Thr Leu Ser Ala Lys Gly Val Gly Gly Phe Asn Thr Ile Leu Lys Glu
      100                      105                      110
Ile Glu Glu Arg Ala Pro Leu Lys Arg Asn Val Asp Gln Val Glu Val
      115                      120                      125
Gly Lys Thr Ala Ala Tyr Leu Leu Ser Asp Leu Ser Ser Gly Val Thr
      130                      135                      140
Gly Glu Asn Ile His Val Asp Ser Gly Phe His Ala Ile Asn Xaa Ile
      145                      150                      155                      160

```

Ile Gln Gln Leu Gly Phe Thr Val Tyr His Ile Leu Trp Ser Lys Ser
 165 170 175
 Phe Xaa Gly Phe Ile Asn Asn Xaa Ala Asp Gly Lys Leu Leu Asp Ile
 180 185 190
 Ser Thr

(2) INFORMATION FOR SEQ ID NO:560:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:560:

Met Lys His Ser Asp Ile Val Val Thr Val His Asp Ile Asp Gln Tyr
 1 5 10 15
 Thr Asn Asp Asn Arg Gln Leu Asp Gln Arg Leu Asn Asp Leu Gln Gly
 20 25 30
 Gln Gln Ala Asn Lys Glu Ala Asp Lys Gln Arg Leu Ser Gln Gln Ile
 35 40 45
 Gln Gln Tyr Lys Gly Lys Arg His Gln Leu Asp Asn Asp Val Glu Ser
 50 55 60
 Leu Asn Tyr Gln Leu Val Lys Ala Thr Glu Ala Phe Glu Lys Tyr Thr
 65 70 75 80
 Gly Gln Leu Asn Val Leu Glu Glu Arg Xaa Glu Lys Ser Ile
 85 90

(2) INFORMATION FOR SEQ ID NO:561:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:561:

Met Glu Leu Leu Glu Asn Ile Ser Asn Glu Ile Ser Glu Ala Xaa Asp
1 5 10 15
Thr Tyr Lys Ser Leu Lys Ser Lys His Xaa Arg Thr Gln Cys Cys His
20 25 30
Ser

(2) INFORMATION FOR SEQ ID NO:562:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:562:

[illegible]

(2) INFORMATION FOR SEQ ID NO:563:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:563:

```

Met Asp Leu Asn Gln Ile Xaa Ala Val Val Phe Asp Leu Glu Gly Thr
 1             5             10             15
Leu Leu Asp Arg Val Lys Ser Arg Glu Lys Xaa Ile Glu Glu Gln Tyr
             20             25             30
Glu Arg Xaa His Asp Tyr Leu Xaa His Val Gln Leu Ala Asp Phe Lys
             35             40             45
Lys Ala Phe Ile Glu Leu Asp Asp Asp Glu Asp Asn Asp Lys Pro Asp
             50             55             60
Leu Asp Lys Glu Ile Ile Lys Arg Phe His Val Arg
65             70             75

```

(2) INFORMATION FOR SEQ ID NO:564:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:564:

```

Met Thr Val Asn Asp Leu Ala Asp Val Thr Asn Val Ser Thr Ala Ser
 1             5             10             15
Ile Val Arg Phe Ser Arg Lys Met Thr His Gln Gly Phe Gln Glu Leu
             20             25             30
Lys Ile Ala Ile Ser Arg Tyr Leu Pro Glu Asp Ile Ala Thr Asn Pro
             35             40             45
His Leu Glu Leu Ile Glu Asn Glu Ser Val Glu Thr Leu Lys Asn Lys
             50             55             60
Met Ile Ala Arg Ala Thr Glu Tyr Gly Cys Asp Leu
65             70             75

```

(2) INFORMATION FOR SEQ ID NO:565:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:565:

Met Leu Thr Glu Asn Gln Ser Val Asn Ala Lys Gly Lys Tyr Glu Lys
 1 5 10 15
 Met Tyr Arg Leu Tyr Asp Thr Asn Gln Leu His Gln Tyr Tyr Ser Gly
 20 25 30
 Pro Ser Phe Asp Leu Thr Asn Leu Ser Gly Leu Gln Ser Arg Leu Leu
 35 40 45

(2) INFORMATION FOR SEQ ID NO:566:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:566:

Met Asn Arg Leu His Gly Xaa Xaa Val Xaa Ile Gly Tyr Gly Asp Asn
 1 5 10 15
 Thr Ile Ile Asn Lys Leu Asp Val Glu Xaa Pro Xaa Gly Lys Val Thr
 20 25 30
 Ser Ile Ile Gly Pro Asn Gly Cys Gly Lys Ser Thr Leu Leu Lys Ala
 35 40 45
 Leu Ser Arg Leu Leu Ala Ala Xaa Xaa Gly Glu Val Phe Leu Asp Gly
 50 55 60
 Trp Lys Ile Phe Asn Thr Gln Ser Thr Lys Glu Ile Ala Lys Lys Ile
 65 70 75 80
 Xaa Ile Leu Pro Gln Ser Pro Glu Val Ala Arg Trp Leu Asn Leu Leu
 85 90 95
 Gly Asn

(2) INFORMATION FOR SEQ ID NO:567:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:567:

```

Met Xaa Pro Asn Pro Pro Gln Glu Leu Leu Gln Gln Leu Gly Phe Ser
 1             5             10             15
Ser Glu Phe Thr His Gln Thr Tyr Thr Phe Ser Asn Met Glu Leu Pro
          20             25             30
Trp Val Ser Phe Ile Val His Phe Ser Phe Ser Ile Val Ile Ala Ile
          35             40             45
Ile Tyr Cys Ile Leu Val Lys Lys Tyr Ala Tyr Leu Ala Ile Gly Gln
          50             55             60
Gly Ala Val Phe Gly Ile Ala Ile Trp Val Leu Phe His Leu Ile Ile
65             70             75             80
Met Pro Ile Met His Thr Val Pro Ala Val Trp Asp Gln Pro Tyr Gln
          85             90             95
Glu His Leu Ser Glu Phe Phe Gly His Ile Val Trp Met Met Thr Ile
          100            105            110
Glu Leu Val Arg Gln His Phe Val Tyr Arg Tyr Lys Leu Asn
          115            120            125

```

(2) INFORMATION FOR SEQ ID NO:568:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:568:

```

Met Met Asp Tyr Asn Thr Thr Gly Asp Gly Leu Leu Thr Gly Ile Gln
 1             5             10             15
Leu Ala Ser Val Ile Lys Met Thr Gly Lys Ser Leu Ser Glu Leu Ala
          20             25             30
Gly Gln Met Lys Lys Tyr Pro Gln Ser Leu Ile Asn Val Arg Val Thr
          35             40             45
Asp Lys Tyr Arg Val Glu Glu Asn Val Asp Val Lys Glu Val Met Thr
          50             55             60

```


Lys Val Glu Val Glu Met Asn Gly Glu Gly Arg Ile Leu Val Arg Pro
 65 70 75 80
 Ser Gly Thr Glu Pro Leu Val Arg Val Met Val Glu Ala Ala Thr Asp
 85 90 95
 Glu Asp Ala Glu Arg Phe Ala Gln Gln Ile Ala Asp Val Val Gln Asp
 100 105 110
 Lys Met Gly Leu Asp Lys
 115

(2) INFORMATION FOR SEQ ID NO:569:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:569:

Met Ile Gln Gly Ala Glu Asn Val Ala Lys Met Tyr Asp Val Ser Arg
 1 5 10 15
 Glu Leu Gln Asp Glu Phe Ala Tyr Arg Ser His Gln Leu Thr Ala Glu
 20 25 30
 Asn Val Lys Asn Gly Asn Ile Ser Gln Glu Ile Leu Pro Ile Thr Val
 35 40 45
 Lys Gly Glu Ile Phe Asn Thr Asp Glu Ser Leu Lys Ser His Ile Pro
 50 55 60
 Lys Asp Asn Phe Gly Arg Phe Lys Pro Val Ile Lys Gly Gly Thr Val
 65 70 75 80
 Thr Ala Ala Asn Ser Cys Met Lys Asn Asp Gly Ala Val Leu Leu Leu
 85 90 95
 Ile Met Glu Lys Asp Met Ala Tyr Glu Leu Gly Phe Glu His Gly Leu
 100 105 110
 Leu Phe Lys Glu Trp Cys Tyr Gly Arg Cys
 115 120

(2) INFORMATION FOR SEQ ID NO:570:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:570:

```

Met Pro Ala Tyr Val Val Asp Thr Thr Lys Gln Ile Ile Lys Ala Leu
 1             5             10             15
Ser Gly Asn Lys Val Thr Val Phe Gly Leu Thr Tyr Lys Gly Asp Val
          20             25             30
Asp Asp Ile Arg Glu Ser Pro Ala Phe Asp Ile Tyr Glu Leu Leu Asn
          35             40             45
Xaa Xaa Pro Asp Ile Xaa Val Cys Ala Tyr Asp Pro His Val Xaa Leu
          50             55             60
Asp Phe Val Glu His Asp Met Ser His Ala Val Lys Asp Ala Ser Leu
65             70             75             80
Val Leu Ile Leu Ser Asp His Ser Xaa Xaa Lys Asn Leu Ser Asp Ser
          85             90             95
His Phe Asp Lys Met Lys His Lys Val Ile Phe Asp Thr Xaa Asn Val
          100            105            110
Val Lys Ser Ser Phe Xaa Asp Val Ser Tyr Tyr Asn Tyr Gly Asn Ile
          115            120            125
Xaa Asn Phe Ile Asp Lys
          130

```

(2) INFORMATION FOR SEQ ID NO:571:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:571:

```

Met Gly Leu Val Ile Glu His Val Thr Lys Arg Phe Gly Lys Met Thr
 1             5             10             15
Ala Val Asn Asp Ile Ser Leu Glu Leu Glu Ser Gly Lys Met Leu Gly
          20             25             30
Phe Leu Gly Arg Asn Gly Ala Gly Lys Thr Thr Thr Phe Arg Met Ile
          593

```

```

      35              40              45
Leu Gly Leu Ser Glu Pro Thr Glu Gly His Ile Thr Tyr Asn Gly Lys
      50              55              60
Lys Leu Asp Lys Thr Met Tyr Asn Arg Ile Gly Tyr Leu Pro Glu Glu
      65              70              75              80
Arg Gly Leu His Ala Gly Asn
              85

```

(2) INFORMATION FOR SEQ ID NO:572:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:572:

```

Met Lys Ile Leu Xaa Tyr Ile Gly Tyr Leu Leu Leu Gly Gly Ile Val
 1              5              10              15
Gly Gly Ile Ile Gly Gly Ile Leu Xaa Asn Phe Asp Gly Leu Gly Ile
      20              25              30
Glu Asn Leu Thr Phe Ala Thr Tyr Asn Asn Val Val Val Ile Ser Ile
      35              40              45
Val Ala Thr Met Ile Ile Ile Leu Val Glu Ala Ile Val Leu Met Asn
      50              55              60
Gln Xaa Xaa Ala Leu Lys Tyr Lys Arg Leu Val Asp Glu Glu Val His
      65              70              75              80
Ile Asp Ala Thr Asp Gln Tyr Glu Leu Leu Ala Asn Arg Tyr Val Leu
      85              90              95
Asn Gly Ser Ile Leu Ser Val Ile Xaa Thr Ile Ile Ala Phe Val Val
      100              105              110
Leu Leu Ile Phe Val Val Gly Gln Ala Glu Ala Asn Ala Met Leu Phe
      115              120              125
Phe Leu Leu Pro Phe Phe Xaa Ser Ala Xaa Xaa Asn Thr Gln Phe Thr
      130              135              140
Leu Phe Asn Arg Lys Phe Asp Asp Arg Met Pro Lys Ile Ala Asp Lys
      145              150              155              160
Asn Tyr Thr Glu Lys Arg Leu Glu Ile Leu Asp Glu Gly Glu Arg His
      165              170              175
Ile Arg Ile Asn Cys Ile Ile

```

180

(2) INFORMATION FOR SEQ ID NO:573:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:573:

```

Met Asp Asn Ser Asn Lys Ser Thr Asp Tyr Leu Lys Gln Ser Asp Glu
 1             5             10             15
Phe Ala Asp Leu Tyr Arg Asp Lys Leu Asn Asp Ala Asn Lys Leu Ser
          20             25             30
Lys Tyr Asn Phe Thr Gln Lys Tyr Gly Val Ser Pro Asn Asn Tyr Lys
      35             40             45
Asn Lys Thr Ile Val Ala Asp Gly Gly Asn Ser Glu Gly Gly Ala Gly
      50             55             60
Ala Lys Tyr Gln Gly Ala Lys His Pro Asn Glu Lys Val Val Ala Thr
65             70             75             80

```

(2) INFORMATION FOR SEQ ID NO:574:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:574:

```

Met Arg Gln Arg Val Met Ile Ala Met Ala Leu Ile Leu Lys Pro Gln
 1             5             10             15
Ile Leu Ile Ala Asp Glu Pro Thr Thr Ala Leu Asp Ala Ser Thr Gln
          20             25             30
Asn Gln Leu Leu Gln Leu Met Lys Ser Leu Tyr Glu Tyr Thr Glu Thr
      35             40             45

```

595

Ser Ile Ile Phe Ile Thr His Asp Leu Gly Ala Val Tyr Gln Phe Cys .
 50 55 60
 Asp Asp Val Ile Val Met Lys Asp Gly Ser Val Val Glu Ser Gly Thr
 65 70 75 80
 Val Glu Val Phe Leu Asn Arg His Asn Ile Pro Ile Gln Asn Ala
 85 90 95

(2) INFORMATION FOR SEQ ID NO:575:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:575:

Met Leu Ser Xaa Leu Val Lys Asp Xaa Lys Ile Ile Ala Asn Tyr Gly
 1 5 10 15
 Ala Gly Phe Asn Asn Ile Asp Ile Glu Tyr Xaa Arg Xaa Lys Ser Ile
 20 25 30
 Asp Val Thr Asn Thr Xaa Lys Ala Ser Xaa His Ala Xaa Ala Asp Leu
 35 40 45
 Thr Ile Gly Leu Val Leu Ala Val Ala Arg Arg Ile Val Glu Gly Asp
 50 55 60
 Gln Leu Ser Arg Thr Thr Gly Phe Asp Gly Trp Ala Pro Leu Phe Phe
 65 70 75 80
 Arg Gly Arg Glu Val Ser Gly Lys Thr Ile Gly Ile Ile Gly Leu Gly
 85 90 95
 Glu Ile Gly Ser Ala Val Ala Arg Arg Ala Arg Ala Phe Asp Met Asp
 100 105 110
 Val Leu Tyr Thr Gly Pro Asn Arg Lys Glu Glu Xaa Glu Arg Glu Ile
 115 120 125
 Gly Ala Lys Tyr Val Arg Phe Arg Tyr Thr Ile Lys Glu Cys Arg Phe
 130 135 140
 Tyr His Tyr Gln Arg Cys Leu
 145 150

(2) INFORMATION FOR SEQ ID NO:576:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:576:

```

Met Ser Gly Gly Ile Ala Xaa Val Ile Pro Ser Asp Val Glu Ala Phe
 1             5             10             15
Val Glu Asn Asn Gln Leu Asp Thr Leu Ser Phe Thr Lys Ile Lys His
          20             25             30
Gln Glu Glu Lys Ala Phe Ile Lys Gln Met Leu Glu Glu His Val Ser
          35             40             45
His Thr Asn Ser Thr Arg Ala Ile His Val Leu Lys His Phe Asp Arg
          50             55             60
Ile Glu Asp Val Val Val Lys Val Ile Pro Lys Asp Tyr Gln Leu Met
65             70             75             80
Xaa Gln Lys Ile His Leu His Lys Ser Leu His Asp Asn Glu Asp Glu
          85             90             95
Ala Met Leu Ala Ala Phe Tyr Asp Asp Ser Lys Thr Ile Asp Ala Lys
          100            105            110
His Lys Pro Ala Val Val Tyr
          115

```

(2) INFORMATION FOR SEQ ID NO:577:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:577:

```

Met Gln Leu Asp Ala Lys Thr Pro Ser Lys Ile Ser Leu Gln Tyr Lys
 1             5             10             15
Thr Ala Val Gly Gln Lys Glu Glu Val Ala Lys Asn Thr Glu Lys Val
          20             25             30
Val Ser Asn Val Leu Asn Asp Phe Asn Lys Asn Leu Val Glu Ile Tyr
          35             40             45
          50             55             60
          65             70             75
          80             85             90
          95             100            105
          110            115            120
          125            130            135
          140            145            150
          155            160            165
          170            175

```

```

      35              40              45
Leu Thr Ser Ile Ile Asp Asn Leu His Asn Ala Gln Lys Asn Val Gly
      50              55              60
Ala Ile Met Thr Arg Glu His Gly Val Asn Ser Lys Phe Ser Asn Tyr
      65              70              75              80
Leu Leu Asn Pro Ile Asn Asp Phe Pro Glu Leu Phe Thr Asp Thr Leu
      85              90              95
Val Asn Ser Ile Ser Ala Asn Lys Asp Ile Thr Lys Trp Phe Gln Thr
      100             105             110
Tyr Asn Lys Ser Leu Leu Ser Ala Asn Ser Xaa Thr Phe Arg Val Asn
      115             120             125
Thr Asp Tyr Xaa Val Ser Thr Leu Ile Glu Lys Gln Asn Ser Leu Phe
      130             135             140
Asp Glu His Asn Thr Ala Lys Asp Lys Met Leu Pro Asp Tyr Lys Ser
      145             150             155             160
Pro Lys Asp Met Trp Asn Leu Ile Thr Ile Ser Met His
      165             170

```

(2) INFORMATION FOR SEQ ID NO:578:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:578:

```

Met Asn His Ile Met Glu Ser Val Thr Asn Ala Ile Tyr Pro Ile Gly
  1              5              10              15
Met Met Leu Leu Ile Xaa Gly Gly Gly Gly Thr Phe Lys Gln Val Leu
      20              25              30
Xaa Asp Gly Gly Val Gly Asn Thr Ile Ala Lys Met Phe Glu Gly Thr
      35              40              45
Glu Met Ser Pro Ile Leu Leu Ala Trp Xaa Val Ala Ala Arg Ala Thr
      50              55              60
Tyr Arg Ile Arg Phe Gly Tyr Ser Ser Cys Asp Phe Asn Tyr Arg Tyr
      65              70              75              80
Cys Leu Thr Ile Ile Thr Ile Ile Arg Cys Lys Cys Cys Ile Ser Cys
      85              90              95
Thr Cys Asp Arg Cys Arg

```

100

(2) INFORMATION FOR SEQ ID NO:579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:579:

Met	Lys	Ala	Ala	Tyr	Lys	Asn	Lys	Gln	Val	Asp	Gly	Phe	Thr	Thr	Asn
1				5				10						15	
Pro	Ser	Leu	Met	Pro	Lys	Ala	Ala	Val	Ser	Arg	Leu	Gln	Ser	Phe	Cys
			20					25						30	

(2) INFORMATION FOR SEQ ID NO:580:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:580:

Met	Asp	Arg	Ala	Lys	Pro	Met	Asp	Glu	Xaa	Ile	Xaa	Asn	Gly	Glu	Asp
1				5				10						15	
Tyr	Ala	Ser	Leu	Ile	Xaa	Xaa	Ala	Lys	Xaa	Lys	Gly	Leu	Ser	Asp	Ile
			20					25						30	
Pro	Asn	Thr	Lys	Ile	Phe	Lys	Tyr	Arg							
		35					40								

(2) INFORMATION FOR SEQ ID NO:581:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:581:

```

Met Met Gln Val Arg His Pro His Val Val Ala His Leu Tyr Asn Lys
 1             5             10             15
Lys Asn Lys Ser Tyr Ile Asp Ile Lys Thr Asp Phe Phe Val Pro Asn
          20             25             30
Asn Val Gln Val Gln Ser Leu Thr Glu Ala Ile Arg Ser Asp Ile Lys
      35             40             45
Lys Asn Val Glu Tyr Phe Thr Glu Met Pro Val Arg Lys Leu Glu Val
      50             55             60
Asn Val Arg Asp Gln Lys Thr Ser Gly Pro Arg Val Leu
65             70             75

```

(2) INFORMATION FOR SEQ ID NO:582:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:582:

```

Met Glu Ala Asn His Ser Lys Ala Lys Val Pro Ile Gly Asn Gln Ile
 1             5             10             15
Val Thr Val Glu Arg Gly Gln Arg Leu Thr Ser Ile Leu Xaa Leu Ser
          20             25             30

```

(2) INFORMATION FOR SEQ ID NO:583:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:583:

```

Met Gly Gly Asp Tyr Asp Ala Leu Glu Thr Leu Met Ala Ser Arg Pro
 1             5             10             15
Asp Ile Leu Asn His Asn Ile Glu Thr Val Arg Arg Leu Thr Pro Arg
      20             25             30
Val Arg Ala Arg Ala Thr Tyr Asp Arg Thr Leu Glu Phe Leu Arg Arg
      35             40             45
Ser Xaa Glu Leu Gln Pro Asp Ile Pro Thr Lys Ser Ser Ile Met Val
      50             55             60
Gly Leu Gly Glu Thr Ile Glu Glu Ile Tyr Glu Xaa Met Asp Asp Leu
65             70             75             80
Arg Ala Asn Asp Val Asp Ile Leu Thr Ile Gly Gln Tyr Leu Gln Pro
      85             90             95
Ser Arg Lys His Leu Lys Val Xaa Lys Tyr Tyr Thr Pro Leu Glu Phe
      100            105            110
Gly Lys Leu Arg Lys Val Ala Met Asp Lys Gly Phe Lys Gln Cys Gln
      115            120            125
Leu Asp Leu
      130

```

(2) INFORMATION FOR SEQ ID NO:584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:584:

```

Met Ile Asn Met Lys Ile Leu Val Val Cys Gly His Gly Leu Gly Ser
 1             5             10             15
Ser Phe Met Val Glu Met Asn Ala Gln Glu Ala Leu Arg Gln Leu Asn
      20             25             30
Ala Pro Ser Asp Ile Glu Val Glu His Ser Asp Ile Met Thr Ala Ser
      35             40             45
Pro Glu Met Ala Asp Leu Phe Ile Cys Gly Arg Asp Leu Ala Arg Lys
      50             55             60

```

Cys Arg Thr Pro Lys Gly Cys Leu Ser Xaa
65 70

(2) INFORMATION FOR SEQ ID NO:585:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:585:

```

Met Ile Leu Pro Ile Leu Ala Thr Leu Ser Val Ala Val Gly Val His
 1             5             10             15
Pro Leu Leu Leu Met Ala Pro Ala Ala Met Ala Ala Asn Cys Ala Tyr
      20             25             30
Met Leu Pro Val Gly Thr Pro Pro Asn Ala Ile Ile Phe Gly Ser Gly
      35             40             45
Lys Ile Ser Ile Lys Gln Met Ala Ser Val Gly Phe Trp Val Asn Leu
      50             55             60
Ile Ser Ala Ile Ile Ile Ile Leu Val Val Tyr Tyr Val Met Pro Ile
      65             70             75             80
Val Leu Gly Ile Asp Ile Asn Gln Pro Leu Pro Leu Lys
      85             90

```

(2) INFORMATION FOR SEQ ID NO:586:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:586:

```

Met Asn Ala His Ile Tyr Leu Glu Leu Ala Gly Asp Tyr Gln Ala Leu
 1             5             10             15
Ala Ile Leu Pro Leu Trp His His Asp Asp Thr Tyr Leu Phe Asp Leu

```

```

                20                25                30
Leu Leu Arg Lys Ile Glu Asp Met Ile Leu Pro Lys Lys Ser Val Ser
                35                40                45
Lys Val Lys Gln Thr Gln Leu Leu Thr Thr Glu Gly Asn Tyr Lys Pro
                50                55                60
Thr Thr Leu
65

```

(2) INFORMATION FOR SEQ ID NO:587:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:587:

```

Met Phe Ile Ile Glu Leu Ile Lys Gly Ile Ile Leu Gly Val Val Glu
 1                5                10                15
Gly Xaa Thr Glu Phe Ala Pro Val Ser Ser Thr Gly His Met Ile Leu
                20                25                30
Val Asp Asp Met Trp Leu Lys Ser Ser Glu Phe Leu Gly Ser Gln Ser
                35                40                45
Ala Phe Thr Phe Lys Ile Val Ile Gln Leu Gly Ser Val Phe Ala Ala
                50                55                60
Ala Trp Ala Phe Arg Ala Lys Arg Phe Leu Glu Ile Leu His Ile Gly
65                70                75                80
Lys His Lys His Val Glu Gly Glu Asn Asp Gln Gln Arg Arg Ser Lys
                85                90                95
Pro Arg Arg Leu Asn Leu Leu His Val Leu Val Gly Met Val Pro Ala
                100                105                110
Gly Ile Leu Gly Leu Leu Phe Asp Asp Phe Ile Glu Glu His Leu Phe
                115                120                125
Ser Val Pro Thr Val Met Ile Gly Leu Phe Val Gly Ala Ile Tyr Met
                130                135                140
Ile Ile Ala Asp Lys Tyr Ser Val Lys Val Lys Asn Pro Gln Thr Val
145                150                155                160
Asp Gln Ile Asn Tyr Phe Gln Ala Phe Val Ile Gly Ile Ser Gln Ala
                165                170                175
Val Ala Met Trp Pro Gly Phe Ser Arg Ser Gly Ser Thr Ile Ser Thr

```

	180	185	190
Gly Val Ile Asn Glu Ile Lys Ser			
195	200		

(2) INFORMATION FOR SEQ ID NO:588:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:588:

Met	Lys	Lys	Trp	Ala	Asn	Gly	Leu	Pro	Leu	Thr	Asp	Lys	Arg	Ile	Ser
1				5				10					15		
Pro	Ile	Asn	Gly	Thr	Ile	Glu	Gly	Leu	Pro	Pro	Val	Tyr	Met	Phe	Gly
			20					25					30		
Gly	Gly	Arg	Glu	Met	Thr	His	Pro	Asp	Met	Lys	Leu	Phe	Glu	Gln	Met
			35				40					45			
Met	Leu	Gln	His	His	Gln	Tyr	Ile	Glu	Phe	Tyr	Asp	Tyr	Pro	Lys	Met
	50					55				60					
Val	His	Asp	Phe	Pro	Ile	Tyr	Pro	Ile	Arg	Gln	Ser	His	Lys	Ala	Ile
65					70				75					80	
Lys	Gln	Ile	Ala	Lys	Ser	Ile	Asp	Glu	Asp	Val	Thr	Gln	Asn	Asn	
				85					90					95	

(2) INFORMATION FOR SEQ ID NO:589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:589:

Met	Asn	Tyr	Gln	Asn	Ala	Ser	Tyr	Leu	Ser	Ala	Phe	Thr	Ala	Gly	Leu
1				5				10					15		

Gly Ile Tyr Phe Ile Met Lys Gly Ser Val Lys His Lys Trp Ile Tyr
 20 25 30
 Val Leu Phe Thr Ile Ile Asp Ile Pro Ile Val Phe Ile Pro Gly Arg
 35 40 45
 Arg Gly Ser Ala Ile Leu Leu Ile Leu Tyr Gly Phe Ile Cys Ile Tyr
 50 55 60
 Thr Tyr Tyr Val
 65

(2) INFORMATION FOR SEQ ID NO:590:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:590:

Met Lys Val Ser Ala Lys Asn Val Met Lys Gln Lys His Phe His Lys
 1 5 10 15
 Gly Ile Glu Gln Leu Val Gln Glu Gly Ala Ile Gln Tyr Tyr Lys Thr
 20 25 30
 Leu His Thr Asn Gln Ile Ile Leu Gly Ala Val Gly Gln Leu Gln Phe
 35 40 45
 Glu Val Phe Glu His Arg Met Lys Asn Glu Tyr Asn Val Asp Val Val
 50 55 60
 Met Glu Pro Val Gly Arg Lys Ile Ala Arg Trp Ile Glu Asn Glu Asp
 65 70 75 80
 Gln Ile Thr Asp Lys Met Asn Thr Ser Arg Ser Ile Leu Val Lys Asp
 85 90 95
 Arg Tyr Asp Asp Leu Val Phe Leu Phe Glu Asn Glu Phe Ala Thr Arg
 100 105 110
 Trp Phe Glu Glu Lys Phe Pro
 115

(2) INFORMATION FOR SEQ ID NO:591:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:591:

```

Met Ser Asp Tyr Asn Gly Met Asn Lys Ile Asp Met Met Asn Gln Ile
 1             5             10             15
Lys Val Asp Thr Met Leu His Gly Tyr His Ala Gly Phe Leu Phe Ala
             20             25             30
Leu Leu Ile Thr Val Val Ser Phe Phe Leu His Arg Ile Ile Gln
             35             40             45

```

(2) INFORMATION FOR SEQ ID NO:592:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:592:

```

Met Asn Glu Met Leu Met Ala Asn Tyr Leu Phe Asn Thr Ser Asp Asn
 1             5             10             15
Pro Arg Phe Lys Arg Trp Val Ile Gly Ser Ile Leu Ser Arg Thr Tyr
             20             25             30
Tyr His Asn Met Val Thr His Leu Leu Glu Ala Ala Tyr Gln Arg Glu
             35             40             45
Val

```

(2) INFORMATION FOR SEQ ID NO:593:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:593:

```

Met Leu Arg Glu Ala Tyr Asp Gln Arg Trp Ile Asp Phe Ala Arg Asn
 1             5             10             15
Lys Gly Lys Asp Thr Gly Ala Phe Cys Xaa Ser Pro Tyr Phe Thr His
             20             25             30
Ser Tyr Val Phe Ile Ser Trp Thr Gly Lys Met Ala Glu Ala Phe Val
             35             40             45
Leu Ala His Glu Leu Gly His Ala Gly His Phe Thr Leu Ala Gln Lys
             50             55             60
His Gln Pro Tyr Leu Glu Ser Glu Ala Ser Met Tyr Phe Cys
65             70             75

```

(2) INFORMATION FOR SEQ ID NO:594:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:594:

```

Met Asn Gln Asp Leu Tyr Gln Asp Thr Leu Cys Gly Gln Arg Val Gly
 1             5             10             15
Asn Tyr Lys Asp Tyr Gly Met Tyr Trp Ile Lys Asn Glu Val Lys Pro
             20             25             30
Asp Ala Ile Ile Glu Phe His Leu Asp Ser Ala Ser Pro Gln Ala Ser
             35             40             45
Gly Gly His Val Ile Ile Ser Asp Arg Phe Pro Ala Asp Asp Ile Asp
             50             55             60
Lys Ala Leu Ser Ser Ala Leu Asp Lys Thr Val Gly Lys Ile Arg Gly
65             70             75             80
Val Thr Pro Arg Gly Asp Leu Leu Asn Ala Asn Val Ser Ala Asp Leu
             85             90             95
Asn Leu Asn Tyr Arg Leu Ile Glu Leu Gly Phe Ile Thr Ser Thr Lys
             100             105             110
Asp Leu Asn Tyr Ile Xaa Asn Asn Leu Asp Ser Phe Xaa Lys Arg Ile
             115             120             125

```


Ala Glu Ala Ile Ile Gly Arg Gln Ile Asp Ala Pro Ser Ser Asn Pro
 130 135 140
 Ser Ala Asp
 145

(2) INFORMATION FOR SEQ ID NO:595:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:595:

Met Trp Phe Ile Arg Pro Phe Tyr Ala Lys Glu Thr Thr Ala Asn Lys
 1 5 10 15
 Leu Arg Ser Ala Val Thr Pro Val Lys Gln Asp Lys Leu Ser Gln Gly
 20 25 30
 Lys Lys Ile Met Leu Val Ala Gly His Gly Ile Gly Ala Tyr Ser Thr
 35 40 45
 Asp Pro Gly Ala Val Ala Asn Gly Glu Asn Glu Arg Asp Phe Xaa Arg
 50 55 60
 Lys Asn Ile Ile Pro Arg Val
 65 70

(2) INFORMATION FOR SEQ ID NO:596:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:596:

Met Met Gln Gln Leu Ser Leu Lys His Arg Leu Asn Asn Gly Asp Ser
 1 5 10 15
 Val Tyr Gly Ile Phe Asn Ser Ile Pro Asp Pro Leu Met Ile Glu Val

```

                20                25                30
Ile Ala Ala Ser Gly Tyr Asp Phe Val Val Ile Asp Thr Glu His Val
                35                40                45
Ala Ile Asn Asp Glu Thr Leu Ala His Leu Ile Arg Ala Ala Glu Ala
                50                55                60
Ala His Ile Ile Pro Ile Val Arg Val Thr Ala Val Ile Asp Arg Asp
        65                70                75                80
Ile Ile Lys Val Leu Asp Met Gly Ala Arg Gly Ile Ile Val Pro His
                85                90                95
Val Lys Asp Arg Glu Thr Val Gly Ala Tyr Trp
                100                105

```

(2) INFORMATION FOR SEQ ID NO:597:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:597:

```

Met Glu Thr Leu Lys Asn Lys Val Asp Gln Val Asn Thr Asp Lys Ala
 1                5                10                15
Gln Pro Asn Tyr Thr Glu Ala Ser Thr Asp Lys Lys Glu Ala Val Gly
                20                25                30
Ser Ser Val Thr Ser Cys Thr Xaa His Tyr Arg Ser Asn
                35                40                45

```

(2) INFORMATION FOR SEQ ID NO:598:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:598:

```

Met Thr Lys Leu Lys Val Gly Val Ile Gly Val Gly Gly Ile Ala Gln
 1              5              10              15
Asp Arg His Ile Pro Ala Leu Leu Lys Leu Lys Asp Thr Val Ser Leu
      20              25              30
Val Ala Val Gln Asp Ile Asn Thr Val Gln Met Ile Asp Val Ala Lys
      35              40              45
Arg Phe Asn Ile Pro Gln Ala Val Glu Thr Pro Ser Glu Leu Phe Lys
 50              55              60
Leu Val Asp Ala Val Val Ile Cys Thr Pro Asn Lys Phe His Ala Asp
65              70              75              80
Leu Ser Ile Glu Ala Leu Asn His Gly Val His Val Leu Cys Glu Lys
      85              90              95
Pro Met Xaa Met Thr Thr Glu Glu Cys Asp Arg Met Ile Glu Ala Ala
      100              105              110
Asn Lys Asn His Lys Leu Leu Thr Val Ala Tyr His Tyr Arg His Thr
      115              120              125
Asp Val Ala Met Thr Ala Lys Lys Ala Ile Glu Ala Gly Val Val Gly
      130              135              140
Lys Pro Leu Val Ala Pro Leu Ser Xaa Arg Cys Val Gly Val Lys Xaa
145              150              155              160
Leu Gly Gly Ala Phe Leu Pro Asn Lys Thr Val Ala Arg Trp Arg
      165              170              175

```

(2) INFORMATION FOR SEQ ID NO:599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:599:

```

Met Val Pro His Glu Val Leu Gly Lys Thr Tyr Asn Gln Leu Ser Lys
 1              5              10              15
Gln Pro Asn Gln Ile Asn Asp Trp Gly Thr Phe Asp His Thr Lys Phe
      20              25              30
Asp Val Asp Asp His Val Thr Ser Tyr Met Thr Phe Ala Asn Arg Ala
      35              40              45
Ser Met Gln Phe Glu Cys Ser Trp Ser Ala Asn Ile Lys Glu Asp Lys
 50              55              60

```

Val His Val Ser Leu Ser Gly Glu Asp Gly Gly Ile Asn Leu Phe Pro
 65 70 75 80
 Phe Glu Ile Tyr Glu Pro Arg Phe Gly Thr Ile Phe Glu Ser Lys Ala
 85 90 95
 Asn Val Glu His Asn Glu Asp Ile Ala Gly Glu Arg Gln Ala Arg Asn
 100 105 110
 Phe Val Asn Ala Cys Leu Gly Ile Glu Glu Ile Val Val Lys Pro Glu
 115 120 125
 Glu Ala Arg Asn Val Asn Ala Leu Ile Glu Ala Ile Tyr Arg Ser Asp
 130 135 140
 Leu Asp Asn Lys Ser Ile Gln Leu
 145 150

(2) INFORMATION FOR SEQ ID NO:600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:600:

Met Xaa Ile Glu Glu Lys Pro Asp Gly Phe Met Ala Phe Val His Ala
 1 5 10 15
 Leu Tyr Arg Ala Asp Asp Ile Val Asp Lys Asp Met Ser Lys Ala Leu
 20 25 30
 Asp Ala Leu Met Ser Ile Asp Phe
 35 40

(2) INFORMATION FOR SEQ ID NO:601:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:601:

```

Met Leu Lys Phe Glu Arg Val Ile Asp Ile Phe Asn Lys Lys Asn Asn
 1             5             10             15
Gly Ala Trp Asn Phe Cys Pro Gln Asn Ala Gly Tyr Trp Glu His Ile
      20             25             30
Pro Lys Ser Ile Thr Lys Leu Ser Asp Leu Lys Ile Val Gly Leu Asp
      35             40             45
Phe Tyr Ile Thr Thr Glu Glu Ser Lys Arg Phe Thr Asp Phe Pro Lys
      50             55             60
Asp Phe Lys Gly Ile Ala Gly Trp Ile Leu Glu Val Lys Ser Asn Thr
65             70             75             80
Pro Gly Asn Thr Thr Gln Val Leu Arg Arg Asn Asn Phe Pro Ser Ala
      85             90             95
His Gln Phe Xaa Val Arg Asn Phe Gly Thr Arg Leu Val Ala Leu Val
      100            105            110
Asn Gly Ser Leu Phe Glu Gly Lys Val Val Glu
      115            120

```

(2) INFORMATION FOR SEQ ID NO:602:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:602:

```

Met Val Met Glu Asn Leu Ala Ser Lys Leu Asn His Gln Ser Lys His
 1             5             10             15
Arg Leu Asp Gln Leu Asp His Leu Asn Asn Ala Gln Lys Gln Gln Leu
      20             25             30
Gln Ser Gln Ile Thr Gln Ser Ser Asp Ile Ala Ala Val Asn Gly His
      35             40             45
Lys Gln Thr Ala Glu Ser Leu Asn Thr Ala Met Gly Asn Leu Ile Asn
      50             55             60
Ala Ile Ala Asp His Gln Ala Val Glu Gln Arg Gly Asn Phe Ile Asn
65             70             75             80
Ala Asp Thr Asp Lys Gln Thr Ala Tyr Asn Thr Ala Val Asn Glu Ala
      85             90             95
Ala Ala Met Ile Asn Lys Gln Thr Gly Gln Asn Ala Asn Gln Thr Glu

```

```

          100              105              110
Val Glu Gln Ala Ile Thr Lys Val Gln Thr Thr Leu Gln Ala Leu Asn
          115              120              125
Gly Asp His Asn Leu Gln Val Ala Lys Thr Asn Ala Thr Xaa Ala Ile
          130              135              140
Asp Asp Leu Thr Ser Leu Asn Asp Pro Gln Lys Thr Gly Leu Lys Asp
          145              150              155              160
Gln Val Thr Gly Gly Thr Leu Xaa Thr Gly Gly Gln Gln Ile Gly Thr
          165              170              175
Lys Trp Xaa Phe Gly
          180

```

(2) INFORMATION FOR SEQ ID NO:603:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:603:

```

Met Ser Ala Thr Ile His Thr Pro Gly Gly Gly Arg Ser Leu Asn Gly
 1              5              10              15
Ser His Ala Ser Leu Val Val Ser Ile Asn Asp Val Phe Tyr Val Thr
          20              25              30
Asp Val Gly Phe Gly Asp Leu Pro Leu His Ala Ile Pro Ile Thr Ser
          35              40              45
Ser Glu His Thr Gln Pro Ile Thr Asp Ile Ser Gly Thr Phe Arg Ala
          50              55              60
Ile Phe Asn Asn Glu Asp Lys Asp Ile Phe Tyr Val Gln Lys Phe Glu
          65              70              75              80
Asn Asp His Trp His Thr Lys Tyr Glu Ala Glu Phe Lys Pro Lys Gln
          85              90              95
Ile Glu Asp Phe Asn Ser Asn Ile Glu Tyr Asn Gln Thr His Pro Asp
          100              105              110
Ser Ile Phe Val Gln His Leu Leu Ile Thr Met Pro Gln Ser Phe Gly
          115              120              125
Arg Ala Thr Met Ser Glu Asn His Leu Thr Leu Thr Arg Asn Gly Ser
          130              135              140
Ser Glu Lys Phe Asp Val Thr Lys Asp Asn Tyr Lys His Phe Leu Glu
          145              150              155              160
          165              170              175
          180
613

```

145 150 155 160
 Lys Tyr Phe Gly Leu Asn Val Thr Ile Asn Arg Ile Glu Lys Gln
 165 170 175

(2) INFORMATION FOR SEQ ID NO:604:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:604:

Met Pro Lys Phe Leu Lys Ser Phe Phe Asn Glu His Pro Phe Ile Asp
 1 5 10 15
 Val Ser Leu His Val Lys Asn Glu Asn Ile Glu Lys Asp Ile Asn Asn
 20 25 30
 His Thr Tyr Asp Ile Gly Ile Ser Arg Asn Gln Pro Lys Leu Arg Glu
 35 40 45
 Val His Ser Glu Lys Val Cys Glu Gly Lys Ile Val Leu Ile Ala Pro
 50 55 60
 Asn Lys Glu Asn Asn His Leu Leu Thr Glu Ala Ser Leu Phe Glu Lys
 65 70 75 80
 Tyr Lys Ile Ile Ser Asp Asn His Pro Glu Tyr Trp Ser Ser Leu Lys
 85 90 95
 Asn Asn Ile Leu Asn Ile Tyr Gly Lys Ala Gln Phe Leu Ser Ile Asn
 100 105 110
 Asp Val His Thr Ser Ile Lys Leu Ile Glu Met Asn Gln Gly Ile Ser
 115 120 125
 Phe Leu Pro Ile Tyr Ile Asn Asn Arg
 130 135

(2) INFORMATION FOR SEQ ID NO:605:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:605:

```

Met Ile Leu Lys Tyr Met Asp Ile Thr Glu Lys Val Pro Met Ser Glu
 1             5             10             15
Ser Glu Val Thr Gln Leu Leu Lys Gly Lys Gly Ile Leu Glu Asn Arg
      20             25             30
Gly Lys Val Phe Leu Glu Ala Gln Glu Lys Tyr Glu Val Xaa Val Ile
      35             40             45
Tyr Leu Val Ser His Ala Leu Val Glu Thr Gly Asn Gly Lys Ser Glu
      50             55             60
Leu Ala Lys Gly Ile Lys Asp Gly Lys Lys Arg Tyr Tyr Asn Phe Phe
      65             70             75             80
Gly Ile Gly Ala Phe Asp Ser Ser Ala Val Arg Ser Gly Lys Ser Tyr
      85             90             95
Ala Glu Lys Glu Gln Trp Thr Ser Pro Asp Lys Ala Ile Ile Gly Gly
      100            105            110
Ala Lys Phe Ile Arg Asn Glu Tyr Phe Glu Asn Asn Gln Leu Asn Leu
      115            120            125
Tyr Gln Met Arg Trp Asn Pro Glu Asn Pro Ala Gln His Gln Tyr Ala
      130            135            140
Ser Asp Ile Arg Trp Ala Asp Lys Ile Ala Lys Leu Met Asp Lys Ser
      145            150            155            160
Tyr Lys Gln Phe Gly Ile Lys Lys Asp Asp Ile Arg Gln Thr Tyr Tyr
      165            170            175
Lys

```

(2) INFORMATION FOR SEQ ID NO:606:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:606:

```

Met Arg Glu Lys Phe Xaa His Tyr Cys Glu His Glu Val Leu Ser Ser
 1             5             10             15

```

615


```

Ile Ile Asn Gly Ser Tyr Ile Ile Val Lys Thr Ser Pro Gly Phe Ala
      20                      25                      30
Gln Gly Ile Asn Tyr Phe Ile Asp Gln Leu Asn Ile Glu Glu Ile Leu
      35                      40                      45
Gly Thr Val Ser Gly Asn Asp Thr Thr Leu Ile Leu Thr Ala Ser Asn
      50                      55                      60
Asp Met Ala Glu Tyr Val Tyr Ala Lys Leu Phe Lys
      65                      70                      75

```

(2) INFORMATION FOR SEQ ID NO:607:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:607:

```

Met Lys Gly Thr Asp Ser Asp Ala Asn Leu Asp Ala Val Ala Ile Ala
  1                      5                      10                      15
Lys Lys Ala Tyr Ala Ile Tyr Lys Thr Ala Ile Val Ile Thr Gly Lys
      20                      25                      30
Glu Asp Val Ile Val Gln Asp Asn Lys Ala Ile Val Leu Ala Asn Gly
      35                      40                      45
Ser Pro Leu Leu Ala Arg Val Thr Gly Ala Gly Cys Leu Leu Gly Gly
      50                      55                      60
Val Ile Ala Gly Phe Leu Phe Arg Glu Thr Glu Pro Asp Ile Glu Ala
      65                      70                      75                      80
Leu Ile Glu Ala Val Ser Val Phe Asn Ile Ala Ala Glu Val Ala Ala
      85                      90                      95
Glu Asn Glu Asn Cys Gly Gly Pro Gly Asn Val Phe Thr Ile Val Ala
      100                      105                      110

```

(2) INFORMATION FOR SEQ ID NO:608:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:608:

```

Met Glu Thr Lys Thr Leu Gln Met Pro Lys Asp Lys Ala Asn Ala Phe
 1             5             10             15
Val Asn Ser Leu Asn Gly Leu Asn Gln Gln Gln Asp Leu Ala His
      20             25             30
Lys Ala Ile Asn Asn Ala Asp Thr Val Ser Asp Val Thr Asp Ile Val
      35             40             45
Asn Asn Gln Ile Asp Leu Asn Asp Ala Met Glu Thr Leu Lys His Leu
      50             55             60
Val Asp Asn Glu Ile Pro Asn Ala Glu Gln Thr Val Asn Tyr Gln Asn
      65             70             75             80
Ala Asp Asp Asn Ala Lys Thr Asn Phe Asp Asp Ala Lys Arg Leu Ala
      85             90             95
Asn Thr Leu Leu Asn Ser Asp Asn Thr Asn Val Asn Asp Ile Asn Gly
      100            105            110
Ala Ile Gln Ala Val Asn Asp Ala Ile His Asn Leu Asn Gly Asp Gln
      115            120            125
Arg Leu Gln Asp Ala Lys Asp Lys Ala Ile Gln Ser Ile Asn Gln Ala
      130            135            140
Leu Ala Asn Lys Leu Lys Glu Ile Glu Ala Ser Asn Ala Thr Asp Gln
      145            150            155            160
Asp Lys Leu Ile Ala Glu Lys Ile Lys Gln Glu Glu Leu Ala Asn Gln
      165            170            175
His His Gln Gln His
      180

```

(2) INFORMATION FOR SEQ ID NO:609:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:609:

```

Met Thr Gln Ala Arg Pro Gly Asn His Tyr Met Leu Ser Arg Leu Lys
      617

```

```

1           5           10           15
Pro Asn Gly Gln Phe Ile Asp Arg Leu Leu Val Lys Asn Gly Gly His
           20           25           30
Gly Thr His Asn Ala Tyr Arg Tyr Ile Val Gln
           35           40

```

(2) INFORMATION FOR SEQ ID NO:610:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:610:

```

Met Thr Glu Pro Asn Gly Gln Ser Ile Gln Val Asn Leu Asn Asn Ala
1           5           10           15
Gln Gly Asp Leu Gly Tyr Leu Thr Ala Gly Asn Tyr Tyr Ala Thr Arg
           20           25           30
Val Pro Asp Leu Pro Gly Ser Val Glu Ser Tyr Glu Gly Tyr Leu Ser
           35           40           45
Val Phe Val Lys Asp Asp Thr Asn Lys Leu Phe Asn Phe Thr Pro Tyr
           50           55           60
Asn Ser Lys Lys Ile Tyr Thr Arg Ser Ile Thr Asn Gly Arg Leu Glu
65           70           75           80
Gln Gln Trp Thr Val Pro Asn Glu His Lys Ser Thr Val Leu Phe Asp
           85           90           95
Gly Gly Ala Asn Gly Val Gly Thr Thr Ile Asn Leu Thr Glu Pro Tyr
           100          105          110
Thr Asn Tyr Ser Ile Leu Leu Val Ser Gly Thr Tyr Pro Gly Gly Val
           115          120          125
Ile Glu Gly Phe Gly Leu Thr Ala Leu Pro Asn Ala Ile Gln Leu Thr
           130          135          140
Lys Pro Asn Val Val Asp Ser Asp Gly Xaa Gly Gly Gly Ile Tyr Glu
145          150          155          160
Cys Leu Leu Ser Lys Thr Ser Ser Thr His Phe Lys Asn Arg Gln Arg
           165          170          175
Cys Val Phe Arg Phe Arg Gln Asn Ile Arg Phe Trp Asn Glu Cys Gln
           180          185          190
Gln Ser Tyr Tyr Asn

```

195

(2) INFORMATION FOR SEQ ID NO:611:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:611:

```

Met Met Lys Met Ile Tyr Pro Thr Phe Lys Asp Ile Lys Thr Phe Tyr
 1             5             10             15
Val Trp Gly Tyr Tyr Lys Asn Glu Gln Ile Lys Trp Tyr Val Asp Lys
      20             25             30
Gly Leu Ile Asp Lys Glu Glu Tyr Ala Leu Ile Thr Gly Glu Lys Tyr
      35             40             45
Pro Glu Thr Lys Asp Glu Lys Ser Gln Val
 50             55

```

(2) INFORMATION FOR SEQ ID NO:612:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:612:

```

Met Phe Gly Phe Thr Lys Arg His Glu Gln Asp Trp Arg Leu Thr Arg Leu Glu
Glu Asn Asp Lys Thr Met Phe Glu Lys Phe Asp Arg Ile Glu Asp Ser Leu Arg
Ala Gln Glu Lys Ile Tyr Asp Lys Leu Asp Arg Asn Phe Gly Arg Ile Lys Ala
Arg Gln Gly Arg Arg

```

(2) INFORMATION FOR SEQ ID NO:613:

(i) SEQUENCE CHARACTERISTICS:

619

- (A) LENGTH: 168 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:613:

```

Met Gly Leu Pro Asn Pro Lys Thr Arg Lys Pro Thr Ala Ser Glu Val
 1             5             10             15
Val Glu Trp Ala Lys Ser Asn Ile Gly Lys Arg Ile Asn Ile Asp Asn
      20             25             30
Tyr Arg Gly Ser Gln Cys Trp Asp Thr Pro Asn Phe Ile Phe Lys Arg
      35             40             45
Tyr Trp Gly Phe Val Thr Trp Gly Asn Ala Lys Asp Met Ala Asn Tyr
      50             55             60
Arg Tyr Pro Lys Gly Phe Arg Phe Tyr Arg Tyr Ser Ser Gly Phe Val
      65             70             75             80
Pro Glu Pro Gly Asp Ile Ala Val Trp His Pro Gly Asn Gly Ile Gly
      85             90             95
Ser Asp Gly His Thr Ala Ile Val Val Gly Pro Ser Asn Lys Ser Tyr
      100            105            110
Phe Tyr Ser Val Asp Gln Asn Trp Val Asn Ser Asn Ser Trp Thr Gly
      115            120            125
Ser Pro Gly Arg Leu Val Arg His Pro Tyr Val Ser Val Thr Gly Phe
      130            135            140
Val Arg Pro Pro Tyr Ser Lys Asp Thr Ser Lys Pro Ser Ser Thr Asp
      145            150            155            160
Thr Ser Ser Ala Ser Lys Ser Gln
      165

```

(2) INFORMATION FOR SEQ ID NO:614:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:614:

```

Met Glu Thr Leu Glu Leu Gln Gly Ala Lys Leu Arg Tyr His Gln Val
 1           5           10           15
Gly Gln Gly Pro Val Leu Ile Phe Ile Pro Gly Ala Asn Gly Thr Gly
          20           25           30
Asn Ile Phe Leu Pro Leu Ala Glu Gln Leu Lys Asp His Phe Thr Val
          35           40           45
Val Ala Val Asp Arg Arg Asp Tyr Gly Glu Ser Glu Leu Thr Glu Pro
          50           55           60
Leu Pro Asp Ser Ala Ser Asn Pro Asp Ser Asp Tyr Arg Val Lys Arg
65           70           75           80
Asp Ala Gln Asp Ile Ala Glu Leu Ala Lys Ser Leu Ser Asp Glu Pro
          85           90           95
Val Tyr Ile Leu Gly Ser Ser Ser Gly Ser Ile Val Ala Met His Val
          100          105          110
Leu Lys Asp Tyr Pro Glu Val Val Lys Lys Ile Ala Phe His Glu Pro
          115          120          125
Pro Ile Asn Thr Phe Leu Pro Asp Ser Thr Tyr Trp Lys Asp Lys Asn
          130          135          140
Asp Asp Ile Val His Gln Ile Leu Thr Glu Gly Leu Glu Lys Gly Met
145          150          155          160
Lys Thr Phe Gly Glu Thr Leu Asn Ile Ala Pro Ile Asp Ala Lys Met
          165          170          175
Met Ser Gln Pro Ala Asp Thr Glu Glu Gly Arg Ile Glu Gln Tyr Lys
          180          185          190
Arg Thr Met Phe Trp Ser Glu Phe Glu Ile Arg Gln Tyr Thr His Ser
          195          200          205
Asp Ile Thr Leu Asp Asp Phe Thr Lys Tyr Ser Asp Lys Ile Thr Leu
          210          215          220
Leu Asn Gly Thr Asp Ser Arg Gly Ser Phe Pro Gln Asp Val Asn Phe
225          230          235          240
Tyr Ile Asn Lys Glu Thr Gly Ile Pro Ile Val Asp Ile Pro Gly Gly
          245          250          255
His Leu Gly Tyr Ile Gln Lys Pro Glu Gly Phe Ala Asp Val Leu Leu
          260          265          270
Ile Cys Gly Cys
          275

```

(2) INFORMATION FOR SEQ ID NO:615:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 197 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:615:

```

Met Gly Arg Ala Gln Asp Gly Phe Leu Asp Gln Asp Lys Tyr Asp Ile
 1             5             10             15
Ile Phe Lys Thr Ala Glu Asn Leu Gly Thr Ile Pro Ile Tyr Leu His
      20             25             30
Pro Ala Pro Val Asn Ser Asp Ile Tyr Gln Ser Tyr Tyr Lys Gly Asn
      35             40             45
Tyr Pro Glu Val Thr Ala Ala Thr Phe Ala Cys Phe Gly Tyr Gly Trp
      50             55             60
His Ile Asp Val Gly Ile His Ala Ile His Leu Val Leu Ser Gly Ile
65             70             75             80
Phe Asp Arg Tyr Pro Lys Leu Asn Met Ile Ile Gly His Trp Gly Glu
      85             90             95
Phe Ile Pro Phe Phe Leu Glu Arg Met Asp Glu Ala Leu Phe Ala Glu
      100            105            110
His Leu Asn His Ser Val Ser Tyr Tyr Phe Lys Asn Ser Phe Tyr Ile
      115            120            125
Thr Pro Ser Gly Met Leu Thr Lys Pro Gln Phe Asp Leu Val Lys Lys
      130            135            140
Glu Val Gly Ile Asp Arg Ile Leu Tyr Ala Ala Asp Tyr Pro Tyr Ile
145            150            155            160
Glu Pro Glu Lys Leu Gly Val Phe Leu Asp Glu Leu Gly Leu Thr Asp
      165            170            175
Glu Glu Lys Glu Lys Ile Ser Tyr Thr Asn Gly Ala Lys Leu Leu Gly
      180            185            190
Leu Ser Ser Asn Asn
      195

```

(2) INFORMATION FOR SEQ ID NO:616:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 109 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:616:

```

Met Thr Glu Gln Ser Val Lys Asn Thr Pro Gln His Glu Thr Gln Ser
 1           5           10           15
Lys Pro Lys Gln Lys Thr Val Lys Leu Ile Ile Lys Arg Gln Asp Thr
           20           25           30
Ser Asp Ser Lys Pro Tyr Glu Glu Thr Phe Glu Ile Pro Tyr Arg Glu
           35           40           45
Asn Leu Asn Val Ile Ala Cys Leu Met Glu Ile Arg Arg Asn Pro Val
           50           55           60
Asn Ile Lys Gly Glu Lys Thr Thr Pro Val Val Trp Asp Ile Glu Leu
65           70           75           80
Leu Arg Arg Ser Met Trp Ser Met Phe Tyr Gly Tyr Gln Trp Ala Gly
           85           90           95
Gln Arg Gln Ser Trp Ser Leu Arg Leu Val Ser Pro Asn
           100          105

```

(2) INFORMATION FOR SEQ ID NO:617:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:617:

```

Met Pro Glu Ala His Lys Lys Val Asn Ser Asn Ser Phe Ile Glu Xaa
 1           5           10           15
Asp Asp Glu Arg Leu Val Arg Asp Phe Leu His Asp Ala Phe Phe Phe
           20           25           30
Ile Asn Ile Ala Glu Ile Ile Leu Phe Ile Glu Lys Gln
           35           40           45

```

(2) INFORMATION FOR SEQ ID NO:618:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:618:

```

Met Pro Xaa Xaa Ile Tyr Ile Asn Met Leu Ile Asp Glu Glu Asp Ala
 1             5             10             15
Ile Pro Phe Asn Ala Leu Tyr Ala Ser Asp Lys Asp Gly Leu Pro Phe
          20             25             30
Ile Glu Lys Trp Ile Lys Gln Tyr Gly Ser Gly Ser Leu Asp Gln Ser
          35             40             45
Asn Phe
          50

```

(2) INFORMATION FOR SEQ ID NO:619:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:619:

```

Met Ser Val Val Leu Pro His Gly Val Leu Phe Arg Gly Ala Ala Xaa
 1             5             10             15
Gly Val Ile Arg Arg Tyr Leu Ile Glu Xaa Lys Ser Xaa Leu Glu Xaa
          20             25             30
Val Xaa Gly Leu Pro Xaa Asn Ile Phe Tyr Gly Xaa Ser Ile Pro Thr
          35             40             45
Cys Ile Leu Val Phe Lys Lys Cys Arg Gln Gln Asp Asp Asn Val Leu
          50             55             60
Phe Ile Asp Ala Ser Asn Asp Phe Xaa Lys Gly Lys Asn Gln Asn His
          65             70             75             80
Leu Ser Asp Ala Gln Val Glu Arg Ile Ile Asp Thr Tyr Lys Arg Lys
          85             90             95
Ala Thr Ile Asp Lys Tyr Ser Tyr Ser Ala Thr Leu Gln Glu Ile Ala
          100             105             110
Asp Asn Asp Tyr Asn Leu Lys Ala Tyr Arg Ala Ile Cys
          115             120             125

```

(2) INFORMATION FOR SEQ ID NO:620:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:620:

```

Met Ser Asn Thr Gln Thr Lys Asn Val Pro Glu Leu Arg Phe Pro Gly
 1           5           10           15
Phe Glu Gly Glu Trp Glu Glu Lys Lys Leu Gly Asn Leu Thr Thr Lys
      20           25           30
Ile Gly Ser Gly Lys Thr Pro Lys Gly Gly Ser Glu Asn Tyr Thr Asn
      35           40           45
Lys Gly Ile Pro Phe Leu Arg Ser Gln Asn Ile Arg Asn Gly Lys Leu
      50           55           60
Asn Leu Asn Asp Leu Val Tyr Ile Ser Lys Asp Ile Asp Trp Met Arg
65           70           75           80
Leu Lys Asn Ser Arg Thr Tyr Tyr Gly Asp Val Pro Phe Xaa Tyr Tyr
      85           90           95
Arg Ser Ile Asn Xaa
      100

```

(2) INFORMATION FOR SEQ ID NO:621:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:621:

```

Met Arg Met Lys Arg Phe Leu Thr Ile Val Gln Ile Leu Leu Val Val
 1           5           10           15
Ile Ile Ile Ile Phe Gly Tyr Lys Ile Val Gln Thr Tyr Ile Glu Asp

```

```

                20                25                30
Lys Gln Glu Arg Ala Xaa Tyr Glu Lys Leu Gln Xaa Lys Phe Xaa Met
      35                40                45
Leu Met Xaa Lys His Gln Glu His Val Arg Pro Gln Phe Glu Ser Leu
      50                55                60
Glu Lys Ile Asn Lys Asp Ile Val Gly Trp Ile Lys Leu Ser Gly Thr
      65                70                75                80
Ser Leu Xaa Tyr Pro Val Leu Gln Gly Lys Thr Asn His Asp Tyr Leu
      85                90                95
Asn Leu Asp Phe Glu Arg Glu His Arg Arg Lys Gly Ser Ile Phe Met
      100                105                110
Asp Phe Arg Asn Glu Leu Xaa Asn Leu Asn His Asn Thr Ile Leu Tyr
      115                120                125
Gly His His Val Gly Asp Asn Thr Met Phe Asp Val Leu Glu Asp Tyr
      130                135                140
Leu Lys Gln Ser Phe Tyr Glu Lys His Lys Ile Ile Gly Phe Asp Asn
      145                150                155                160
Lys Tyr Gly Lys Tyr Gln Leu Gln Val Phe Ser Ala Tyr
      165                170

```

(2) INFORMATION FOR SEQ ID NO:622:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:622:

```

Met Asp Gly Met Asp Gln Leu Met Lys Ile Val Lys Lys Asp Phe Thr
  1                5                10                15
Gly Ile Ser Phe Leu Asn Leu Val Asp Phe Asp Ala Leu Tyr Gly His
      20                25                30
Arg Arg Glu Lys Pro Gly Tyr Ala Gln Ala Ile Lys Asp Phe Asp Asp
      35                40                45
Xaa Leu Ala Arg Ser Leu Phe Ser Asn Leu Xaa Gly Arg Arg Phe Ser
      50                55                60
Asn Tyr Tyr Lys Gln Thr Met Val Met Thr Pro Thr Ala Pro Gly Xaa
      65                70                75                80
Gly Thr Asn Thr Arg Glu Tyr Ile Pro Val Ile Ile Val Lys Ser Arg

```

85 90 95
 Xaa Leu Lys Val Xaa Gln Cys Thr
 100

(2) INFORMATION FOR SEQ ID NO:623:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:623:

Met Asp Val Phe Ser Trp Ser Asn Gly Tyr Glu Lys Arg Tyr Gly Leu
 1 5 10 15
 Phe Tyr Val Asp Phe Glu Thr Gln Glu Arg Tyr Pro Lys Lys Ser Ala
 20 25 30
 Tyr Trp Tyr Lys Glu Leu Ala Glu Thr Lys Glu Ile Lys
 35 40 45

(2) INFORMATION FOR SEQ ID NO:624:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 592 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:624:

TTCGAGCAAT ATGGATTAAA TGTTGAGAAC CCAAAAAACT TTTAAGCAAG AGGAGCGTAT 60
 AAAATGCAAT TTTCATTACT AATATATATA GTCGTAATTT GTGCGGTTAT GTATTTCTTG 120
 ATGATCAGAC CACAACAAAA ACGTGCGAAA CAGCATCGTG AGTTGATTAA TAACATTCAA 180
 TCTGGTCAAA GAATTACAAC TATTGGTGGT ATTAAAGGTA CTGTTAAAGC AGTAGATGAA 240
 ACAACTGTTG TTATTACAGT TAATGGTCAT GGTACTGAAT TAACTTTCGA AAAACCTGCT 300
 ATTAAACAAG TTGGACCCNT CATAACGAGA AGTGGTATTA AAAAGGATGA AACGAATAGC 360
 GTNTCATCCC TCCTTAAGTT ATNAGTAGNA TTGTAGGAAT NGCTGATTTN NATNCCAAAA 420
 AANGAAATTG NGANACATAA TANNNGNNA NTTTAANTCA AATNTATCTA TGA CTAGTCT 480

TNNNACTCCC AGCTCTAGNA TGTTATTNTG TATTTGGTTA ATAATNTCTC GNCAGNNNNG	540
ATTTANCTCG CGNTATAAAT TAGNATACAA GTNTTCTAAT ANCATACGAC AA	592

(2) INFORMATION FOR SEQ ID NO:625:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:625:

CGGGCAGNCT TTANAATTAT TTNAATGATG ATTAGCAATG CATATACGAT TAATTCGATT	60
ATGGNITATA TCTNNATTGA TTAANTCACT TATATTTTAC AAGTGTGTTG CTTTGGAGCG	120
TCAACGATGC TATCACATAT TACGGCATAT GAAATTTTAT CTGAAATTCG NAAAAAATTA	180
GCTCAAAAAT TAATGCGCCT CCCTTTAGGN GTAGTGAAT CTAAGAAAAT AGGTGAATTA	240
AAAAATATAT TTGNCGATAA GGTGAAACA ATAGAATTAC CTTTAGCACA TATGATTCCT	300
GAAGTTATNG GAAACTTACT TGTGGCAGCT GCTATCTTCT TATACATAAT GNTCATNGAT	360
TGGCGTATTG GATAGGTGNC TTANTAGATA ACGATACCAA TNTCAATTTN CGCTTCTAAA	420
AAAGTNATGT CTTGGATTTT AATGAGANAA TTTGCTGGAC AAANTGAAAT CCAATTTNTN	480
TTTTTNATTT GNCGNAATGG	500

(2) INFORMATION FOR SEQ ID NO:626:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:626:

GAATTCGCGA CATAAGGAAG TCTTCATAAT CCATCGTTAA TCCAAATAAG ATACCTATGG	60
TAATATACCG GGAAANANGN TAGNATTGGT CCGGNCGTTG CANTACCAAT CAGACCTTNC	120
ATAAAACCAT CTTGCATTAC TAATGTTGTA AATCCTAGCG TTGCCATTAN TGANAAGACA	180
NATCCTAAAA CTGCTNTTAN CGGTATNAGA ATTGNTCGGC AGACAATCAN TATTANGAAT	240
CATGCCATTN CACACNTCC TGTCGTATAT AATGGTGTG TCTCAATTTN CTTTTNAGAC	300
ATATCANTAT TATTTGNCAC TTNGGCCCG ANNTCTCCNC CNTNGGAGCC CATATNGATC	360

TTGGTGCATC TNGATGGANT ATCCTCGCTN ATCCATGCAA CTNAANTCAT TTGGTGCTCT 420
 CTTNCATNTA GGCNCCTGGT TA 442

(2) INFORMATION FOR SEQ ID NO:627:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 808 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:627:

ACCCTGTTGT CCCCNGGGGT CAATAGACCC CGACATACTT TNNGGCTTCT GAAAATAAAA 60
 TTTCAGGNNC GCACTTTAAA GATGGACGTC GATGTCGACT AATGTGATGA CNGCCTTTCA 120
 TCTTTTTTAAA AANTCATTAA TTTCCCTTCT TGTTTAANAC GTACATANAA GAAATACGCA 180
 TACGGTACTA ATAAAATAGT TGTATATGTT GCGTGTGTTA ATAATAATAC ACCGATTAAT 240
 TCAGGAATGA TGTTTAAGAA GTAATTTGGG TGTTTTGGTA ATTTTATATA ATCCAGATTT 300
 AATAATAGGA TGGTTAGGTA AAATGAATAA TTTTAATGTC CAAATACCAC CTAAAGTTTT 360
 AATAACCATA AATAACATGA TATAAGCAAA GATTAATATA ACTAAGCCAA TACCATTTCG 420
 AAAGCTAAAT GTATCTTTAT TAATAAATGC CTCTACACCA GCCAATACAT AAATTAAAAC 480
 GTGTGTTATT GCTAAAACT TCGAATTTTT AACGCCATAT TCAACTGCAC CGTCTGCTTT 540
 TAATTGTTTT GAGTGANTAA TACATATCTT TAAGCTGACA AGTCTGATAC AGAGAAAGAT 600
 AAGTAATATA GATAGANTCA TGATGTCCTC CGTCATTATG TCATATGTAT AAGCGTTGAT 660
 TTTGACAACA TAAAGTATTT TATAGATAAA ACTTGTCACA TACTATTAAC TATTTATTAA 720
 TTTTAGTACA TAAATATGTT TCTAAGTATG TGTTTATGTT CAGTATTTTG GATAATTTAA 780
 TAATTTTAAG GATATTAAGC GCTTACAG 808

(2) INFORMATION FOR SEQ ID NO:628:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:628:

GAATTCGTGT TCAAGGAGGT AAAAAATAAT GGGTGAAAAT AAAACAATT TGTCGATTAA 60

CGACGATCAT TCTAATGCAG CTATGACGCA TACCTCTGAC GCTATCGCAT CATCTGATTT	120
TATTATTAGA GAATTAGACT TGAATCAGGA ACCTGAAATG CAACGAGAAA GCACANNCTC	180
NCGGCAAGAT GCTTGGNCTC AGTTAAAACG AAANAAGTTA GCTGTNGTCG GTATGATAGG	240
TGGTNGTTNT CATTGNCCNA TTTGNTTTTA TCGGTCCAGC CNATAAATTA AACATGATTA	300
TGCCTGAACA AAATGTTGAA CATAGAAATC TTCCNCCAAN AAATACCTGT ATTAGACAAA	360
GTTCCCACCC CTNGCCTCCG GTGGGNANNG TTNNAGATTG GNAAAGATTC TTATTAAAGC	420
AGGNAANNNN TAGNGNGAAT ATTGGTNGGG GGTGGNCACG GGGTCCGTGT TTTTGGTAAN	480
AAAAC	485

(2) INFORMATION FOR SEQ ID NO:629:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 672 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:629:

CTACAATGAT AAATCTGATT GATCTTTGAC AAAAATAACA ACTACACTTA ATACAATACC	60
AGACGCAACA ATATTACTGA GGCTAGGAAT TTTAACTTT TCAGNTCCAG CATAAAACCA	120
TGAAATATCG AGTGCTGCAC CTATAATATA GATTCCTTGT AGTAGGAAAA TAAGATAGTA	180
ATCATCAATA AATATAGTAA TTACGACCAT ATACACCGCA AAAACTGTTA ACGCTAAAAA	240
TAATTTACTG ACAAAGATAT CCCAAAACG CTGAGACAAT TGCCGTTTGT CGTTAACAGA	300
CTTCGCGATA ACTCTATTAA AATATAACTG AACGCCAACA CTTGCAATCA TCAAAAAGTA	360
TTGCACGATA TTGAAAGAAA ATGAAACAAT ACCCACACCA CTGGGACCAA ATGCACGTGA	420
AATAATGGGT ATTGTAATCA GTGGTGTGAT CGTTCTAATC AATTGGTATA GCCCTTGATA	480
AATAATATTT TCTTTTAGTG AATCACTCTT CATTACGATC CCCNTTNCCA TCTTGGCATA	540
TTTGAACAAT AAAGACGANN CTTCTAANA ATNAAAGNG AAATGTCTTG AGTTATGACT	600
GATACTGGTA GCTTGTAAGT TAGCATCGGN CAACATNNAA CCANTTTGCN GGGANATTTT	660
TCCCAGTAAT GT	672

(2) INFORMATION FOR SEQ ID NO:630:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 974 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:630:

ATGCCTGTTT	TNGTAANTTT	GGGTTCCGAG	ACANAATCGG	ANAAATTTTT	TCCCAATAAT	60
AAGNCCCTAG	TGTTTGTTTT	AAATCCCAT	TTTTATCCAT	ATAAGATNCA	TCGCATTTAA	120
ATGTATGATG	ATTATCAAAA	ATTGTTTAAT	CCAAAGCCAT	CAAAGTTGTG	ATACAGCGCA	180
CTTAATGTCT	TATAAATTAA	TGGAGCACTA	TTACTTAAAT	CTCGTTCTTT	ATTATTAAGC	240
AGTTTATGAT	TTTCAACATT	TAGAAAAATA	AGCTTTTCTT	GTTCAATATC	CAATTCATTA	300
ATTACTTGTT	TTAAATTTTT	AAAATGCAAA	ATATTTTTC	ATAGTAACTC	ATCACTTTCC	360
CCCATCAAAT	AAGGGCTACT	TAAATTTGCA	TTATCTATTA	TTAACGAATC	GAATTTAAGT	420
CGCTTTATTT	GTGATACTAG	TGATTTAAAA	ACTGAAGGTT	TTTCAAATAA	ACAGGTAATG	480
TTCAATCCTA	ATTTACACATT	CAACATGATG	TTATGCAATT	TTAATATCAT	TCGATAAATT	540
GTTCTAATTT	CCATCAAGGA	TAAATCAAAA	ACAAAATGCA	CTTCGTAATT	ATTATGATTA	600
CTTAATTCGT	TTGGAGATAT	TTGTCTGAAA	ACACTCATAA	AAGCTTCTTC	AACAAAATAA	660
GTGCTATTGA	TGTAAAGCCG	TACTATCAAC	TTTGTAAGC	TAAAGGCTTA	TTGTCAATT	720
TCGACAATAC	TTTTTTAACA	CCTTATCTTT	CAACACCATT	AGCAGAAGGT	GCTGATATAG	780
TCTTACATTC	AAGCTACGAA	ATATATTGGG	TGGGACAATA	ACGATGGTAC	TTAGCAGGGT	840
NGTCGGNAAC	CGTCAAAAGA	TGGAATCACT	CGGCGCAACA	AGNNGGGTTG	GATTTNNCAC	900
AACAATGACT	TGGGGCAACA	CTTCCAACCA	ATAGATTGGN	TATTTGGGTG	GGTACNGTNG	960
GACTTTAAAA	CTTT					974

(2) INFORMATION FOR SEQ ID NO:631:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 622 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:631:

CAGAAAGTTT	TTAACGAAGC	TTTTCATGTG	AATAATTACG	ATATAAATGT	AACTACACCA	60
GTTATTTCTG	CACATACTGG	TCAAGGTGCG	ATTGGCCTCG	TAGTCCTTAA	GAAGTAAATT	120
TAATCTTTTC	AGTGTTAATT	NCPTCCATTT	CANTCCTTTA	TAGACTAAAT	TTATAATTAG	180
NTAGATAGAG	GAGGTAATTC	ATATGACAAA	AGAATATGCA	ACATTAGCAG	GAGGATGTNT	240
CTGGTGCATG	GTTAAACCAT	TTACATCATA	TCCAGGCATC	AAGTCAGTCG	TATCTGGTTA	300
TAGTGGCGGN	CATGTTGATA	ACCCTACTTA	TGAACAGGTA	TGTACGAATA	AAACCGGCCA	360
TGTCGAAGCA	GNACAAATTA	CGTGTGATCC	AGAGGTTACT	TCCTNTGAAA	ATATATTAGA	420
CATATATTTT	AAAACATGTG	NACCCANCTG	ATGATCAAGG	GCAATTTNNC	GATAGAGGCG	480
AAAGCTATCA	NCCAGTCATT	TTCTNTCATG	ATGAGCATCA	GAAAAAGGCT	GCTGAGTCTA	540
ANAAGCAACA	ATTAANTGAA	CAAGGTATTT	CAAAGAACCC	AGGGATTACA	CCTATNACCC	600

ATATTAAAAA TTCTATCCAG GT

622

(2) INFORMATION FOR SEQ ID NO:632:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 749 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:632:

ATTAACGTGC ACNCTATCGT TTTTATTATG AANGTTGGTA ACGCTCATGA GTTTCATC	60
TACTATNTAA TATTAATATT GATTAATCTA TGGAAAATGT TATCAATATC TNCGACAGGA	120
CAGNCAATTT TNACATCTTT TATCCAATGT ATAAAACCTA CACTCAACGA GTCATAAATA	180
TAAAATATGA GATTATCTGG GATGTCGCTG ACAATATCGA TACGGTCTCT ATTATTTGCG	240
ATATCGGTAT GCATAATTTT AATGGAGACA TTTNNTAATA CTTTATTTAAA TACAGCGTCT	300
TCTTCTTGGA ATTCTGCGAT TTCTCTCAAA TCCTCTTTAT TATTAATCGT ATCACTCATC	360
GTGTGGAATG GATGATTAAG ACGGNCACTG ATATCTCTAG CAAAGTAGTC TTTAGTCAAT	420
TGATTGAACA AATACTCTAG AAGATCATAT TTATCATAAA AATGTTTATA AAATGTTGTG	480
CGGTGTACGA GTGCATTGTC GCAAATNTGA TTGACAGTAA TCGTNTGGAA TAATTGCTGN	540
TCTAACAATT GTAGCAAGCT ACTCGACAAT GCTTTTGTG TCTTTATAAC TCGNAAATCA	600
GTCTCTNTCA TCTACATNTC TCCTNTGTGT GTAGGGNTTA ATATGACAAA AATTNNCCAA	660
TTGGATTCTT TTAAGAGGNN CGGNGGATTA GATACTTATT ANTCGAACAN ATAATCTTAC	720
ACTNGTATTT TTAAACTTA TAACGCNGG	749

(2) INFORMATION FOR SEQ ID NO:633:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1095 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:633:

CTGGTAATTT ATTTGGATGA AATATAATTC TTAAACTCT ATTGATTAAT CAAATATGTA	60
TCTATCAAAA TTCGTCTTAT TTATTCACCTC TGACATATCC AAATACGCAA AAAGACTATT	120
TCTACCTTGC ATCGATAGAA ATAGTCTTTT TATACTTAAT TGGTTTAATT TCACATAAAA	180

TTTTATACTT	TTTTAAAAAT	GGGATGAAAT	ATATTTTCCT	GAAACATGTA	ANTCATGTTC	240
GNTACAAATT	GATAAAATAT	GATTAAGTGT	TGGGTGCAAA	TGACATTTTC	TCAAAAAGCG	300
CTTCACTATC	AATTGGGTAC	TTGTGTGTGA	ATTTTCAGCAA	AGTCGCTGCG	ATAAATATTN	360
GNNCAACTTA	AATTGGGCAA	NAACTTTTAT	TACGGNGCGC	CAGNTGGATA	ATGCATCAAN	420
GGTTTCAACC	ACATTTTCAA	CGCTTTGATA	TNGCTGAATT	AACTTAATAG	CCCGNTTCT	480
CACCCAATTC	CTTTAACACC	TGCATATCCA	TCTGCTGTAT	CACCCATAAA	CGCTTTAATA	540
TCGATTAGTT	GTTGTGGTTC	AAGGGCATAT	TCTTCGTAA	AACGATGTAA	TGTATATCTA	600
TTATAAATGT	TAAAACCTTT	TTTAATTAGC	CAGACTTCAA	CATGTGCATT	AATACATTGC	660
AGTAAATCTT	TGTCGCCCCG	AATAATATAG	ACATCGNNAT	CAGTTGAATA	TTGTTGTGCT	720
AATGTACCTA	TAACATCATC	CGCTTCATAG	TTTTTAACGC	CAATATTTAC	AAAGCCAAAT	780
TGCTCTGAAA	TTTCTTTAAC	ATAATCAAAT	TGTGGTATCA	ATTCTTCTGG	TGGTGCAGAA	840
CGATTTTGGT	TATAACCATC	AAAACATATC	ATTTCTAAAA	GTGATTGTC	CCATATCCCA	900
ACATACAGGT	ACATGTGTAG	GGCGTATTTT	ATGTATTGGC	CGAAAAGATA	TGACGCACAA	960
ATCCTNGTAT	TCCATTTGTA	GGGTACACCT	TGGTGAATTG	GTCATAAATT	GGTNATGGAG	1020
GACTNGTGGC	ATAGAAATGT	CTTAATTATA	GGGCCATACA	ACTTCAAGTN	ATATTNATTA	1080
GGGATTTAAA	CGTCC					1095

(2) INFORMATION FOR SEQ ID NO:634:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 635 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:

GGCGATCGGT	ATCCATATTT	AATATTTGTA	TCTCATCCAA	CATCTTAATA	TCTCTCCAAT	60
CTATGTATCT	TTAATATCTT	NACATTACCC	TAAATTNTCC	AACAAACTCA	ATTAATGCGA	120
ATTATCGCTT	TCAATANNAA	ATATTCANTA	AATCATTNAA	GATATTGAGT	TCCAATACTA	180
TTTTCACTTT	TCATTAATTT	TAGTCAAAAA	AATACCCAAC	CAAAAATGAA	TTAAATCATT	240
CTTAGTTGGT	TTATATATTA	ATATCTATTC	TGATTTTTC	TCTTCATCAG	ACTGTCCGAT	300
AGTAGGTCTC	GCTTCATTAA	ATTCATAGTT	TAATATCACC	CAAATAATTT	GGTGGTTATC	360
GATTTCTGAA	ACAACCCAGC	GATCATAAGT	TGNTTCCACG	TAATCANCTT	GNTGGTAAAT	420
TGGTATTACG	AGATNGGTAA	CCATCCACCC	TATCGNATCA	ACTATCCTCA	AGAGTCAACA	480
AAATNCTTAT	ACCGAACTCT	TCAAGTTAAA	TCATCCAATA	GTAATCTGNC	ATNNTACTTG	540
GAATGCTTNA	TTATCAATTN	NTAACGATAT	CANTCACTTT	CATCATCAAT	CAAAATNCAA	600
TCAAGAATTT	TCTTCCAACC	GATTTCTTCC	TTAAA			635

(2) INFORMATION FOR SEQ ID NO:635:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 760 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:635:

```

CTATTTTATA ATAGGAGGGA ATNTCAAATG ATAGACNACT TTATGCAGGT CCTTAAATTA      60
ATTAAAGAGA AACGTACCAA TAATGTAGTT AAAAAATCTG ATTGGGATAA AGGTGATCTA      120
TATAAACTT TAGNCCATGA TAAGTTACCC AAGCAGTTAA AAGTGCATAT AAAAGAAGAT      180
AAATATTTCAG NTGTAGGGAA GGTTGCTACT GGGAACATA GTAAAGNTCC TTGGATTNCA      240
ATATATCCCC CGCGATGAGA ATATAACAAA AGAAACAAAG GATGGATATT ATNTGGTATA      300
TCTTTCTCAT CCGGAAGGAG AAGGCATATA CTTATCTTTG ANTCAAGGAT GGTCAAAGAT      360
AAGTGATATG TNTCCGCGGG ATAAAAATGC TGCAAAACAA AGAGCATTAA CTTTATCTTC      420
CGAACTCAAT AAATATATTA CATCAAATGA ATTTAATACT GGAAGATTTT ATTACGCAGA      480
AAATAAAGAT TCATCTTATG ATTTAAAAAA TGATTATCCA TCAGGATATT CTCATGGATC      540
AATAAGATNC AAATATTATG ATTNGAATGA AGGATNCACA GAAGAAGATA TGCTAGAGGA      600
TTTAANGAAA TNNNTTNCAG AACTTATTTA NTGAATTAGC TNCAAAAGTT ACAAAAAACA      660
TCCTATTGAT AGCTTGGGTC AATAGCATAG ACGAANTACA AGGAAGACAG NGAAATTGGA      720
GAAACTTAGA NCAGCACAAN NAGATAAGAC ACCANGGCNC      760

```

(2) INFORMATION FOR SEQ ID NO:636:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 704 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:636:

```

CTTATTGTTT TTAAGTTATC ACTTAAAAAT CGGTTGGCAA ATTCGTTGTG ACGCTTGTCC      60
ATCTTCTAAT GAACAGAATT TGTGATAAAA TACCGCGCGT GCTTCAATAT ACTCATNTGN      120
AGTCTCATCG ATNTGTTTTA ATGCATCAAT GAGTGCTGTG TGATTNACAA CAATTGGCCC      180
TGGCAACTCT TTTTATAAAT CCATGTAAAA CCCTCTAAGC TCATCGCCAT ATTTATCTAA      240
GTCATATGCA TAGAAAAATGT GCGGACGCTT TAATACACCG AAGTCGAACA TGACAGATGA      300
GTAGTCGGTA ACTAACGCAT CGCTGATTAN GTATAANTCC CGNAAAAAA TGNGGATGNC      360
TACATAATCT GANNCGTCNT TCNCGNAANA TCATCATGNT CATCAAGACG TGTCACNAGC      420

```

TAAATNATAC ATGCGTNATA NAATNACATA ATCATCATCC ANCGCTGGAC GCAAATGCTT	480
CTATATCAAA GTTAACATTA AATTGATATG AACCTTCNCG ANTCGCTTCA TCGTCACGCC	540
AAGTTGGCGC GTACATAATC ACTTTTTTAT CTAATGGAAT ANTTAATCTT GTCTTAATAC	600
CATTAATATA NTCAGTATCA TTGCGTTTAT GTGATAATTT ATCATTTCTT GGATAACCTG	660
TTTCCAAAAT CTTATCTCGA CTAACATGAA ATGCATGTTG AAAG	704

(2) INFORMATION FOR SEQ ID NO:637:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:637:

AAGATAATTT GGTACCCAAT TAATGCCTGN CCAAAGATGT AAATACCTTC CTAATTCNNG	60
GACCCCCATT TGTCCGGAAT AGTTTGCCCA CCCTACCCNA TTGATCCAAT AATACCTGCG	120
ATAATATTGC CTAAAATACC ACCTGGGATA TCTTTACCCA TAATAGCACC AGCAGCCCAT	180
CCAATTAAAGC CACCGACAAT TAACATTCCA ATAAATCCAA ACATAATTTT CAGTCTCCTT	240
TTTCTATTTA TTTTGCGTTA TTCTAAGTAG TACCCCTTAT TTACAATTCT AAAACAAATT	300
CAAATTATTT TTATCCAAAT ATTTTAAAAA GTAGTAATTG AATATCAATT TTATTCAATG	360
TAGCTATCGT TATTTAAAGT CTCTGTACTG GCAATATCAT ATACATTTAC ATTATTTTTT	420
CTGCC	425

(2) INFORMATION FOR SEQ ID NO:638:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 529 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:638:

CTTCATAAAG TTTTAAAAAT ATTCTGTTTT ATCACCTATT ATTAGTGGAA AAGTACAATT	60
GCAATTGTAT ATAGTTTGCA TAACGCTTCA AAAGTAATTT CTTTTTTGTT TAGTTCAAAA	120
AAATTTAGAG GTGATGTTAT ATGAATAACG GTTTTTTCAA TAGCGACTTT GATTCAATTT	180
TTCGAAGAAT GATGCAAGAT ATGCAAGGTT CAAATCAAGT CGGTAACAAA AAGTACTATA	240

TTAATGGTAA AGAAGTTTCA CCTGAAGAAC TAGCGCAACT CACACAACAA GGTAGCAATC	300
AATCTGCTGA ACAAAGTGCG CAAGCTTTTT CAACAAAGCA GCACAAAGAC AACAAAGGCA	360
ACAAGGTGGC AACGGCAATT ATTTAGAACA AATTGGTCGT AACCTTACGC AAGAAGCACC	420
TGACGGTTTA TTAGATCCAG TCATGGTCGT GATAAAGAAA TTCAAGAACT GCTGAAGTCT	480
TAAGTAGACG ACTAAAACAA TCCTATATAG TGGAGAGCTG GTGTGGTAT	529

(2) INFORMATION FOR SEQ ID NO:639:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:639:

CGAAAAGTTT AAAAAAGTAC GTACATCTTT ATTACCTTTG ACTTTCATA AAATGGAGTC	60
TGTTGATAAT GTTTGACCGT TCCACNTTAT CACTAAACNC CACATTCCCTA CCATATGCTT	120
TTCCAACATA GTCATGTGCA TCAGTTTGTA TCGCGACACG CCATTCCATA AATTTTATTG	180
TTGGCGCAAC AAATACTTTA ACAGGGTGAT GCTCTTGTTG AATTGCTTTT AAAGCTTGTT	240
GCTTAATTAC GGCTCTCATT TTAAAACGAA TCATGTAATA AATGATTAGT AAAGCGATTA	300
TAGGAAAGAA GACTGCAAAT GGATGCAAGC CTATAACCCA TAATACAATA CCAATACAAA	360
GAAGTGTGAA AATAATAGGG TCAAATGTGG TTAATCACAC TTNAATTGAA TCCATTTGTT	420
TGTGATAGGT CTAAGCGCTT GTGTACCATA AGAATTGAAT ATATCTACAA AGACATGTAA	480
AAATACTGCG AGCTGAGCCC ACATCCATAC ATGAAAG	517

(2) INFORMATION FOR SEQ ID NO:640:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 648 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:640:

TTATCAGTNT CTTCTATTAT ATTGTCANCT TGTGTTGATG ATATGTANGT GTTGATACGC	60
TCCTNACACA TAATGTNCCC TTTTGGAAG CATTTGNATG TCTTCTTCT ATTGTNTTNN	120
TGGNTTTTNN AANTGNAGAT AAAATANAAG TGTNTTGTA CAATATGTTT GTGAAAATGC	180

CAATTTCTTT ATCTCAAAAA TCAAGANTTT TGTGATATAC TATTTTTCAT AGTCTTGAGT	240
TATAGATGAT ACTGCTAGCC TAAATATAAC CAACATCGGC ATGCACATCT TAGANTTTAA	300
GCTAGTGGCA GCTTATAACT TAAGGCTCTT TATTATTGTC ATACAAGATG TATATACATA	360
AATGGAAGGA TGATATTATG ACATCAATTA AAACAATTAC ACCCAAAGAT TTTATATTTA	420
GAGTTTATC AGGTGTCGCC ATAGGTATTG TTGCGGGTTT AGNTCCTAAT GCGATACTTG	480
GAGAAATTTT TAAATACTTT ATGGATTATC ATCCGATTTT TAAAACGTTA TTAGGCGTTG	540
TCGGTGCAAT TCAATTTACA GTACCTGCTT TGATTGGTGC ATTGGGTTGC CATGAAATTT	600
GACCTATCGC CATTAGCAAT TGCTGTTGTG GCAAGTGCAG CAGGATAT	648

(2) INFORMATION FOR SEQ ID NO:641:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 445 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:641:

TTTGGTCCAG AAATTGAAAC ATTTACACAA GTAGTAGAAG CAATTTATGA TGAAGAAGGT	60
AACAGCTTAG ACGCGGCGCG CCATCCATTA CAAATCGTTC AAATTAAAGT GGATCGCCCG	120
ATATATCCAA ACAACATGAT GAGAAAGGAA ATTGGCTAAT GAAAGCTACT ACAATCATTG	180
GCATAGCTGG TGGATCTGGC TCAGGAAAAA CAACTGTAAC TAACGAAATT ATGAAAAACT	240
TAGAAGGTCA TAGTGTGCT TACTTGCTC AAGATTACTA TTATAAAGNA TCAAAAAGCA	300
CTTGACTTTC GACCGAGCGC CTAGAAACCA ATTATTGANC CATCCATTTG CATTCGGATA	360
ATTGATTTTA TTAATTGGAA AATCTTTAAN GACTTGAAAA ATGGNTAAAG CAGGNNGGAN	420
GTACCCNCAT TTTGATTATG CTAGG	445

(2) INFORMATION FOR SEQ ID NO:642:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:642:

GATATTCGTC TCCGNNACCG GNCCTTNATG NAGATATGNC CGTTNTTGA TGCCGTATTA	60
--	----

AGTTCTGATA CAACAACTTT ACGCATCATC AAGCAATATG AGCAGGCAGT ACNAGCTTAT	120
GCGGATGACC AAAGTGATAA ATTGTTCAAG CGAATGATAG ATGCGCAAGA TGCTATGGAT	180
CAACATGATG CTTGGGACTA TAACGCTGAA ATTAAAACAA TCCTCTCAA ACTAGGTATA	240
CATGATACTA CTAAATACAT TAAAGAATTA TCCGGCGGAC AACAAAAACG TGTGTNCTT	300
GCGTAANACA ATTAATAGGA ACAAACCAGA TTTATTGGTT ATTAGATGGA ACCNACGGAA	360
CCANNTAGGA CTTCGAATCA ATCAGCTGGT GGGTCAANTT ATGTGAAGCA ATNTCCNCAA	420
TNCAGG	426

(2) INFORMATION FOR SEQ ID NO:643:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:643:

CTACCGCGTG CGCTGTAAAC CCAATNCGTC ANCTTTTTC AACTTAGGTG ANATGAAATG	60
TGGTCCCNCG ACGATCGTCA GTAACCAAAT AACAGGCAGT CATTGGATTA TGTTTANCGA	120
AGTAAGTAAA TAAATATTTT GAATTACCTA TATATTGATG ATGATCACCG ATAAAAACGA	180
TGTGATCTTT TAAAACGTTT GGTGCTTCG TATACAGGCC GAAGTTTGT AATTGTTTGT	240
TATCAGCACG TTGCTTTGCT ATTTTATATA ACCATTTAGG TAGCATAAAC TTGGTAGAAN	300
ACAACCAATT ATCTGNCGAA TTAAGTTGTT CTGAATCCTC GATAAAAAGG TTGCGAAAAG	360
GTATAGGATG ATGATCAATA GAAGCCATTT TATTCAAATA AAACGTAGAC ATCATAG	417

(2) INFORMATION FOR SEQ ID NO:644:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:644:

CTACGTTGCC CCATCGTTTT CGCACGAATC GTCTTACCAA ATGCATCTTT AGTTATCTCT	60
CCATCATANA AATCNAACAG ATGTTGAATT GTGTTATTAT GCGCCATTTT AATAGCTGCT	120
TCAACATCTT NAATTGTAAT ATTATTACCT AAATCAATAN CCTNCAGCAA ATTGATTAAT	180

ACTGATTCCG CTTTCTCTAC GTTTTCTATT TGTGGNACCT TTAACGGCAA CTTCTTGTCC	240
TCTTGNATGG ATGACAACAT CGAAACTCTC TNCAATTGCT TTTAAATGTT CATCATNATT	300
TCCAATTAAA GCTTGAGATG GGNTCANATC GTCTATNTGT NTAATTCCAG GCATACACGC	360
GCTCCNNNNC ATATATCATT TATATNCANN CTNTGATGCT NNAATNTCTA CTTANTNATA	420
TCAAGCAATT GA	432

(2) INFORMATION FOR SEQ ID NO:645:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:645:

CAAGAAGAAA TGAAATATAA ACGTCCGTCA GGTGTAGACT TCGGTCCTGT AGATTNTGTA	60
AAATATGCAG AATCATTTGG CGCGAAAGGT TTACGAGTTA CTAATCAAGA AGAATTAGAA	120
GCGGCAATTA AAGAGGGCTA TGAAACAGAT GGTCCAGTAT TAATTGATAT ACCTGTAAAT	180
TACAAAGATA ATATCAAAC TTCAACAAAT ATGTTACCTG ACGTATTTAA CTAAATAAAA	240
GATAAATGTT AAAGAGGAGT GGGAGATTTT ATGACTAATG TTTTATNCCA ACATGGTACA	300
TTAGGCACAT TAATGGCAGG ATTATTAAAA GGAAGTGCAT CAATAAATGA ATTATTGCAA	360
CATGGNGACT TAGGTATCGC TACACTAACA GGCTNCAAAC GGGTGAGGTA ATCTTTTTTTA	420
GATGGAAAAG CTTACCATGC AAATGACATA AAGATTTGGT AGAATTAAAG GTGACGAGTT	480
ACACCATATG CAACTGTAC TAATTTGGNG CAGGNTCAAA GCTTATGAAC GAAAGATAAT	540
CTTCCAGAGC AGGTT	555

(2) INFORMATION FOR SEQ ID NO:646:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:646:

CTAGTACATT CCAAGGAATG GAACTGATTT CTAAATTAGA TTCNAGAACC CAAGTGATGA	60
CGAACGACAA GATTACACTA GCATTTGATA TGAATAAGTG TCACTTTTGG GATGAAAANA	120

CAGGAAATCG	TNTCGTCTAA	GGGGGAGTAT	TCATGTCTAA	AATTTTAAAA	TGTATCACGT	180
TAGCCGNGGT	AATGTTATTA	ATCGTAACTG	CATGTGGCCC	NAATCGCTCG	NAAGAAGATA	240
TTGNTANAGC	ATTGANTANA	GATAATNCTN	ANGACAAGNC	TAACCAACTT	ACGATGTGGG	300
NGGGATGGCG	ACAAAGCAAA	TGGCGTTTTT	NTNAAAAAAT	TACGGCATCA	ATCATACTAA	360
AAAAACTGGC	ATCAANGTAA	AGCTTGGTNA	NTATTGNTCA	AAATNATCCA	NCTAGNANAC	420
ATTCNGCTA	GACGCTCCCG	CAGGAAAAGG	GCCCAGNTAT	CTTNTTCTT	TAGCAACATG	480
ATAATACTGN	NANGTCCNAT	CT				502

(2) INFORMATION FOR SEQ ID NO:647:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:647:

GAATTCCTAA	AATTCCTAA	TTACAAGGAG	GAAACACCAT	GGCTAAAAAA	ATTGTTTCTG	60
ATTTAGATCT	TAAAGGTAAA	ACAGTCCTAG	TACGTGCTGA	TTTAAACGTA	CCTTTAAAAG	120
ACGGTGAAAT	TACTAATGAC	AACCGTATCG	NTCAAGCTTT	ACCTACAATT	CAATACATCA	180
TCGAACAAGG	TGGTAAAATC	GTAATATTN	CACATTTAGG	TAAAGTGAAA	GAAGAAAGTG	240
ATAAAGCAAA	ATTAACTTTA	CGTCCAGTTG	CTTGAAGACT	TATCT		285

(2) INFORMATION FOR SEQ ID NO:648:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:648:

ATTGACCCAT	TCGTTAATNA	ATCGNNNATN	AGNANATGTT	CCTNATAANT	NTCATGATAA	60
TACCNAANCA	CATCNAATAA	TGTTAGTTTT	CCNACCGCCT	CTTATGCCNA	ANCCNAATAA	120
TAANATANAC	NGGCGCNATG	TACTGTAGTA	ATGTTGCAAT	CGCAGCATTA	CCTGTATTAA	180
TAGATGCCAT	ATAAGCATAT	TGTACAACATA	ACATGCCCCAG	TATACTGAAG	ATAAGTAANT	240
TGCCTAACAT	ACGTCGATCN	TGGAATACGC	TAAATANTGA	ACGNNTGGGT	TGCATCATTC	300

TGTACATAAT	ACAGTNAGNA	AACACCACTG	ACTACAAGTC	GACCAGTGAC	GTNCCAATCG	360
ACATTAATAT	TCTTATATGT	GNACAAGAAA	GCAGANACAG	TNCCACCTAA	TCCCCATAAA	420
CAAGCACCGA	CAATGGCAAG	TATAATTCCT	TTTAAACGCA	AAGCTGAATG	ATTATTCGCC	480
AAGTATCTCA	CCCCTTTAAA	ACTTAACACC	AACAACATAA	AATATGTCGG	TGTATGATAA	540
TGATTTAATT	CATTAGGAAT	TCCG				564

(2) INFORMATION FOR SEQ ID NO:649:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:649:

TATAGAACCT	ACTATATCTT	TGTCTAATGC	CATGTTATTC	TCCTNCGATT	CTTGTATTCT	60
TTATTATTAT	AACATGTGTG	AGTCATTCTA	TCATTACAAC	TTATATGAGG	TCGAAACTGT	120
GACGATAATA	TGATATAATT	CTTCCGCTAG	AATATCGAAT	GAAAAAAGG	AGAAAATGCA	180
TGTTACAAGT	AACATGATGTG	AGTTTACGTN	GTGGAGATCG	NAAACTATTT	GAAGATGTAA	240
ATATTAAATT	TACAGAAGGT	AATTGTTATG	GATTAATTGG	TGCGAATGGT	GCAGGTAAAT	300
CAACATTCTT	ANNAATATTA	TCTGGTGAAT	TAGATTCTCA	AACAGGACAA	TGNTTCANTA	360
GGGTAAAAAT	GAACGNCTAG	CTGGNNTTTA	AAACAGGACC	ACTATGCTTA	TGAAGATGAA	420
CGCGTGCTTG	GATGTTGGTA	ATTAAAGGGT	CACGAACCGT	CTTTA		465

(2) INFORMATION FOR SEQ ID NO:650:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:650:

CAATAACTAG	GGTGGTACCA	CGACGATCTC	GTCCCTTGTA	TAGGGGCGGG	ATTTTTTGT	60
TTTTTCAGAC	ATAAATGTTT	GTTGGTGTCA	TATATTCCTT	GTTTATTGTT	AATAGGTTTA	120
ATGTTAAAC	GATGATTGTT	GTTCAATTTT	TTAACGAGGT	CAGATAAAAG	TATTTATAAA	180
GCAAATAGGA	GGGTTTAAAC	TGGAACAAAT	TAATATTCAA	TTCCAGATG	GTAATAAAAA	240

GGCGTTTGAT AAAGGTACTA CTACTGAAGA TATAGCACAA TCAATTAGTC CTGGATTACG	300
TAAAAAAGCT GTTGNCGGCA AAATTTAACG GGCAACTTGT AGATTTAACT AAACCGCTTG	360
AAACTGATGG ATCAAATTGA AATTGTGACA CCAGGTAGTG AAGAAGCGTT AGAGGTATTA	420
CGTCATTCTA CTGNACATTT AATGGCACAC GCGATTAAAA GGTATATGG TAATGTTAAN	480
TTTGGGNGTA GGTCCCTGTA ATAGAAAGTG GNTTCTTCTA TGACTTCGNA TGACCAA	538

(2) INFORMATION FOR SEQ ID NO:651:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:651:

CCGTCTATTA TCAACTCGTC TAAAGGNCAA GTGTTTANTG AAGNTTGAGN GTATTACACA	60
ANCATCAANT CAGCCGATTT GAAANCACAA GATTAAAANG TCAATATGAT GGCATNANTN	120
NCCACTGTGN ANTTNANACA TCGAACNCCC CCTANTTANC GGGTAAAANC ATNNNTAACC	180
AAGATAGTGA TATCAGNTAT ATCACACAGN NTTTTAAATA CAAANTCNAC GTTCCAAGAG	240
ACGCATGATA ANTCATCANA CATGATTGAT AAGGATGATG TTCATGNTGA AACGAAAGAT	300
GTTGGATGGC AACACATCTT NTGGANNATG ANCANACNTC AATANNTTAA CNTCAATTTT	360
CGAGAAACAT TTAAGTGACG AAAAATCAGA ACAATTATTG CATCATNTGC GNTCGGGNNT	420
AACTTTGCTT GATTCAATGA GAATAGTTAG TGCCGGAGNN AAACAGTGAC AAACAN	476

(2) INFORMATION FOR SEQ ID NO:652:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:652:

GACTTCCTNA AGGCAGTAAT GGCAGCAACA TTGGGGAGTT AATCACTAAA TGGAACGATA	60
TGAACATGAT GTGTCTGATG ATATAAGTGT CATGTACAGA CACCTCATAT TGGTATTAAN	120
GGAGAAATGA ATATGAACGA NTCAGGAGAT AACAACTCA GTAAATCTTC TTTAATTGGN	180
CTAGTTATAG GANCCATGAT TGGTGGCGGT GCGNACAATA TAATGTCTGA TATGGGCGGT	240

AAAGCCGGTG GATTAGCCAT TATTATTGGG TGGATTATTA CAGCTATAGG AATGATNNCA	300
TTAGCGCTCG TATCACAAAA TTTANCCAAT GAACGGCCGG AGCTAGACGG GGGTATTTAT	360
AGCTATGCTC AAGCAGGATT TGGCGATTNT GTAGGATTNA TCAAGCGCTT GGAGATATTG	420
GNTCTCAAGC GTCTTTAGGC AATGTTGGCT ATGCAACACT ATTGATGTCA AGCAAGTAGG	480
TAACCTTCTC CCGATTNTTA AAGGAGGCAA CACATTACCA GTATTATTGT CGCTCGTTAC	540
TACTCT	546

(2) INFORMATION FOR SEQ ID NO:653:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:653:

TATCNGCANT AACAGTATCC GCCATCTAAG GCATNNCGAA TAAATTGTTT GTNGGGGGGA	60
ATAAATATAT CCTNCCATAT CCTCATCTTC AGGTCTTAAG AATCNCAAAN CCTTTTTTAT	120
CTTGACNTAA CGTTCCTTT ATCAANTNTG ANTGACCTTN TGNACTATGC TTTNTTTGAT	180
ATCTGNCTGN TTTNGTACGT TCAATTAATC CNGATNGTTC TAATTCTACG ANCACCTNAA	240
TTAAATCTCT AAATGAGTCG GCACTACTTA AACCTAATGC ATCTTGAAAA TCTGACACTG	300
ACATAGGTTT ATATTGAGT TGATTAATAA TCTCTTCTAT TGATTGCTTT AAATTCATTA	360
NGCCCTCCT TTCTAANGTT AAAATCTCTT TTTAG	395

(2) INFORMATION FOR SEQ ID NO:654:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 616 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:654:

TGAGGTGAGC AGAGATGAAC TTTTTTGATA TCCATAANGA TNCCGANCAA AGGCATTCCA	60
TTATCGGTAC AACGTAAATT ATGGCTTAGA AACTTCATNC AAGCTTCCTT TGTAGTGTG	120
CTTTGTTTAT ATGGCTATGT ATTTAATTCG AAACAACCTT AAGGCGGNCC ANCCGTTTTT	180
ANAAGAGGAA ATTGGATTAT CTACATTAGA ACTTGGTTAT ATCGGATTAG CAGTTAGTAT	240

CACGTACGGT	TTAGGGAAAA	CATTACTTGG	ATATTTNGTC	GATGGACGTA	ACACAAAACG	300
TATTATCTCG	TNCTTACTTA	TCCTATCTGC	GATTACAGTT	TTAATTATGG	GATTTGGTTT	360
TAAGTTACTT	TGGTTCTTGT	AATGGGATTA	TTAATTGGTA	CTTTGGGGGA	CTTAACGGGG	420
TGTTCCAATC	AAGNTGGGTG	GGACCTGCAA	AGTTATTCCA	ACGANTTCAA	GGATGGGCGC	480
CAAGGACGAA	ACGGTGGGCC	GATACTTTAG	GATTTTGGGG	NATACANCAC	ATAAATATCG	540
GNNGGNNGCC	AATTGAGGTG	GCGGTNGGNA	CTTTNGGGGG	GGGTTAANGT	TTTCNTCCC	600
CAGGAAATTG	TTATAG					616

(2) INFORMATION FOR SEQ ID NO:655:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:655:

CAAAATTATT	TACNGANANT	GATTTGAANG	ATGATGAAGT	CATTTCATA	TTTGTTCG	60
ATAAGTCAAT	AGAATAAGTG	TTGCTGGTGT	AAGGTACACG	GTGCTGTNTG	CTAACTTCGC	120
TTTGAACCTA	ACAATAATTC	AAGGGGGTGG	TATGTCAAAC	GGTGCCGTTT	TTTGNGNCAT	180
ATTTTTAAAA	CAAGCAACAT	GCAACACGTA	CTTTAAGGAA	GTCAAAATTT	ATCATTTAGG	240
AGAGATGGAT	ATGAAAATCG	NAGNATTATT	TCCAGAAGNA	GGAGAAGGTC	AAGAAAATCA	300
ATTANTTAAT	ACTNAAAAAG	NAATAGGATT	AAAAACATTT	TNAGAGGAAA	GAGGGACATG	360
ANTNCCACNA	TTTTAGCAGG	TTATGGGGGA	AGACNTAGAT	AAACATTTNC	CACGATCTTG	420
GT						422

(2) INFORMATION FOR SEQ ID NO:656:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 719 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:656:

TTTGATAGGG	GTACAGCATT	AAAAGAAATT	GATTGCACCA	TTTTTGGTAT	TCATCCAAGG	60
AAGANNCGTT	AGTTATTGGA	GATAGCGACA	ATGATAAGAC	CAATGTTTTG	AATTTGTTCAT	120

TAATACAAGT	TGCTATGAAA	AATGCACGCC	CTGAAATCCA	AGCATTAACT	TCAGATGTAA	180
CGGCATACAC	GAATGAAGAG	GATGGCGCAC	CAAAATATTT	AGCAAAGCAT	TTTTTAGCTG	240
ATTAATAAAA	TAGGTAGTTA	TTTATTATTT	AATTTACAAT	AGTTGATGAG	TAATGTACAA	300
AGANCAGTAA	AGTTATTTTC	TATAAGAAAA	TGCTTTACCT	GCTCCTTTGT	ATGCTAGTAA	360
TCCAGATACT	AGTGTTACTT	CTTCTTTTTT	GTCTTTCTTC	TCCATATATG	GAATGAAGNA	420
AATCACCAGA	ATAGGGCACA	GAGTATAGCT	ACAATTGAAC	CGTATGTCAT	ATTAGCATCA	480
CCTTTTATAT	GGTTTATGCA	TTTAAGTATA	CTATAACAAC	TACCGTTATT	TTAAGTAGGG	540
GTGTATTTGC	GTTAGAGCCC	CTAACAACTC	CAAAATCGCA	TTTGTGATTT	TGGGATAATC	600
AAACATTTCA	TTCCATAAGT	AAGATATGTT	TCACTTTATA	TGAGTTTTTT	ACATTACAT	660
TCTGTAGTGG	TTGTAAGAAA	ATTTTTTCTT	TCTCTTAGGC	AGTAATAGGC	AATTTACCG	719

(2) INFORMATION FOR SEQ ID NO:657:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 650 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:657:

CAATTCACGT	GAGACTTCCA	AATGATTTGC	CTCAAAATTT	TTCAAAGTGT	CGTCGTAAAA	60
ACTGTCTAGT	AAATACTAAT	AGTATGTCGT	AGACCTATGA	CAAATCTGAA	TTATGACGAA	120
GATCAATCAA	GAAAAACAGC	ACCAAGATCA	TTTCAATNGG	CACGAGTACC	TTACTGCTGT	180
TCTTTATTTA	TTACATTTCA	ATCTTAATAA	TGACCGTAAT	ATCACGTGAT	TGTCATTTCC	240
TTGTNATCAT	ACCTAAAACA	ACAATTAATC	CTGTGCGTGT	CGCTGACTTT	CTTTAGTATG	300
AATTAAATCA	GTAATAAAGC	GATTGACTGG	CGCTTCAATA	TGACGTTGTT	TACCCAATGT	360
TGCAACTGCG	CCATTAATAT	AATCAATTTT	AGTTTTTCTA	TTATTAACAA	TTAAATCTTG	420
ATACATGGAT	GGATAATGCG	CACCAACTTT	TTCATTTAAA	TCAACTAAAT	ATTCAAATAC	480
TTCATCAACA	TTTAAATGAA	CATTATCAAT	CGGCGGTTAC	ATGCACTATT	TCTTGCGGTT	540
AATTTATTAA	TCAAAACACT	TCGGATAACT	ACTTTCAATC	AGGGGATGCC	ATATTACACT	600
CCAACACTGG	TGCTTTAATG	CATTTGGCCG	GACCAATAAC	ACAAATCTTT		650

(2) INFORMATION FOR SEQ ID NO:658:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:658:

GAATTCATT GAGATTCATC TTCATTAGCA CGTTTTAACA TAGTATTNTG GAAAATTTTCG	60
TATACCTCTT CTGAAACATT AAAACGTTTT TCAGGATCTA AACCGTAATT TTCGAATGTT	120
AATTTTCTTT CAACTTCACC TAAAGGTGCC CCATGAACAC CATTAGTTCC TGCTTTATTC	180
GGTGAACCAA ATCCGATTGT TGTTTTAACT TCAATAATCG NTGGNCCTTC TTGAGATTTA	240
GCTGTAGTAA TCGCTTTATC AATTTCCTTCT AAATCATTAC CATCTTTTAA CTAGTAAGTA	300
ATTCCAACCA TATGCTTCAA AACGAGCTTN TGTGTTTTCA GAAAAAGCTT TGTTTAATTC	360
GCCATCTAAT GAAATATCAT NTGAATCGTA TAAACAACCT AATTACTTA ATTTATTATG	420
TCCAGCAAAT GAAGNTGGTT CATGCGATAT ACCTCCATT AAAATCAACC GNCAGAAGCT	480
TAATACATAT GTGTAATGGA TCTTACAAAA ATTATATCCC CCTTTAATTA AATTTCCCG	540
GTAGGTGGAT CTCCTGNTA AAGGTTAATC CCACTG	576

(2) INFORMATION FOR SEQ ID NO:659:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 611 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:659:

TTAATCCTGG TNGGCNTTGT CCTNTCNATG NCTCTAGTTG TTTAATTGTA TAAACCCGCT	60
TCGCTGTCNC TCCATATGCT ACTTGNAAT GAAGNCAGTA CATGAAACAT TTGATACAAT	120
NCCATGACAA TAGTTGCCCT TGCAGCAGGC GTATTTTCCA ATGAATCTNC TAATTTTAGT	180
GCTGCTTCAT ACGTNTCAAA TGATTTATTT CTATTATCTT CGAACCATTG CTCAATTACA	240
TGTTTCACTG AAGCAATTGT TTNCATGATC ATACCAATCT GTTTGAAAAG CGTTACATTC	300
CCCGAAANAT GCATTTCTTT TGTCATCAAT CAATTCGATA AACANACAAT CNCGATGCGT	360
TAAAGTGACT TTCGGTGTTA CAATTTGTGA CTTNAATGGC TCACTATATT TATNNAAATG	420
CAAAGCTGTC AACTTCATCA AATCATCCTC TATACAACCT ATTTNCTCTG TAATTTACCC	480
GTTGATGTAG AAGGTAAAGT ATCAACCTTT TCAAAGTGTT TCGGTACTTT ATATTTTCGCT	540
AAATGTTTTG ATAAATATGC AATCAATTGT GCCTTTGAAA TGTCACCTTC ACTGACAAAA	600
TATAATTTAG G	611

(2) INFORMATION FOR SEQ ID NO:660:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:660:

GAATTCCTTT CTGCCTCAAT GCGTGTGTA GGGATACTGT TAGTAAGTGC TTTAATCACG	60
TTACCAATTG CAATAAGTAT GCGAATAACA AAAAGTTTTA AGCAATTGAT ATTACTAAGT	120
GTATTTTTAG GTGAATTATC AGTAATATTA GGCTTAGTCC TAGCTTTCTA TATGGACATT	180
TCTCCGGGTG GNGTAATTGT AGNTCTACTA GTTATTTTAC TTATGATTAC AATGGNTTAT	240
CAGAAAATGC GAATGAAGTT TAAAAAGGGA GCTAATATCA ATGAATACAA ATGATGCTAT	300
TAAAATTTTA AAAGAGAACG GGTAAAAATA TNCAGATAAA CGTAAAGATA TGTTAG	356

(2) INFORMATION FOR SEQ ID NO:661:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:661:

GAATTCCTGT ATTAACAATA ATCGCATCAT TATTAGAAGT TTATGTAACC ATAAATTAAG	60
GAAGTGTATC ATGCTAGTTT TAAATAATCT TCAAAAAAAA TTTACTAATT CAAAAATGGT	120
TTTGAATAAT GTGAATGCTA AGTTTAGAAG TGGGAGCATC AATTGCATAG TGGGAGTAAA	180
TGGGGCAGGT AAAACGACTT TGTTAAATAT TATTAGTAGT ATATTGATGC CAACAAAAGG	240
TGATGTATAT TTAAATAGTG AAAGTATTTT TGAAAATAGC ACACTTAAAA AAAGAGATTT	300
TTCACACACC AGNAAATCCC TTTTNTATG AAAATTTAAG TGCTAAAGAT AATTTGTACT	360
TAATATGTAG CCTATATAAT CGGAAAATAG ATCAAATACT ATTGAGAAA	409

(2) INFORMATION FOR SEQ ID NO:662:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:662:

GAATTCCTTC	TTTAAGTAAA	TGGTTAATTA	CAGCCCCACC	GATACAGTTT	GATTGATTTA	60
CATTTGACGC	ATTGTAAATG	TCATACTTTC	AATTACATTC	GTTAAGGCAT	TAGCTGTATC	120
TAAAGATGTC	AAACATGGAA	TACCATTTTC	AACTGTAGTA	CGTCTAATTT	GGAAGCCATC	180
CCTTTCTACT	TCTTTACCTT	TAGTCATTGT	ATTTATAACG	ATTTGAACAT	CACCATTTTG	240
ANTACGTGTT	AATAAATCAT	TTTCGCCACC	GATTTTG			277

(2) INFORMATION FOR SEQ ID NO:663:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:663:

GCAACAAATA	AGGTTTATTC	CGAGTTTTC	TGCAAGCCAG	GCTTGACGCT	ATCCGCTGCC	60
GGGATTTATT	CATATACTCC	TGGCGACTTG	TATTCAGCTA	AGACACTGCA	CTGGATTAAG	120
ATGAAAACGA	TTGAAGTTGA	TGATGAACTC	TACAGCTATA	TTGCCAGCCA	CACTAAGCAT	180
ATCGGCGAGA	GCGCATCCGA	CATTTTACGG	CGTATGTTGA	AATTTTCCGC	CGCATCACAG	240
CCTGCTGCTC	CGGTGACGAA	AGAGGTTCCG	GTTGCGTCAC	CTGCTATCGT	CGAAGCGAAG	300
CCGGTCAAAA	CGATTAAAGA	CAAGGTTCCG	GCAATGCGTG	AACTTCTGCT	TTCGGATGAA	360
TACGCAGAGC	AAAAGCGAGC	GGGCAATCGC	TTTATGCTGC	TGTTGTCTTC	ACTATATTTT	420
TCTTGACGNC	CAGGCGTTTG					440

(2) INFORMATION FOR SEQ ID NO:664:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:664:

GAATTCCACA	TTTTCAGGAT	TAAAAAACGG	TTTGGAGTTT	ATATTTAAAT	TCAAATAAGT	60
TTAGACCATC	AATCGCAACC	CTATCTGGT	AAACGTTTCGN	TGCTGATATA	TCTGTAAAAT	120
TGTGTGGACC	GACACCTGCA	ATAAACTTAA	ACTCTGCTTC	ATCTACCAA	TAATCATACG	180
CTTGTGTATG	TCTATCCTGT	GCGCCATGTG	GAAATACAAA	CATATCTTGT	TTTACCTACA	240
ATTGGNTCAA	CTTCATCTTT	CCATCTTTTA	GTATCACGTN	TAATACCNCC	TAAAGATGTT	300

(2) INFORMATION FOR SEQ ID NO:665:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:665:

GAATTCCTGC	TTTAGTGTTA	AAAATCTATA	TCTGCACTAA	TTAAACGGTG	TGATTCACCC	60
GCTTCATCTC	TAACAATTAG	ATAGCCATCG	TAATCTAAAT	CAATTGCTTG	TCCTTTAAAC	120
TGTTTATCAT	TTTCTGTAAA	TAGCAACGTT	CTATTCCAAA	TATTAGAAGC	TGCAATATAT	180
TCTTCACGAA	TTTCAGAAAA	AGGTAACGTT	AAAAATTGAT	TATATCTTTT	NTCAATTTCT	240
TGAAGTAATC	TCTCTAAAAA	TGATATCTA	TCTAATTTAT	TTNTATCATG	TAATTGTATA	300
CTTGTGCTC	TATGTCTAAT	ACTTACCATC	AAAGTTTTCT	AGTTG		345

(2) INFORMATION FOR SEQ ID NO:666:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:666:

GAATTCCTCA	TATTACTAGG	AACATCAACT	ATACATGCAA	TCGAGAGAGG	TATGGCACGA	60
GGTTTAGGTA	CTATTTTAGG	TGTGTTAGTA	CTTTCAGTCA	TATTGTTGTT	TTCAATACCA	120
ACACCTGTTG	CAGTAATTTT	AATGGGCATT	GCAGCATTGT	TTACTGAAGC	ATTGGTGGGA	180
GCAAATTATG	CGATTGCAGT	AGTTTTTATT	ACAATACAAG	TTATTTTAAT	GAATGGATTA	240
GCATCACAGA	ATTTAACAAT	TAACATTGCG	TNTCCAAGAG	TTATTGACGT	TGCAATAGGT	300
ATTGTGATTG	CAATCATAGG	TTTATTTGGC	CCNTGGACAA	CGTACCGCAT	CCCGTATTTG	360

GTTCCTAAT TTTAATTGGC TTGAGG

386

(2) INFORMATION FOR SEQ ID NO:667:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:667:

GAATTCCTTA	GATTCTGAAA	TTTCAGTGTG	TACTTCAGCT	ATAGGTGTCA	TTGCCTCATT	60
ACCTGGAATG	ACAAACTCTT	GTTAACTAG	ATTCGATTGA	TTAAGTTTAT	ATGCAAGTGC	120
ATGTTCTCGT	CCACCAGCAC	CAATTACTAA	TACATTTCATT	TATGTTACGC	CCCTTTAAAA	180
TTAGTGTTTA	AAATGTCGAG	TGCCTGTGAC	TACCATTGCA	ATACCATGTT	TATTAGCCAT	240
ATCAATTGAA	TCTTGATCTT	TAATCGAACC	ACCCGGTTGG	ATAATTGCCT	TTATACCATG	300
TTGTGCTGCA	AGTTCAACTG	TATCTCCCAT	AGGGAAAAAT	CCATCAGATA	CTAACGCTAC	360
ATGGATCATT	GATTTCATA	GCTCTCTCTT	AACGCAATTT	TAGCAGCAAC	CGACACGATT	420
CATTTGGTCC	AGCANCTATA	CCTACAGGNT	GGNTTATTAT	TACTTAAAAT	AATTGGATTA	480
CTTTNTTACT	GATGGGTACA	ACTT				504

(2) INFORMATION FOR SEQ ID NO:668:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:668:

GAATTCCTGA	CGAAAAAAGT	CAAGAAATNT	TAAGTGATCT	AGAAAAGGTT	TGTATCGNAA	60
ACGTATGTTA	AGTTATGGNG	GCTTACTTAA	AGAAAAGCAT	AAANTTTTAA	ACTTAGACGA	120
TGCCGAAGAT	GGTAATTTGA	TTAATACAAN	TGATGAAGAT	AAAACGACAG	ACGAAGAAGA	180
AAAAGCACAT	TCGANNACAG	NANTNTGGNA	TNTCGAAANG	CAAAATTATT	ATTTACAAAA	240
TTTAAGGAGT	TANAAATATG	AACACTAAAA	TTTTCACTGG	AATGACTGGA	AGTTCTCTAN	300
GAACGAAAAA	TCAATANTTT	TATTAATGAT	CCNAATCGA	AGTCATGGAT	ATTAAGTTGN	360
CAAAGTTCTN	TNTTCCNATT	GAGG				384

(2) INFORMATION FOR SEQ ID NO:669:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:669:

```

GAATTCGTC TAAATAATAT TTAAGTGCNG TCAGTAAGAA ACTAAAAATT GCGATACTAA      60
TCGCGATTAT GTCCATACTT ATCACCTCCT TAGGTTGATA ACAACATTAT ACACGAAAGG      120
AGCATAAACA ATATGCAAGC ATTAAAAACA AAATCGAACA TCGGCGAAAT GTTCAACATA      180
CAAGAAAAAG AGAATGGAGA NATCGCAATC AGCGGTCGAG AACTTCATCA AGCATTAGAA      240
GTTNCAACTA GGTACGATAA GTGGTCCGAA AGAATGACGG AATATGGTTT GGAGANCGGG      300
ATAGGATTTT ATTTCCGAAG TTGGANAANG TACACGGGGC AAANNAAGGG CGCGGTNCTT      360
ATTGAACAAA GTTAATCAAT ATTGCTCAAC TCTCGG                                396

```

(2) INFORMATION FOR SEQ ID NO:670:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:670:

```

TTCAATTGCA ATATGTTTCTAG CATGCGCCGT TGGTTGTTGT NGTGTTTCTC TTAAATTATG      60
TGCTCTAGCG ATAACTTCAT CATCTTTAGT GATGATAGCA CCTATAGGTA CTTCGCCTAG      120
TTGAGCTGCT TTTTCTAGCTT CTTCAATCGC TAATGTCATA ANNTNTNTGT CATNTGTCAT      180
TTATGTCCAG ATACCTCACT TATGGTACAA TACTCAATGT CTATTTTAAC ATTTGGAGAT      240
GTGAATATGA ACAAACCTTT TATAGCAATT GAAGGTCTTA TTGGCGTAGG TAAATCTTCA      300
CTTGACACACA AATTAAGTCA AACTTTAGAT TTTTATGAAG AAAAAGAAAT CATCACAGAA      360
AATCCATTTT TATCAGACTT TTTATGAAGA TATCTCTAAA TGGAGTTTTT CAAACTTGAA      420
ATGTTCTTTT TATGCAATAG ATAT                                444

```

(2) INFORMATION FOR SEQ ID NO:671:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:671:

GAATTCCTAT CGATAGCGTT TACCGACACA ATCGTAACGA CAATGAAAAT CGTCATCGAC	60
TGTAAC TACA TTATTGACAT AAATATCATC TGGTAACGTT CGGTTCATTG CATATTGCCA	120
TTGTGACATA GGTATATTCA GCTCTGTGTC GAAATGAAAG TACTGCTGTA TCGCATGTAC	180
ACCTCTATCA GTCCTACTTG AAGGATGGAT TCTCACATGT CTTTATGCA TGC GTTGTA	240
TAGCTTTTCA AATTGTTGCT GTACCGTACG TCCATTCTGT TGAATTNGAA AGCCTAGAAA	300
ATTATTTCTT NGATACGCAA TTCTACTAA TATACGCATG AATTTACACT CCTGAATATT	360
TCAATACGAA TTAAGAATAA TTGCAATTGG GATAATCATG GGCTAAAGAT ATCCGTATCT	420
CTCAANTTGC CATTTAGCTG TCTGTAGTC CGCCCTCTTA ACATTGGAAT CAATAACCCC	480
TAACTTCCAA TTGNACCGC TAATTCTTCC GGTGCGTTGG AAAGCTGAGA TGATTAGGGG	540
GACTANGCAA TGGAT	555

(2) INFORMATION FOR SEQ ID NO:672:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:672:

GAATTCAGTA ATTAAATAAA GAAAAATACA AACGTTTGAA GGAGTTAAAA ATGAGTCGTA	60
AAGAATCCCG AGTGCAAGCT TTCAAACCTT TATTTCAATT AGAAATGAAG GACAGTGATT	120
TAACGATAAA TGAAGCGATA AGTTTATTA AAGACGATAA TCCAGATTTA GACTTTGAAT	180
TTATTCATTG GCTAGTTTCT GGCGTTAAAG ATCACGAACC TGTATTAGAC GAGACAATTA	240
GTCCTTATTT AAAAGATTGG ACTATTGGAC GTTTATTAAA AACGGGTCGT ATATTTTAAG	300
AATTGGAACA ATATTGAAAT TATTACACAG GGGGATACAC CTGCTTAAGG CCGGGNAATG	360
AATTGAAGGC AGGTGGAATT TAACAAAANC AATTCAAGTG ATGATGATCC ATTATTAAAT	420
TTTA	424

(2) INFORMATION FOR SEQ ID NO:673:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:673:

```

ACACATAAAG ACACCAAAC CTCATCAATA GTTCCGTAAA TTTTATTGA CAGAACTTAT      60
TGACGGCAGT GGCAGGTGTC ATAAAAAATA CCATGAGGGT AATAAATAAT GATGAAGCGC     120
AATATTCTGG CAGTGATCGT CCCTGCTCTG TTAGTAGCAG GTACTGCAAA CGCTGCAGAA     180
ATCTATAACA AAGATGGCAA CAAAGTAGAT CTGTACGGTA AAGCTGTTGG TCTGCATNAT     240
TTTTCCAAGG GTAACGGNGA AAACAGTTAC GGTGGCAATG GCGACATGAC CTATGCCCCG     300
CTTGGTTTTA AAGGGGAAAC TCAANTCAAT TCCGANCTTG ACCGGTTATG GTCAGTGGGA     360
ATATANCTTC CAGGGTAACA CTCTGANGGC GCTGACNCTC AACCTGGGT      409

```

(2) INFORMATION FOR SEQ ID NO:674:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:674:

```

GAATTCCCGC GTGGTGATAT TTNTGTACGT GGTGCAATCA AAGAACATAT GGCGAGTTTA      60
GTCTATAAAC TAGAAGAAAT GGGCGTTGAA TTGGACTATC ACGAAGATGG TATTCGTGTA     120
CGTGCTGAAG GGAATGACA ACCTGTAGAC ATCAAAACAC TACCACATCC TGGATTCCCG     180
ACTGATATGC AATCACAAAT GATGGCATAG TTATTAACGG CAAATGGTCA TAAAGTCGNA     240
ACCGAACTG TTTTGAATA CCGTTTTATG CATGTTGCAG AGTTCAAACG TATGAATGCT     300
AATATCAATG TAGAAGGTCG TAGTGCTAAA CTGAAGGTA AAAGTCAATT GCAAGGTGCA     360
CAAGTTNAAA GCGACTGATT TAAGAGCAGC AGCAGCCTTT AATTTTAGCT GGATNAGCTG     420
GTGATGGNAA AACAAGCCGT TACTTGAATT AACGCACCTA GATAGAGGCT ATTGTTGACT     480
T                                                                 481

```

(2) INFORMATION FOR SEQ ID NO:675:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:675:

GAATTCCTAT GTATTTGTAT TGCCTATTGG GCTTAACAAT CAATTAGATT AGATCAATTT	60
TTTAAAAAAG GATACGCCAC TCAATTACAA GTGTGTATGA TATGTGTTGC TATTTTATTA	120
GGCACTGCAG TAAGCAATTT TATGTAGAT GTGTTACAAT ACTCGACGCA GGTAATATAT	180
TTAATAAAAT AAGTCTAACT CTATGATGTG TAATCAAAAC TAGATATAAT TAAATAATGA	240
CTTAAATATA TTTTAAATA GGGAAATGTA AAGTAATAGG AGNTCTAAGT GGAGGATTTA	300
CGATGGATAA AATAGTACTC AAAGGTGGAA ATAAATTAAC GGGTGAAGTT AAAGTAGAAG	360
GTGCTAAAAA TGCAAGTATT ACCAATATTG ACAAGCATCT TTTATTAGCT TCTGATAACC	420
CGAGTAAATT AGGTTAATGC TCCAGCTTTA AGTGATGTAG AACAATAAAT AAT	473

(2) INFORMATION FOR SEQ ID NO:676:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:676:

GAATTCCTAG TCTATATCTT TTTTCGTTTG ATTGAGTCTC TTNTGTAAAT TCAATAAATC	60
ATCCGCTTTA CCATNCAATG CCGATTTAAC TAAATTAAAA ATTTTATTGT GATCTGTTTC	120
TATTTTAGTA ATTAAATCTG CCAGTAATTG TGCCNTGTGT CTTTCTATAC GTGTTGCTAA	180
AATCGTNTCA ATAGCTTGCT TTTTATCTT TGGCATTATN CAAAATTGCT TNTAATATAT	240
CATCTGAAGA CGTGTCGCCA G	261

(2) INFORMATION FOR SEQ ID NO:677:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:677:

```

TTTTCGAACT AACATTCAAT TAATGGATTA CCTGCGATAA AAATGCCCTC GTACGCTCTG      60
ATTTAGGATG CGCAAAAAAT TCATCAGGTG CAGCTTGCTC CACTATTTC CCACGATCCA      120
TAAAAATTAC CCGGTCAGCG ACGGTTCTGTG CAAACCCCAT CTCATGTGTT ACACACAACA      180
TTGTCATACC CGACTGCGCC AGCCCAATCA TCGTATCCAG CACCTCTTTC ACCCATCTCA      240
GGNATCGGAG CGCCGACGGT TGGGCTCAAT CAAAACAAAC AATAATTTC NGGCTTCCAT      300
ACACA                                           305

```

(2) INFORMATION FOR SEQ ID NO:678:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 375 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:678:

```

GAATTCAGAT ATACATCGAT CTCGTCTATT AAATTCAAAA TACGATGAGA TGGGTGGAGA      60
TGTAATGAGA GATTATTATN CACTAATTTT CTTAGAAAAA TNNCAATGAG GGGTATTTAT      120
GATTANTGAN GCTTCACTAG CGATATTAGA TGATATTGAT GANCTAGCTG ATATGATAGT      180
TGCATCAGAT ATNTATGCAT CATTTGAGCA AGCTAAACAG GCGCTCGANA ACAATGANGA      240
AGCACATCTA CTTTATCAAT CANCTCNACA ATCAAAAGAG AAATNTGATG AGGTAGTGCG      300
TTTCGGGAAA TATCATCCNG GATTATGAGA AAGGTCATGT TAGGAGACAN AGACAACGCC      360
ATTNGAGCAT CTGAA                                           375

```

(2) INFORMATION FOR SEQ ID NO:679:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 240 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:679:

GAATTCATTA TATATTTATA TACGTAAGAC TTTAGTGAAT ATATCTATAA TTATTTACTT	60
GGTAAGCTGG TACCGATCTG TAAGTTAAAA TACCTGGTGC AGNTGAATAG NTCANTTCTG	120
AAACTAAAAT NCTACCATCG NTATTTACAC GTTCTACAAA CATAACATGA CCATAATAAC	180
CTACATCTGT TTGAGCGATA GAACCTACAG NAGGTCTATT GTCGATAGTG TCAACCATCT	240

(2) INFORMATION FOR SEQ ID NO:680:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:680:

GAATTCCTAT GATCCAGAGT GTTTCATCGA TTTAATCGGT TGAGGATTCC ATTCGTATCC	60
TTTATCTTTA CCAATTGTTA GACCACCAGT AGAGTGATCT GCTGTTGCAA CGACAAGTGT	120
ATCTTTATGT TTCTTAGCAT ATTGAATGGC GTCATCGAAT GCTTTTTCOA AACCTTCCAT	180
TTCAGACATA ACGCCTGTAA TATCGTTGGA ATGCGCTGAT TTATCTATAG AAGCACCTTC	240
GACCATTAAG AAGAAACTTT TTTATTACGC TCAAGCTTAC TAAGTGCACT TTGTTGCATA	300
TCAGCTAATG ATGGTTCCGT CTTTTAGAAG CATCTTTTGC AAGTGGCATA TTTTATCT	360
TGCAACAAA CCAAGACTTT ATCTTTTATC AAGATTTTGA TGAATCCTTA TTGTCCNGGG	420
GAAGGTCNGG NACCATCTTN NNGATG	447

(2) INFORMATION FOR SEQ ID NO:681:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:681:

GAATTCCTTG CAACACAGGA CGTTCTCAG CGTATAATTT ATATTTATTT ATCTGTAAAC	60
GTATGTTTAT TTACATCTAC TATTTTCAAG GTTGTATTT NGTCTGGATA TTCAGGAAAA	120

TACCATTTAA AATATTCTGT GCCAGTAACA AATGTCATTG TTCCATCACC TTCATTATCT	180
GAGTATAGTA TGTATTATTT ATTAAC TAAC ATAGAATCTA ATTTATTTCAT TATTTTCAAA	240
ACATCTTCAC TAGATAATAG TGCTCTTTGT ATATCTTTAC TCATCTTTCT ATTATTTATT	300
TNNTCTTNAN CATAATGTTT CATTAATTGA CTTCAATAAA CTCATTTAAA AAGTAAATTT	360
CATTAAGT ACCACCTACT AATGCAATTC ATTTNGTCAG ATGATTGTAA TACAATNGNG	420
TGGGTTCAAG GA	432

(2) INFORMATION FOR SEQ ID NO:682:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:682:

GAATTCGCT TTAAAAACA AAATCCCTTC AACTGAAATC GTAGCGGAAA CAATTTATCA	60
AATTGTTAAA GAAATTTGG CATCGCTCGA ACACCAACCA AAATGTATTC AAGTATTTGT	120
AAGAGAAACA CCAACAAGT ATGTTGTATT TAGACCAAAG GAACAGGTGT AACTAATGGC	180
TAAAATTCCT GACTCGAAA TATTCGGTCC AACCATTGAG GGTGAAGGTC GAGTAATCGG	240
TAGAAAAACG ATGTTTGTGA GAACAGCTGG ATGTGATTAT CGCTGTAGCT GGTGTGATTC	300
TGCATTTACT TGGGATGGTA GTGCTAAAGG CGATATTAAA ACTCATGACC GCTGAAGAAA	360
TTTATGTATG AATTAACG AATTGGGTGG CGATTTTATT TAATCACGTT ACAATTCCTGG	420
TGGGGTANCC CAGCATTAAT TAAGGGTNTC CAG	453

(2) INFORMATION FOR SEQ ID NO:683:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:683:

GAATCCCAG AAAC TAGATT TTNTCATAAT CGACCTATCT TTTGTCCAGA TACAGTGAGA	60
CCCTTGTCAT TTAAATGATT TTTAATTCGT CTGTACTAA AGACTTTTCT ATTAGAATTA	120
AAAATATTTA TGGCGGCACG TTCTACGTGT GAATCATCTT TAGTGATTTT ATTATCTTNT	180

CTTTTATAG AATCATAATA GGTACTTCTT GGTATTTTTA GGACTTTACA CATTGCTGGT 240
 ACTGAATATT GATGTGCATT CTTGTGAATG ACTTCTTATT TGNGCCCATAT ATCAGCTCT 299

(2) INFORMATION FOR SEQ ID NO:684:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:684:

GAATTCCTNA CCATCCATAG CTGTGNACAC AACATGATCT TTATCAATCA TCATAATGTT 60
 GCAAAGGGAT TTCTTTNATC AAATCAGGT GCATATGCTC GNACTTCTTC CATAGTTANG 120
 GGCAATTTTCG TTGGGGTTAA AGGGTGTGTT GGATGCCCCCT CTGGNNCCAA GCTCTCAGAA 180
 TAAGTTAACT CATCTGTCTT ATCACTATCT TTTACATGTT GTANCCATGA AAAAAAGTTA 240
 ATATCTTGTG GTAATCTNGA AAATTTAAAA CTGTGACTTA TTAATGTGTG TCTGTGAGAC 300
 ATGTGNTTAT ATGTCACATC TAACTATCT CGACTGTGTA TTANCTCCTT CGNNGTAGTC 360
 GCTCTGANNA NTAGGGATAT CAANGGTCAT GACTCAACAC ATCTAACAAC NCCTTCTTAA 420
 NGGTTATTA 429

(2) INFORMATION FOR SEQ ID NO:685:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 413 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:685:

GAATTCCTAC AAGCGTCGTT GTAAATGGCG AATTGTANTA TCTCTATGTG CAATGACAAT 60
 CATCGTTGTA TCTTTAAAAT GTTGAAACAG AACGTTCTGA ATCATGTGTT CTGTTTGAAT 120
 ATCTAAACCA GTTGCAGGCT CATCAAATAT AACGAGATCT GGCTTCATAA CTAAAAGACG 180
 GCAAAGTTCT ATGCGTCTCA TCTGTCCACC AGATAACATT TCGCCTCCTT CACCTATTAT 240
 TGTGTTAATG CCTTTTGTGA AAGATTGCAC TTTGTCTAAT AAACCTACTT CGNCTAGCAC 300
 TTCTTCAATA GNATTATTTT CTATATCTTN AAACATCGNN ATATTCTCTT TNATAGAAGC 360
 ACTGAAAATA TATGGCTGGN GACTAAGTAT TCCCATATTT NAANTCACGC TGG 413

(2) INFORMATION FOR SEQ ID NO:686:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:686:

```

GAATTCGAAG AAACGAATTT GCATAAAAGA CTAGCTCTTT TAGTGTTATC AATTGTTGGT      60
AATAAAACTA GAAATATAGT TATTGGAGCA ATTATCGTTT CAATTGTACT TGCATTTNTC      120
GNTCCTTCTG CAACAGCTAG AGCAGGGGCA GNTGTNCCAA TCTTGCTGGG TATGATTGCG      180
GCATTTAAAG TTTCCAAAGA TAGCAAGTTA GCGTCTTTAT TAATAATTAC TTCAGNACAA      240
GCTGTGNCAA TTTGGAATAT NGGTATCAAA ACGGCGGCAG CACAAAATAT CGNAGCGAAT      300
TAANTTGATT AACCCATCAA NNAGGATTNG NTGGTTCCAA NGGGGCGAAT TGGTTCCTTAT      360
NT

```

(2) INFORMATION FOR SEQ ID NO:687:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:687:

```

GAATTCCTGG TAATACTAGT TGAAAAGGAG TGTAGTCATC ATGTCAGAAA CAATTTTCGG      60
CAAAATTTTA ACTGGAGAAA TTCCTAGCTT TAAAGTATAT GAAGACGATT ATGTCTATGC      120
CTTTTtagat ATATCACAAG TTAATAAGG ACATACGTTA TTAATTCCCTA AAAAAGCTTC      180
TGCTAATATC TTTGAAACTG ATGAAGAAAC AATGAAACAT ATCGGTGCAG CATTACCTAA      240
AGTAGCAAAT GCTATTAAGC GTGCATTTAN TCCTGANGGT TTAAACATTA TTCAAAATAA      300
TGGTGAGTTT GGAGATCAAT CTTGTATTTT ATATTCCAAN NCCACTTAAT TCCNCGATAC      360
GAAAATGATA TTTGATNGGT TTGGGTTATT AGNCGGGAAA CCACACCGAN NGCCATT      417

```

(2) INFORMATION FOR SEQ ID NO:688:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:688:

GAATTCAAAA AAGGTTAAGT ACAATTACTG ATTCGTACT TAACCTTTT TAAACTCTAA	60
TCATATGTTA GTTATTTTCAT TCTTCGTAAT AATATTAAGA AGTATGGTGC ACCGATAATT	120
GCAATGATAA CCCCTACAGG AATATCCAGT GGCGGATGAA TGCCACGGGC TAAACCATCT	180
CCAAATGTTA ACAATATAGC ACCAATTAAC CCCGACATGA TAATAACGTG TAATGTTTTA	240
TTTCCTATTA ATTGGCTCGC AATATGAGGT GCAATTAATC CTAAAAAGCT AATACCACCG	300
ACAACTGAAA TTGCGGATCC CGCTAATATT ACTGCTAAAA TTAGCATAGC ATTTTAATTA	360
G	361

(2) INFORMATION FOR SEQ ID NO:689:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:689:

TAGAATAGAA GCGTGTGAAA ATATAGAATT AAATATAATT TGAGGTGGAA AAATGATACT	60
AGTAATGTTA TCTCCATTAT TAATCATATT CTTTATAGTG TTGTCTATTT TAGAGGAGCG	120
TAAACGTACG AAGAAAAAGC AACTCGAGAA AGAAAAAGCA AATACACTAA ATCAAAATAC	180
AAATGACACG GAAAGTTCAA ATCAAGAGCC GTCATTGCAG CAGACTAAAG AACAAAAAGA	240
TAACAAAGGA TAATNCAATT GAAGGAAGAA GATTATAGAT GAAAATATTA ATTGTTGAAG	300
ATGATTTTGG TTATAGCAGA AAGTTTAGCA TCTTGAACCT AAAAAATGGA ATTACGGNGT	360
TATTGTCGGT GGAACAANTT GGATGATATT ACTTGTCCTA TCTTTTAACC CAACATCAAC	420
CCCAAGCTTG GTNPTGGCTA GATATTTAAT TTGGGCAACG NTAAATGGGT TTCCACTGGG	480
GGTCAAGGAA ATCCCGAAAA CATCTTAT	508

(2) INFORMATION FOR SEQ ID NO:690:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 562 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:690:

ATCCCTAGGA TATACGAATG TNCCTGTTAA ATTAGATAAA GAAGTTGAAG GTACAATTCTG	60
CGTACACACA GTTGANCAAT AAAGTTGGAT TGAAATAAGA GGTGTAACCA TTCATGGATA	120
GAATGTATGA GCAAAATCAA NTGCCACATA ACAATGAAGC TGAACAGTCT GTCTTAGGTT	180
CANTTATTAT AGATCCAGAA TTGATTAAATA CTACTCAGGA AGTTTNGCTT CCTGAGTCGT	240
TTTATAGGGG TGCCCATCAA CATATTTTCC GTGCAATGAT GCACTTAAAT GAAGATAATA	300
AAGAAATTGA TGTGTGAACA TTGATGGATC AATTATCGAC GGAAGGTACG TTGAATGAAG	360
CGGGTGGCCC GCAATATCTT GCAGAGTTAT CTACAAATGT NCCAACGACG CGAAATGTCC	420
AGTATTATAC TGATATCGNC TCTTANGCAT GCATTAAANA CGTAGGATTG ATTCAAACCTG	480
CAGATAGTAT TGCCAATGAT GGATATANTG ATGAACTNGG ACTAGATGCG ATTTAAGNGA	540
TGCAGAACGT CGNATTTTAG AG	562

(2) INFORMATION FOR SEQ ID NO:691:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 596 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:691:

CATAAGATAT TCTCACAAGT ATTCTTTTATT GTNAAATTTG GTATATCAAT GAGACTCATC	60
ATATCCACCT CGTNGTTTTA GCAATCTATC TCTTAGCGCA TCTCCGGTTA AATTAAAAAT	120
TAAAATAGTT ATAGCAATGA CTGAAGCAGG TGCAATCAAC ATAATTGGAT GAGACGAAAT	180
AAAATCACGA CCTTGTTGNA ACATAGCGCC CCACTCTGGT GPTGGCGGTT GTGCACCTAA	240
CCCAATAAAT GATAGTGAAC TTATATATAA AATGATTTTA CCGAAATCAA CGACCATCAA	300
AACGATAATA GCCGGTATAA TTTTAGGTGT TAAATGACGT ATTAATATTG TNCITGTAGG	360
TACATGAAAT AATTGTGCCA TTTTATATA AGGCTTATTC ATTTGCTAT TAACTATACT	420
TCTTAGTCAA CCTTGTGTAA TTCATCCCAT TTTATTTACT TGTAATTGGA GATAACTAAA	480
TTNCCACAAA AGATGGTTGA AAAAAGCTTG CTTAAAAGCA ATCAATGATG ATANTTCTTG	540
GAATACTTAG GACCACATC AATAANCTA ACAATTATCG GTCAATCCAC CCTTTT	596

(2) INFORMATION FOR SEQ ID NO:692:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:692:

```

GAATTCCTCGG TAAAGAACTT TGTATAAGAC AGAATGATAT TATTAAGAAT AAGTGTATTT      60
ATAATGAAAA TGTGGTAACT TAATATAAGT AGAGGTGANA TAAATGGGTT TGAAANTAAA      120
AGAGTATATA AATGATAGTA ATAGGAAATT GGATAAAGAA ACAGTTAGAA AGCACTTAGT      180
AGATATACTA AATTACACTG TNGAAGAAAA TAGTTTNCTA GATCAAATGA CAGNTGGCAA      240
AAGACTATAT TCAAATCAAT ATAAAACTC GCCCTCTNTA TCATTAAC TG NAAANCATAA      300
AATCAAAATA AATGAAGGCG ACGAGNGATT TTAGCTATAA ATTTTCTGAT AATGAAACTC      360
AAACTTTTAA CCTNTCAAAN GAGTTAGGAG TAGCNGGCGN NATGGNTAGN ATNGGGNCCC      420
AAAACT                                           426

```

(2) INFORMATION FOR SEQ ID NO:693:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:693:

```

AATAAGGAAT TTTAAATTGT GACTTTTNCG GAATATTAAA TTTTAAAAAT ATGAGGTTTG      60
TGAAGCGGAT TTCTCACAAA ATTTTAAAAA ATTTAAGCCT GAAAATGATA AAGCGGTAGG      120
GAACGTTTCT CTGAAAGTTA GTGATACAAT AGTTTAAAGT TGAAATACAG GAGGATGAAT      180
AACATGAATC AGTCAGTCAA NTTACTTAAA CATTTAACAG ATGTAAACGG CATTGCTGGT      240
TATGAAATGC AAGTTAANGA AGCAATGCGT NACTATATAG AGCTGTCAGG ANCAAATATT      300
GGAGATAACT TGGGTGGGAA TTTGGGGNAA GAAAAATGCT GAGAATGG      348

```

(2) INFORMATION FOR SEQ ID NO:694:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:694:

GAATTCCGAC GTTAGATCAA TTGAAATCCA AAGATCGAAA CATTGGGACA TATTTATTAA	60
CGACAATGGC TTCAACAGGA TTTGGTTCAT TCGGAAAATA TTTATTGGGC ATCATTGTGG	120
CGCTGGCATG TCTAACTACA GCATGCGGGC TTATTGTTGC AGTTTCTGAA TATTTCCATA	180
GAATCGTACC TAAAGTATCA TACAAAGCAT TTGTATTAGT TTTCATTTTA ATGAGTTTTA	240
TTATTGCTAA CCAAGGTTTA AATGCTGTTA TCTCAATGTC AATCCCGTA TTAAGCATTG	300
TATACCCAGT AGCAATAACT GTTGTATTAT TAATTNNAAT TGNCAAATTC ATACCGACAA	360
AACGCATTTT ACAAACAAAT TCCAGTTATT ATCGTATTTT ATATTGGTCG GATTTTCAAG	420
TGGTTATTAG GTAAGTTAGG GTTGGGCTTG AAAAATTAAC TTTTATT	467

(2) INFORMATION FOR SEQ ID NO:695:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 771 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:695:

GGGGGGGCTG TTATTAAGCC TANGNGGGNA CCAGCAATGC CANGGCGGNN GCATTANCAA	60
ANACGANCTT ACCGCAAAAN CCGNNATGGG NGGGCGTTCC AAAATGTCGC TAAATTAATG	120
ACAAGCTGCC GGTAGTAGTA TTTTGTAAAA ANTTACCTAT GATTTTCGCA TTAGGTGTCTN	180
CAATCGGATT AGCTGGCCGT GATGGCGTAG CAGCTATCGC AGCATTCGTC GGTTACATAA	240
TCATGAACAA AACAATGGGC GACTTTTAC AAGTTACACC TAAAAATGTT ANTGAACCAA	300
CGAGTGGTNA CCNCTAGCAA TTNAGGTAAA ACCAACATNA CAANNAGGTG TGTTCCGGCGG	360
TATTATTATC GGGGCCCTGG CAGCTTGTGT TATAACAAGT TCNATAACAT TAACTTACCA	420
TCTTATTAG GTTCTTCGC TGGTAAGCGT TTCGTACCTA TTATGATGGC TACAACATCA	480
TTTATTTTAG CATTTCCAAT GGCATTAATT TGGCCAACGA TTCAATCAGG ATTAAATGCA	540
TTCAGTACAG GATTATTAGA TTCAAATACT GGTGTTGCCG TATTCTTATT TGGTTTCATC	600
AAGCGTTTAT TAATTCATT CGGTCTACAT CACATTTTCC ACGCACCATT CTGGTTCGAG	660
TTTGGTTCAT GGAAAAATGC AGCTGGTGAA ATTATTCACG GTGACCAACG TATCTTTATC	720
GAACAAATTC GTGAAGGCGC ACATTTGACA GCTGGTAAAT TCATGCAAGG T	771

(2) INFORMATION FOR SEQ ID NO:696:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:696:

```

CTTGCGCTTG TCGACGTTTA CTTTCATGAC TAAGCGAATG AATTTGCCTG AAGTTGACCT    60
TGAAAAAGTA ATAGCACCAT GGAAAGAAAT ACTAGCGACT AATAGAGAGA TACCAAATTT    120
AGATAATCAA ATGTGTATTG GTGGTTTAGA CTTTGCAAAC ATTCGAGATT TTGNAAGTGT    180
AGGGCTATTA TTCCGAAAAA ACGATGATTA CATTGCGTTA GGACATTCGN TTGTAAGACA    240
AGGGTPTTTG GATGATGTCA AATTAGAACC TCCTATTAAA GAATGGGGAA AAATGGGGTT    300
ATTGACCATN GTCGATGATG ATGTCATTGA AATTGAATAT ATAGTTGGAN TGGGTTTTTN    360
ANACCAAAG GCTAGAGAAA AATATGGGAT TGAAAAAGTC ATAGGCTGAT AATTATAGAA    420
CTGATATTGT AAGACGTGCG TTAGGGATG CTGGCATAAA ACTTGAGTA CTTAGAAATC    480
CCA                                                                    483

```

(2) INFORMATION FOR SEQ ID NO:697:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:697:

```

CAGTTAAAGT GTCTGTATCA ACTAACTACA ATACAATTGT TGAAGCTATG AAGTCTAAAA    60
AAGTTGATGT TGGTTTCTTA CCACCAACGG CATAACATT AGCACATGAT CAAAAAGCAG    120
CTGATTTATT ATTACAAGCA CAACGTTTTG GTGTAAAAGA AGATGGTTCA GCAAGTAAAG    180
AACTTGTTAGA TAGTTATAAA TCAGAAATTC TTGTTAAAAA AGACTCAAAA ATTAAAAGCT    240
TGAAAGATTT AAAAGGTAAG AAAATTGCCT TACAAGATGT AACATCAACT GCTGGATATA    300
CATTCCCACT TGCGATGTTA AAAAACGAAG CAGGTATTAA TGCAACTAAA GATATGAAAA    360
TTGTGAATTG TTAAAGGTCA TGACCAAGCA GGTATCTCAT TATTAAATGG AGATGTAGAT    420
GCTGCGGCTT GTATTTAACG ATGCACGTAA TACTGTGAAA AAAGACCAAC CAAATGTATT    480

```

TAAAGACACA	CGAATTTTAA	ATTAACACAA	GCTATCCCGA	ATGACACAAT	TTCTGTAAGA	540
CCAGATATGG	ATAAAGATTT	CCAAGAAAAA	TTGAAAAAAG	CTTTTATAGA	CATTGCTAAA	600
TCAAAAGAAG	GTCACAAAAT	TATTAGCGAA	GTTTATTTCAC	ATGAAGGATA	CACAGAAACG	660
AAAGATTCAA	ATTTTCGACAT	TGTAAGAGAG	TACGAAAAAT	TAGTTAAAGA	TATGAAATAA	720
TCATTATCGA	ATTTGGTATT	AAAAGCTTTC	GTCAATAGAT	ATATTCTAGA	TAAATATTGG	780
AAANGCTAGG	CGCTAACCTG	AAACAGATAT	AGAAAGGTGT	CGCTGTACAT	TTGAAACCAT	840
TTGTACACAG	AAACCCAATG	TCTATGATAT	TTCAGTTTAC	CTTGGCTTTT	CTTTATTAAA	900
GAAAGGTGTC	AAACATGAGT	CAAATCGAAT	TTAAAAACGT	CAGTAAAGTC	TATCCTAACG	960
GNCATGTAGG	CTTGAAAAAT	ATTAACCTAA	ATATTGAAAA	AGGTGAATTT	GCAGTTATTG	1020
TCGGACTATC	TGGTGCTGGG	AAATCCACGT	TATTAAGATC	TTGTAAATCG	TNTGCATGAT	1080
ATCACGTCAG	GTGAAATTTT	CATCCAAGGC	AAATCCATCA	CTAAAGCCCA	TGGTAAAGCA	1140
TTATTAGAAA	TGCGCCGAAA	TATAGGTATN	GATTTTCCAA	CANNTNAATT	TAGTTAAACG	1200
GNCAAGTGTA	TTTACGAAAT	GTNCTAAGTG	GACGTGTAGG	TTTATCANCC	CACCTGGGAA	1260
AATGGTATTA	GGGTTTANTC	CC				1282

(2) INFORMATION FOR SEQ ID NO:698:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 607 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:698:

CGTCTTGCCC	GATCGAAACC	ATGCTTCCAA	AACTTGATTT	CCCATTGTC	ATCCTAAAGG	60
TGCATATATG	TATGGTTGGA	AACCCCGCC	TGGTTATGAC	AGCGACCAAT	TTGACCAATT	120
TTTAGTGCAA	GAGAAGTCAA	TACTTGTTGC	TCCAGGGAAA	CCATTTGGAG	AGAATGGTAA	180
TCGTTATGTG	AGAATTTTCAT	TGGCGTTAGA	TGACCAGAAA	TTAGACGAAG	CTGCAATAAG	240
ATTAACAGAA	CTAGCATATT	TATATGAATA	ATAAAGTTAA	GGGTGATGTT	AAAATGACAA	300
AAATTAAAAT	CATGAGTGTA	CGTGATGAAG	ATATGCCTTA	TATCAAGGCG	TGGGCAGAGA	360
AACATCATGT	TGAGGTAGAT	ATTACTAAAG	AAGCATTAAC	TGATGACAAT	GTTGAAGGTG	420
TCGCTGGTTA	TGATGGCTTA	TCGCTATCAC	AACAAATACC	ATTATCAGAG	CATGTTTATA	480
AACGATTAAA	TGAACTAGGT	ATTAAACAAA	TCGCACAACG	TAGTGCTGGA	TTTGATACAT	540
ATGATTTGGA	GTTAGCAAAC	AAGTATAACT	TGATTGTGTC	AAATGTGCCG	TCATACTCTC	600
CGANNCC						607

(2) INFORMATION FOR SEQ ID NO:699:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 969 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:699:

```

GGCACGAGCG CTCACGCACC TCATCTTCAT TTTGAGCACC TATATCTAAT GTTAAATCTT      60
TAATTTCCGG TGCACCTTCA CTACCAGTAC GAAAATGTTT AGGTATATTA GAAACAACAC      120
CGATAATTTT ATCGCCATTT CTATTTTTTAA TTACTAAGCG TTGTCCTTGC CAAATATCAT      180
TTGCAACACC ACCTAAATTT GTGAATTGAA TCATTCCATT TTTAGTGATA TTTGTAATCA      240
TAAATCCGAT TTCATCCATA TGTGCTGCAA TCATTACACG TTTTGCAATTT GGATTTTITAG      300
ATTTTTTTCAC ACCAAAAAAT CCACCCATAC GATTTTCAAT AAATTCATCT ACATACGGGG      360
GCAATTGGTG AGTCATATTA ATTTNNTACT TCTTCTTCCA AAACCTGGGT GNCCCATGAA      420
GGTCAAGTTA AAGTTTGGAT TCCGTTGTAA TGTACTTTT TTATTTATGT TCATAAAAGT      480
TCTCACTCCT TATAAGTTAT TATATCATCT TCAATATGGT AACTAATGA TATGAATTTG      540
AAATCAAGGG AGCATAAATG ATGACTAAAC TGAAATATAT AATCCAACA ATAATTGCAG      600
TAGCCATTGT AATTATTTCT ACCATTTCAA TCATCCAATT TATTAATCGT AAACGCTATA      660
ATCCCGTTAA AGTACTTAAT GAAGTAAAAT CATATTTTAT GAATGTCAA GGCTCATATA      720
TCGTTTATGA ACCATTCGTT CATCCTGAAA CTGATAAATA CCGNITAGTT TATCAAGGTG      780
GGAATTACAA CTATTAAAAA TGGGCAAAAA TATTCAATTA TGATTTNNAT GCAGATGCAT      840
ATTCTGGGGG AAGGTCATTA CATNGCNGGA GCGGTAAATA CGAATTTNNA TCCCATATTN      900
GGACTGGGGC CCGNAAANC TTNAAAATGG AGNCACACCC CAATTAAGNA AGATGGGGTG      960
GNGGNTCAA

```

(2) INFORMATION FOR SEQ ID NO:700:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 943 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:700:

```

AATGACAAAA TATTAATCAA TTGGCGTATT ATACAAGAGT AATAGACATA TAAAAGTCGA      60
ATGTAACACTG GTGAGTACTG ATTTTATTCT TTGTAAATTA CAAGCATTTT ATATCATAAA      120
GTTTGAAAAG AGGTATATTG AAGTGGAGAA AAACGAATAT ACAGCTAAAT ATAATGAATA      180
TAGTCAATTA TTAGACGCTA CTTACTCGCA AGCTGTAGCA TACCTTTTAA ATAAATATGG      240
CGCTGTAACC GATGATTATT ATAAGGAAAA ATCATAACAG CGATTTTTAA ATGGAGAAAT      300

```

CAAAAGTATT	TCAAAAGGAA	AATACACTAG	AGCTAGCGAA	GGATTATATT	GTCATCACAT	360
AAGCGAAGAC	AAATTCCTAAA	ACTTATCTTG	ACCTAAGATT	CATTTCCGAA	TTTAAGTACT	420
CATACAACGT	CAAAAGAAAG	AAAACCTAGT	GTACTGTGAT	CTTATCGAGC	ATTTANTTTT	480
ACATGCAATT	ATTACAAAAG	AATCCAATGG	CAATTGGGGT	GTGGGCTGGA	TTATGTCAAA	540
TGATCAAACC	AACAGTCATT	GATTGGGACA	TTAGCGAATA	TACTCCAAA	CCAGCATGGA	600
TGCAAGCCAC	CAAAGCACGT	GCCTATGTGC	CTAGAATATT	AGTAGAGAAA	CTACTCATT	660
NNATTGACGA	TATGTTAGAA	GGAATAGAAA	TATATGATNT	CCNTGAGTCT	AGATAAATGA	720
TTAANGGAGA	TATATTTTCGT	GNTCGNTGAG	ATTGTGNTAT	AGATAGNNTA	ACCCNNTAAT	780
TAAATATTAT	TCTATNAAAT	AGACCACGCA	TNCCTATCTA	TAAACGGACA	ACGTTTATAA	840
ATGAGTTTGC	ATGGTCTTGA	ATTGTATTAA	ATNTCTTNTT	GGGTTTAAAT	AGNTCACTTA	900
GNGGGTATGT	CAACATTCTT	TNGACAGCTT	CACGTGTATT	TTT		943

(2) INFORMATION FOR SEQ ID NO:701:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 569 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:701:

CANTTGTGAA	NTTGGCGTCC	TTTTTGGANA	CCCGATATAG	CTTTATCTTG	CCACCGNAGT	60
TTCATCTTGA	CGTCCCAACC	NACCTCCGGA	CCAACATGGT	AAATATGCTA	TTTCATTATC	120
AGCCACCGGA	TTTCCGAAAT	ATTCAAGTTA	NCGGATTGAC	ATGATTGTTT	CACCATATGA	180
AATAAGGATT	GATAATTTCC	TTGTAAAGGA	TTTATTAATT	CATCACGGAT	CCGTTAAGTT	240
ATATTTAATC	CTATAAAAAG	CAGGCGTTAA	ATGTAACAAG	AGTTGCTGTG	ATAATTTCTC	300
CTTATCTTCA	ATGTTAATAA	AAGTGATTTG	TTTACAATGG	TGAATCATTT	GAGCGATGGC	360
CATCGTTAAA	TTGATATGT	TATCTGATTC	CTGCAATCA	GTCCATTGCA	CACCTGTTGA	420
AAGTAAGTGT	AATGTCAAAT	ATAACTTTTC	CGTTCTGGC	AAATCAGGCT	CATGTTGCGT	480
CATAATCTCC	GTGCTTGAT	ATTCTTTCGT	ATCCCTCAAA	TACTGATAAT	TAATATTTAA	540
TGGATTCATC	ACATGACCAC	TTTGAAGTC				569

(2) INFORMATION FOR SEQ ID NO:702:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 661 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:702:

```

TCTTTAAAAA GGGNATANTT GTNCCCAANC TGGGACAAAA NTCANACNNA TATNGGTCTA      60
TNCTTTTGAT TTAATAAAGG GANTTTCCCG ATTCNGCCC TATTGGTTAN NAATTGANCT      120
GNTTTAACCA CNAATTTAAA CGCGAATTNT TAACCAAAAT ATTAACGGCN TACCAAATTT      180
GCCAATTCGC CATTCAGNCC TGCNCAACTG TTGNGAAGGG CGATCGGTNC GGNCCCTCTTT      240
CGCTATTACG CCAGCTGGCG AAAGGGGGAT GTGCTGCCAA GACGAGTAAA GTTGGGTAAC      300
CGCCAGGGTT TTTCCAGTC ACCGACGTTG TAAACGACG NCCAGTGAAT TGTAAATACGA      360
CNCNCTATAG GGCGAATTGG GTACCGGACC CCCCCTCGAG GTCGACGGTA TCGATAAGCT      420
TGCCACCTAT AAANTCATAT CTATCNTNCA NATCTTGAAG TTCTTCTTCC GATGGACGTT      480
TACCATGTCT AATATCTGTA TAATATGGCT CTATGTCACT TTCTTTATAA GGTGTGCCAT      540
AAGCCATAAC TAATAACCCC ATTTTTTTAG TCATTGATAA TACCTTCCTT TAAATGAATT      600
ATCTTTCATG TGCTTCAATG TAATACTATG ATTATCTTTG TGTATATGTG TGTACGAAGT      660
C                                                                                   661

```

(2) INFORMATION FOR SEQ ID NO:703:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 638 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:703:

```

CNTNTGTGGG TCACGCGGNG GNGGGCGGCT CGTCTAGAAT AGTGGATCCC CCGGGCTGCA      60
GGAATTCAGA ATCGTACCAA CAACTGTTGC ATTGACAATG ACATTGGACA AATTGGATTT      120
ACCAATTGTC GGCAAACCCA CGTCATATAA GACATTGCCT AATCGTTATA AAGATGTACC      180
GGAAATTGGT CAACCAATGG AGCCGAATGT TGAAGCTGTT AAAAAGTTAA AACCAACACA      240
TGTTTTGAGT GTGTCAACGA TTAAAGATGA AATGCAACCA TTTTACAAAC AATTAAATAT      300
GAAAGGCTAC TTTTATGATT TTGATAGTTT AAAAGGGATG CAAAAGTCGA TTACACAATT      360
AGGTGATCAA TTTAATCGTA AAGCACAAGC AAAAGAATTA ANTGACCATT TAANTTCTGT      420
AAAGCAAAAA ATTGANAATA AAGCAGGTAA ACAAAGAAA CATCCCAANG TATTAATATT      480
AATGGGTGTA CCGGGTAGGT ATTTAGTAGC AACTGATAAA TCATATATTG GGTGATTTAG      540
NTAAAATAGC AGGTGGAGAA AATGTTATTA AAGNGAAAGA TCGCCAATNT ATTTGCGNCTA      600
ATACTGAAAA TTTGTNGAAT NTCANTCCAG ATATTATT                                     638

```

(2) INFORMATION FOR SEQ ID NO:704:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 811 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:704:

```

GACAACTTGC TAAAGCACGT GATGAAAAAG TAAGTGAATA TGGAAATTGAA CAAGCTGATG      60
GTACATTAAT TCAATATGAT AGTGAAGCCA AGATATATGA ACATTTTAAT GTGAATTTTA      120
TACCACCTGC TATGCGAGAA GATGGTAGCG AATTTGATAA AGATCTAAGT AATATCATT      180
CATTAGATGA TATTAATGGT GATATTCATA TGCATACAAC GTATAGTGAT GGTGCGTTTT      240
CTATTCGAGA CATGGTAGAA GCAATATCG CAAAAGGTTA TAAATTCATG GTAATTACTG      300
ATCATTCACA AAGTTTACGT GTTGCTAATG GCTTACAAGT GGAAAGACTT TTTANGACAA      360
AAACGAAGGA AATTAAGGCT TTAGATAAAG AATATAGTGA AATTGGATAT TTATTCAGGT      420
ACAAGAAATG GATATATTAA CCTGATGGCT CGCTGGATTA TGATGATGAA ATTTNAGCAC      480
AACTTGGATA TGTNATTGGA GCTATTCAAC AAAGCTTNAN CCAATCAGAA GAACAAATNA      540
TGGAACGGAT TAGCTAATGC ATGTCGCAAT CCATACGTGC GACATATAGC GCATCCAACA      600
GGGCGTATTA TAGGTAGAAG AGATGGTTAT AAACCGAATA TTGAACAATT AATGGCATTA      660
GCTGAAGAAA CGAATACAGT ATTAGAAATT AATGCCAATC CACATCGACT GGATCTTGAA      720
CGCTGAAATC GNTCGNNAAT ATCCAAATGT GAAATTAAC TTTAACACTG ATGGGCATCA      780
TNCAAATCAA TTNGATTTTN TGGAAATTATG G

```

(2) INFORMATION FOR SEQ ID NO:705:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 568 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:705:

```

AGTAGGAAAT GCTTNCGCCA NTTANTTGNC CNCGGTTTCT ACCAAANTTN CCTGCATCCT      60
CCNAATGGAN ATAANACGNC AACCTCCNAC TAAACTTTGA AAATTCACC CTAAACTAAT      120
CCCCCATAGT AAAATCAGGG ANCCCAAATT TTTAGCGCTG CTAATAATGC CGGACCAATG      180
CGTCAATAAA GCTGGTTGCG TGTTTTCAGT TTCACCCAAT TTACCTTCTT CATCAGTAAA      240
CATTGTCTCT AAAATATCAA AGTCTAACGT CTTTGCTGCT GAAGTTAAAA TTTCAGTTGC      300
TTGATCATTG TTATTAAACA AATCTTGTGC CATACCAACT TTTTGGGCAC CTTGTCCCCG      360

```

AAAAATAATT GCTGTTTTAC TCATTGATT CACCTACAGT CTCTTTCATT GTTGTACAA	420
TATTTTGTTT TCCTGCGATT TTCGCTTGTC TAATTGCAGA ATAAAAAGCT TTAGCATTTG	480
AACTACCGTG TGCTTTAACT ACAGTACCTT CCAATCCTAA TAATACTGAA CCACCGTATT	540
CTGAGTAATC CATCTTTTGA GCGAAGTC	568

(2) INFORMATION FOR SEQ ID NO:706:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 595 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:706:

CCANCGTTTT CTTAATTGCC CAAGCCTTCA AGNNATAAGA AGAATCCCGA ACCNAAGCAT	60
ATCGTCTCTC AATTGGATC CGATTTGNAC ATANNNAAGA TGCTTTAGCC ATTAAGNNNA	120
AGTGNMNAAT NAAGTTGATA AATCTATTAA AACCAAGAAG TGAAGCGATA AGCTCAATAT	180
CAAGTTTAAC CGGAATATTA TTATTTGTAA CATCATTTTT AGGTATTACA TTCTTGATTG	240
CTGTATGTTG CATTATATAC ATTAAGCAAA TAGATGAAAC CGAAGATGAG TTAGAGAATT	300
ATAGTATATT GAGAAAGCTT GGATTTACAC AAAAAGATAT GGCAAGGGGA CTAAAGTTTA	360
AAATTATGTT TAATTTTGGG TTACCTTTAG TTATTGCACT ATCACATGCA TATTTTACAT	420
CATTAGCATA TATGAAATTA ATGGGTACAN CGAATCAAAT ACCGGTTTTT ATAGTAATGG	480
GATTATACAT TTGTATGTAT GCTGTTTTTG CAGTGACGGC TTATAATCAT TCCAAGCGAA	540
CAATTAGACA TTCCATATAA AATATACAGA TGGCTTTCAG TAGAGTAGTG GATTC	595

(2) INFORMATION FOR SEQ ID NO:707:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 992 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:707:

ACCCTGATTT NCCCATCCAA TATATCCAAT TGAAACTTTT TAATTTACCT TCGCTTGTA	60
AGCCAANTTC ACATGATGTC CATGGTTCTA AATCTTCCTA CNNTGNGAAA TGCGTNTCNN	120
GAAACTTCTT AANCCAATCT ATATAAATCC GTCCACAAAT CATAAAATAC TTTTTCAGAG	180

ACATAATACT	CTCTAGGGAT	ATATGTGTAA	TAATTCAATT	CATCACTACC	TGGTTTAGTA	240
TAATTAAGAA	TGACTTCCCC	AGCTTGATCA	GTTACATAAG	CTATTGTAAA	TACTTGCTCC	300
CATTCTACTG	GTATCATCCC	ACTAATCTCA	TTCGCAATCT	CGTTGTACAT	TTGACTTAAT	360
TTTTCTTCAA	AATTCATGTT	ATCGCCCCTA	TAGTTCAGCT	TCATCTTGCT	CTTTAACATA	420
ATCTTTTATT	TTTTTACCCA	ATTTATGGCA	TATTCTTTTT	CAGGCCAAAT	TCCAAATTTT	480
TTATACATGT	AATAATGTTT	TCTTCCCATT	TGTCCAAACT	CTGTATTGAC	CCAATCAATA	540
TAATCAAATG	AAACTAATTC	AATTTGCCGT	CTCTTGTAAG	GTCAAATTCA	CATGATGTCC	600
ATGGTTCGAG	TCCTTCTTCT	TTAAATAAAT	CTCTTAGTTT	ATCAAATNGC	TTATATAATT	660
CATATACTGA	GTCCATAAAT	TCTGATCTTG	ATATATTATA	TTTATTTAAC	ACGCTCGTAT	720
AGTAAATAAA	TTCATCACTT	CTTGGCTCAG	TATAATTGTA	GAACACTTCT	CCACTNCTTT	780
CATTTACATA	AGCCATTGCA	TATACCTTTN	CCCATNCTAC	CGGTATCATA	CTGNTAATTT	840
TATTTGGAAT	TTCATTGGTA	CATTTGACTT	AGTTTTTCTT	CCGAAAGTCA	TATTATCCGC	900
CCCTATTGGT	TCAAGCTTCC	ATCTTNGCTC	TTTAAATATT	TTTGCTCGGA	TTTCTTTTAA	960
TTTCTTCCCA	ATTTTCATATT	CCCATTTCTT	GG			992

(2) INFORMATION FOR SEQ ID NO:708:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:708:

GAATCCTTAG	TTTAAATTAA	ATCCCATATC	AATTGATCTT	CAACATGAAT	ATATCGATGT	60
ATCGGATCTT	TAAAACTTT	TTCTTCTACT	AATTTTAAAT	CTACATATGC	GTTAGTCATT	120
ATTCCCCTCC	TTTTCGTTTA	ATATAATATT	TAATTTACTT	AAAATGCCTT	GTACATAAGT	180
GCTAAGTCTA	ACTTTTCGCC	ATACATTTCT	GGCTGATAAG	AGCGTAAGAT	TGTAAAACCT	240
TGCTCTTTAT	AGTAAGCTAC	TGCTTCTNCA	TTTNTATTAT	CTACTTCTAA	GTAAACACCT	300
ACAAATTTAT	CTTCAAAACG	TGATAATCCT	TCATTTAACA	AATGCTGTAC	CATAACCTGT	360
ATGGTTGGAT	TCTGGTTTAC	ATAATGAGCT	GATAAATATA	ATTCTTCACA	CCGNCAAATA	420
AAGTTAGCAA	AGCCACGATG	TCATTACCTT	CCTCCAACGA	CTAAGAATAA	TGGTCTTGGA	480
GGGCTTNTCT	TTTAAATGAT	GGTCCAATAT	ATGAAGCTCC	TTACAAAGTG	GATAACTGGC	540
GAGGG						545

(2) INFORMATION FOR SEQ ID NO:709:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2247 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:709:

```

AGCAGAATCT TTTTGTAGCAT GATCTGTCAT AATGATCATA CGCTCTGGAT TTAAATCAGC      60
TAAATGTTCA GTGTCTAATT GTAAGTAAGG TCCTTTCAAA TATTTACTTA AACCTTGTGT      120
TACATCGTCA CTTAATGCAT TTTTAAATCC TAGNTCGTTT AAAAATTGTC CAACATATGA      180
ATAGTGTGGA TGTGCTAATA AACCAGCTTT AGCAACTACT GCTGGAAGCA CTTTGTGATT      240
TCTATCAAAT TTAATTTTCAT CTTTATACTT ATTGATTAAT TTATCATGCT CAGCAAGACG      300
TTTNNCGCCT TCTTTNTCTT TATTTAAAGC TTTAGCAATT GTTGTGTAAC GAATTAATAT      360
TGTGGGTGTA GTCTCCATCA AAACCTCTTTA ATGATAATGT GGTGCAATGT GGGCTAATTC      420
TTTATTAATA CCCTTATGTC TACTGCTATC AGNGATAATT AATCCCGGNT TTAATTTACT      480
AATNTCTCTT AAGTTNGCTT GTTACGTGTA CCTACAGAAG TATTACCCCC AATTTTCTCT      540
TTACTGGGTT ATGATACGTT TTTTCTTACC ATCATCAGCA ATACCAACTT GGTNTAACGG      600
CTATATGCTG NTAATGCAAC CTGCAAAATG AGTACTCTAA TACAACGATA CGTTGTGCAT      660
CTTTAGGTAC TTTTACTGTA CCATTTTCAT CTTTACCCG AAATAGTATC TTTAGTTGAT      720
GATTCTTCTT TTAATTGAAT TATCCGTATT ACCACAAGCT GCAACTAAAA GTAAGGCAAC      780
TATTAATCCC AATATACTAA AAGTTTGTAG ACCTCTCATC NGTCCCACTC CTTAATATGT      840
ATANCTTCAT TTATTATTTT ATTGATAACA ATTATCATTG TCAAGTAGCG TTCAATCTTT      900
TTTATATTTT TAAAATGTAT GACTATATAT TTCTCTAAT AATTATGACT ACAATTAGCA      960
CATTTCCCTT GACAAAATAC TGATAATGTA TCATTGCTAT ATCATCTTTG CATTAATACA     1020
ATTGACACCA CTTAGCATGA CCGNTATCCC TGTAATTCAG CTGATATTAT CTGTTGCAAT     1080
TTTATGTGAC GAACTGTTGC ACTTAATTTG ATAANTCAAC AANTACAANA NATCTAAGTT     1140
GAACAATTAT GATACAACCG TGCAAACGAT ATGTAGTATA ACTTGTC AAC TTAGAATTAT     1200
TGATAAATAT ATTAATATTG GTTTACCATA GCAGGAGATT TCACATCAAA ATTTTGAAGT     1260
AGCGTATCAA TCTTTGAATC ATCAATATAT ACCTTATGTA AATTTTTCAT ATACATCGAA     1320
TGAGAAAGTG CTTCATAATT TAATGAAAAA GATATATGAT CTCCAACCTG ATAGTGTCTT     1380
TGACCATTTA AATCAAGCAT TAAATGATCA CTCGAAGCGC CTAAAATATT GATATGCTGA     1440
TCCATAGGTG AAATATTATC GACTTGTGTA TCTNAAATAA CCAATATCTA CAATAGCTTG     1500
TAAGAATGAT TCATGCGTGT GTGTATTAAC TCGAGGTTTA ATTTCTAAAA TCTCAGCCTC     1560
CAATGTAATC GCATCTTGAT ATAACATAGC GAATCGCTTG ATTTGCGTTG TTTCAACAAC     1620
TCTAAACAAC GTNTCANCTA TTCGGAANTC AATTTATTTT TACCCAAATC AATATATAAA     1680
AGGTGGGGGG NAACATGCTC CGAATTACCA CCCGGAAATA ATTTNCANTC GATATCCTAT     1740
TTCTCTTNCA ACAGCTGAGA CGAATCGATT AATCATAAAG ATATCANCAC CACTTGGCGC     1800
ATCAGATTTA AAACACATAA AATTGAATGC TAAACCTACA AAATGGATAT TTTNCAAGTG     1860
AATAATCTCT TTANTATAAT CTAAACATC ATAAGTCAGA ACACCTTCAC GGACATCTTT     1920
CCAATCTACC ATTAATAAAA TCTTATGTTT TTTTCTTAAA ACTTCTGCTA CTTTATTAT     1980
NTGATGTATG GTAGATAATT CTGTGTGGAT ACTCATATCA ACTTTCCTCT ATCATATCTG     2040
AAATCTCTTT TGNGGGAGGC GTACGCAATA ACGTATATGT TAAATCCTGA TCTGCAATAC     2100
TAATTATGTT ATCCAATCTG GATTCTGCAA CATGATTGAT ACCTAACGCT TTTAAGCTTN     2160

```

CTACAATGGT ACGGGCANCA GCTATACACT TAATTACTGG TGTGANTNGN ATATTTTTC 2220
TTTGAAAAC T NNGTGGAGGT ACTTGGG 2247

(2) INFORMATION FOR SEQ ID NO:710:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:710:

TGATGCAAGT TGTATNATTT TCAAACCCCC NNCCAAGAT CAAGTAAGAC AATGTATAAT 60
GTGGCAGCAA CCGCGACAGG TGCAAAAAGT CATTTAAATT GAATTGGATC AAGATGATCA 120
ATTAATTAAA AATCTTGAAA ATAGACAAAT TGTACAAGCA CATCCAATGG GAGGCATACA 180
AATCATACCG GAAACCAATC AAGTTATTAG TCCAAGGTTT GGAACATTAA CAAATATGAT 240
TGCGATAGGT CAAATGACAA ACGGTGTTAA TAACTACGA AATGGTGTGA AAATGATAGT 300
AGAACAAGTT GCGCATACAG TATCTCAATT ATATGATGCT TTAGAATCGA ATGAGCAACA 360
ACAGCGCAGT TACAATCAAT AATTTGTAAC TAGANGATAA TAANGNGAAC GCTCTAGAGA 420
GACGAATTGA AGGTTTGGAT TTTNCTGTCT TGTTAGTAAG CATCATATCA ATGAGATGCC 480
TATNGTCCTC AGATTATATT A 501

(2) INFORMATION FOR SEQ ID NO:711:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 775 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:711:

AAGCTGNCCG ACAATTCAC AATTGAAATC CCACATCATT ACCNAAGATA AAATTAAGAN 60
NNCCAGTAAT GGTGGNACA ATACTGCTGT TGCTACAAGT TCATGATATT TCAAGATACT 120
ATTCANCGGA TTAAGTGGCA TTCCAGTTTC TCANATGGAT GATAACGATA TTGNACGTTT 180
AAAAAATATT TCTAATCGTT TAAGAAGTAA AATCATAGTC AAAGATCAAC CTGAAGNNAT 240
GGTTTCAACG TTGCAATTCTN CCGTAATCGC GCCTGGGGTT TGATGACGGC CAACCCGTCC 300
AATTGGTAGT TTCTTAATTT TGTCGGCCCT ACTTGTGTGT GGTAAACAG AGCTTGCTAA 360

ACAATTACCA	ATTGATCTAT	TTGGTAATAA	AGATGCACTT	ATTCGACTTG	ATATGAGTGA	420
ATATAGTGAC	ACAACAGCTG	TTTCAAAAAT	GATTGGTACA	ACTGCTGGTT	ATGTCGGTTA	480
TGATGACAAT	TCAAATACGT	TAAC TGAAAA	AGTACGCCGT	AATCCATACT	CAGTCATTCT	540
ATTTGATGAA	ATCGAAAAAG	CAAATCCACA	AATTTTAAACA	TTGTTATTAC	AAGTAATGGA	600
TGATGGTAAT	TTGACTGATG	GTCAAGGTAA	TGTCATCAAC	TTTAAAAATA	CAATTATTAT	660
TTGTACATCA	AATGCTGGCT	TTGGCAATGG	CAATGACGCT	GAAGAAAAAG	ATATTATGCA	720
CGAAATGAAA	AAATTCTTCC	GCCCTGAATT	CCTTAACCGC	TTCAACGGCA	TCGTT	775

(2) INFORMATION FOR SEQ ID NO:712:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:712:

ACTTGTGCAC	TGCCAATAAT	AATTAATCCT	TTCATATTTG	ACCCCTCTTT	TTTTTATTAA	60
ACTTGTGTGT	CACGTAATAA	TTTCATAATA	GCTTTTCCAA	CACCACTATT	TTCATTTCGTA	120
TCTGTGACAT	ATTTCGCTAT	TTTTTTAACT	TCTTCTGCAC	CATTTTCCAT	CGCAACTGGA	180
TAGCCAACTT	TCTCTAACAT	TGATAAGTCA	TTTAAATTGT	CACCTATTGC	CATGACATCT	240
TTCATTTCAA	TCCCTAATCT	TTCCGGCAAT	TGTTTCTTAG	CGCAATACCT	TTNTGGTGCA	300
TCTTGAATGC	GTTATTTCTT	ATTTTTTCCT	CTCGAAGATG	ATGATATTAG	CTTAAATTCC	360
GGAGATTCCA	AGTTTAAAAT	TTTTACTTAG	CTTTGGTCAA	ATTTTCTTTA	AATTTTCCAT	420
CAAAATGCTT	ATATTTTCCA	ATAATTAATC	AACCAGGTNT	TTTGTTTTTC	CA	472

(2) INFORMATION FOR SEQ ID NO:713:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:713:

ACTTGTGCAC	TGCCAATAAT	AATTAATCCT	TTCATATTTG	ACCCCTCTTT	TTTTTATTAA	60
ACTTGTGTGT	CACGTAATAA	TTTCATAATA	GCTTTTCCAA	CACCACTATT	TTCATTTCGTA	120

TCTGTGACAT	ATTCGCTAT	TTTTTTAACT	TCTTCTGCAC	CATTTTCCAT	CGCAACTGGA	180
TAGCCAACTT	TCTCTAACAT	TGATAAGTCA	TTTAAATGT	CACCTATTGG	CATGACATCT	240
TTCAATTCAA	TCCCTAATCT	TTGGGCAATT	GTTTCTAGCG	CAATACCTTT	NGGTGCATCT	300
GAATGCGTTA	TTTCTATATT	TCCTCTCGAA	GATGATGATA	TAGCTAAATT	CGGAGATTCA	360
GCTAAAATTT	TACTAGCTTN	GGCAATTTT	TCTTAAATTT	CCATCAAATG	CTAATATTTT	420
CATAATTAAT	TCAACAGGTA	TGTTTTCAAT	AGGATCATAA	TTATCAACAA	CTTTCAACGG	480
TNCCAATATC	TATGCGTCTT	TGNATACCAT	CTTNAATACG	CTCAACGTNT	GGATGTTGAC	540
CTGCACGCTC	AGCAATATCT	ATGTAAATGT	CTAAATCTCT	TGGGGGATCT	TCCAGTATAA	600
ATCGCACGAC	TCGGNTATNC	TGGATAATAA	GTACCTGNAT	CTTTTAAAAC	ATNTGTAATG	660
NGGTGTACTA	ACGATTTATT	ANGGNGTGAA	GTGCTCATTA	CATTGAAAGT	TTCATCACGT	720
TCTTCAGNAC	CATTCAGACA	AATATATGGT	ACTGNTAAAT	CTGTGTCAGC	AANTGGTGCT	780
TGTGCTTCAA	AAAATGCTCG	ACCTGGCACG	AGCGATAACA	ACCGTTATCC	CTTGTTCTTG	840
AGCGTATTNA	NTCGCATCAA	TATTAGGTTG	AGAAATTTCA	TNTGCTGCAT	TAAGGTAGCG	900
NGCCATCCAT	ATCAGNGGNT	ATTAGGTTTN	TCANTATGTT	NCCNCGCCCN	CGNCTTTTCGT	960
AAATTTAAAA	TCTTGTCTT	AAATAAGAAT	ATATACTCAG	CGCACATACT	TTTCTATTAA	1020
CATTTATATT	GTCATTAATT	TATCATATAA	TGTAATTTCTA	ACAAATTTTA	ATTAGTATGT	1080
ACTATCGTCT	TAATTGGTGG	ATTTCTTATT	GGCTCTTAAG	TTTTTAAAAA	ATGTTGGTTA	1140
ATAATGGTGC	TACATGCTTC	TTTTAAGGTA	CAACCTTTAT	CAACAAATTG	GACGGATGAT	1200
TAAAAATTAG	GTNNGGTTGG	AAATAAATTC	AATTAACTT	GCTACTACAA	ACCACC	1256

(2) INFORMATION FOR SEQ ID NO:714:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:714:

GAATTCGCT	GTAGGCGTCC	AATTTCCAAA	TGTACCACCA	CCCATCAAGA	GTAATAGATT	60
CAATATGCTC	AGCGATTCTT	GGATCACGAA	TCAATGNCGT	TGCTACATTC	GNAAGAGGAC	120
CTGTCGCTAC	AGAAGTAACA	GGTGTATCAN	TCTTCTACAC	NCGGTTCAAT	ATCNNNACTC	180
ATGCTGGCAT	TGCAACTGCT	TGACGTGATG	GTGTCGACGG	TAGTTTCGGA	CCATCTAATC	240
CAGATTCCCC	ATGTATTTCA	GAAGCAAAGG	CAGCTGGTTT	AATTAACGGC	CTATCCGCAC	300
CTTTCGCTAC	TGCTATATCT	TGGCGTCCCA	TAATATCCAA	TACGTCCAAG	GCGTTTGTCC	360
TATNCTTGTC	AACTGATTGA	TTACCTGCGA	CTGTTGGTTA	CAGCTTAATA	TCTCTAGTGG	420
ACTTGTCACT	NGNCCCCGCT	TAAAATTAAT	GGTATTGCAT	CAACGGNGTC	CTGGATCACA	480
ATCCATAATA	ATCTTCTTA					499

(2) INFORMATION FOR SEQ ID NO:715:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:715:

```

TCTTATACAG GAGAAAATGG CATAGATGGT ACATCTGGAG CAGCTAAACG CATGATTGGT    60
GCATCTAAAT CGAACAAGCA ATGCTCTGCA ATAATCGCTG ACACTTCTGA CATAATACTA    120
CCTTCTAAAT TATCTTCAGT TACAAGTAAA ACTTTACCTG TATTTTTCAGC ACGATCAATA    180
ATTGTTTCTT TTATCTAATG GATAACAAG NNCGGTAAAT CAACGACTTC AACGTNNGAT    240
ACCCGTCTTG CAGCTAAAAT ATCCCGCTGC TTGGGTAAAC AAATAATTGA CCCATTATC    300
CCATAACAAA AATACTNGTT AAATCTTCCA NCCTCANC GG TTNTACATCT TGCTTTTCCT    360
AAAGGTACAA GGGGTAATAT TCCTCCTNGA ACTTCTTCCC CCNTTAAAGA ACGATAGCTT    420
TTTTATGCTC AAAGTACAAT ACTGGGATCC AATTGGGGTC CGGTAGATGA TAATAAAGGC    480

```

(2) INFORMATION FOR SEQ ID NO:716:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 548 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:716:

```

GAATTCNAAT ACTTCTTCAT AGAANANGTT TGTAACGTTA GATTTAGTAG TTAAAGTAAG    60
GTCATAAATT TACAATATGC CTTGAATTAA ATTATGTTTA GACTGAGCAA AACTCTCATT    120
TTTAACATCC GCTGTAATTT CTNTATCAAC TAATTTTAAA TTAAATTGAT TAAAAATATT    180
CTGTATAAGT TTAGCTCTCG TTTGTGTGTT TATATCAATA CCCAACATTT CTAATNCATT    240
AATCGACAAT CCGACATCTG ATAGACAAAT NNCATTATTA GGNAGTGTAT CAGCATATAT    300
TCTAATAAAA TCACACAAAT GGCTCTTAAN GGGAGTAGTA ATTTCTTGTA GAACTATCTT    360
AANTCTGNNG AAGATATTAA TTGNGGCTTT ACNCAGGTGG ANATATTCCG NAACTCTTT    420
CTTCCGATAG TCTTCACTAA GTATCCCCC ANNTCTTNNA CAAGAAATCT TGGNTCTTNT    480
ATNACAANAT CGGGTNTNTN TTAGGNTTAC TCCAAAAAGG AGGCTTAATG ATCCTATNAN    540
NCCACCTG                                     548

```

(2) INFORMATION FOR SEQ ID NO:717:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 597 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:717:

```

TTGTCATTAT AAGCCCTCCA TTTCATGATT TGATTTGCCA CTCGGAACCA TTGGGGTTAC      60
AGCTTCAGTA GGGGAAATAC GAACCTCAAT TAAAACTGGT CCTTGATAAG CAAACGCTGC      120
ATCTAATTGT TCTTCCAGTT GTTCTGGCTT ATCGATTAAAG AAACCTTTGA CGCCATATGC      180
TTCTGCCATT TTCATAAAAT CAGGTTGACC ATTAAATACT GAGTGTGAGA AGCGTTGATT      240
AAAGAACTTA TCTTGCCATT GTTTAACCAT ACCTAATGTT CCATTATTGA TTAGTACGAT      300
TTTGACATCT AAACCATATT CGGGTAAAAG TGCCATTTCT TGGTTTGGCA TTTGGAAACC      360
ACCGTCACCG ACGAAACATA CGACTGTTTT ATCAGGATTA GCTAATTTGG CACCAATTGA      420
CGAAGGAATA CCGAATCCCA TGGTTCCTAA ACCACCGNTT GTAACCCATT GTCCGTGATT      480
TTTAAATGGA TAAAAATGAG CTGCCCCACA TTTGGATGTT GTCCACGTC TGTAGTAACA      540
ATTGCTTCAN CCATTTGTAA TTTTGGCCGA TATATTCCGA TTGTTTGTG GTGGCTT      597

```

(2) INFORMATION FOR SEQ ID NO:718:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:718:

```

CCAGGAGCCA TATTTANCGA TGATGNACCC ACACCGCTAT TTA CTNAAG AANACATGGG      60
ATGAAAAGAA ACCCGCTTGT ACAGTGATAN CGATGTACCC TCATTTAAGA TGGTGTATTA      120
TCACTCGATC TCACAACTGT TCTTATCCTC AATCAATTAG CTAATACTTG AACCCAAATG      180
GTGCTGTATA TCTTGTAAT CTATTTTCAA ATATTAGAAC ACCCGAAAAC CTCANACATA      240
TCACAAATCC ATACGATGAG CACACTGATA TTCATTTGAT GAAAGCGATT AGTGAAAGTG      300
ACACAGTGAT TCTTGCTTAT GGTGCCTATG CGAAGCGACC AGTTGTTATC GACCGTGTCTG      360
AACAAAGTAT GGAAATGTTA AAACCTCATA AAAAGAAAGT AAAAAAGCTC ATCAATCCAG      420
TAACAAATGA AATTATGCAT CCACTCAACC CTAAGGCACG TCAAAAATGG ATTTTGAAAT      480

```

CATAGCAAAT ACATGGAGGT CAATATGGAA ACAAACAAA TCAACATCGT TTTACTGTAA 540
 ATGATATTGT TGAAACAATT CCTGACAATG AATTTCGAC 578

(2) INFORMATION FOR SEQ ID NO:719:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 932 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:719:

AAATATTGAT AATGCTAGTA NCCCCTGTAC CTTANTCTTT TCAAAACAAT ATCTCCTCTA 60
 TAAGTCGAA AATCAATTGA ATAAGCTTGG AAATACAATA TCTNNCCATG TGTATCATTT 120
 CATGGGCTTG TGTACCCAAA AGACGGCAAC ATTAATATGA TNTGANTTAT CACNAATACC 180
 CATAACTACA ATCTAAGGTT CTTTTTATTA TACCCTAATT TTTGTTCAAT ATTATTTAAT 240
 TTTTGTGAAT TTTATGTTTT CTATAAATTT AATTATTTTA CTTTAACAAT TCATTACGCA 300
 TTTAGCATTT CAAGGCATAC ACAATATTTA TTACTATGAT TTCATTTTAT CTGCTGCAAA 360
 AACAATCATT ATAACTCTTT TTCCATAATT AAATCTGTAT CCGTTACATC ACCTGTGTGA 420
 AAATGATGTT CACCACCCAC TTAAATCCA TGACGTTTAT AAAATGCTTG AGCAGCAGGA 480
 TTATGCTCCC AAATCCTAG CCAAATTTTA TGTTTATTAT GTTCTTGGAG CAATTTTTTC 540
 GGCCAATTCT ATCAATTGTG AACCTCTTCC GCCACCTTGA AAGTCTTTCA AAAAATATAT 600
 GCGCTGCACT TCTAAATAGG TCTCCCCCAT TTCTTCAGTT TGAGCACTAT TAATATTCAT 660
 CTTTATATAA CCAACATTCG CACCATCTTC TTGATAAAAA TAATGAAATG AATCTACATG 720
 GTTAATCTCT TGTGTAAATT TNTCTACAGN ATAATTGTCT TNAAAAAATT GATCAAAATC 780
 TTTGTCATCA TAGTAAGAAC CAACGTGTCA TAAATGTTC TTGTTGNTAA TCAACTAATC 840
 ACTAGCATTT GGTCTGAATT CTTNGATATC CCAGCCATTT AATCCTCCAA TAACAGGGAT 900
 GGATCAAATA TTACTATGTT ATTTNCAGCC AC 932

(2) INFORMATION FOR SEQ ID NO:720:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:720:

TTGAAACAAT	CTAAAGAAAT	TCCATTTATC	ATAATCATCC	AATTTGCCTG	CATATTGATT	60
AATACTGGCC	TTTGGCGTGT	TGCATTACCA	TTGTTTATTT	CCAATATATT	AAAAGAGGGC	120
GTTGGTGTAT	ATGGACTAGC	TACATCATGT	TTAGGTATAG	CATCTTTATT	AATGTCATTG	180
ATTATGGGTT	TACTATCAGA	AAAACGATTA	ATCTTTAAAT	TTAGTATTGG	TGTTTITAGTT	240
TGGGGGATTG	GCTTATCGAT	AATTAATGTG	TTTCCAAGTG	TGGCGATACT	ATATATAGGT	300
GCAACATTAG	TGGGACTTGG	ACAATCTATA	GAGGGACTAA	CAAGATCAGT	TGNCATNCAA	360
ATTAAAAATG	CCAAANCATT	TGGATGGGGG	AAAGGTATTT	AGGNATATCT	CANCTTACAA	420
TCGGAATCTA	CGCAGGNCGG	ATNCAATTAT	CTTTAGGGAC	TNGATAAGGT	TTTAATTATA	480
CCCTTTACTT	AAGCTTAAAG	TAATATT				507

(2) INFORMATION FOR SEQ ID NO:721:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 659 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:721:

GAATTNCCAT	ATNGNACTAA	AATATCTCCC	AATCTGNGCA	TGAGTTTATC	TNGATTGTAT	60
CTATAGTTGA	CTGTACGCGG	TTTTTTATAT	GACCAACGAC	TGTGNGATAT	TAANTCTACA	120
ATACTTCACA	AGTTACTCTG	TAATTGCATN	ACAAATACTG	ACATAACTCC	CCCTACTTAC	180
TTATTGAATA	TTGTTGNGAT	ATATTGTGCC	CAATGATACA	GNCAATTGTT	AGTTATCGGT	240
GGACATTTCA	CACTGATGTG	ACACATTATT	TTTAATGTTA	ATGTGTCACA	ANTCTATTAA	300
CATTATTAGC	AATGTACTTA	CTCAAACATN	CACCTGAGAC	TAAAGCAGNA	CCAATCAAAG	360
GTATGAAAGC	AGAAGCTAAA	AAGTGTGACG	TTATTGGTTT	AGACATTINA	GTAGGGACGA	420
TGTTAAGTTT	AAATGTAATC	ATCACACAGA	CGTCTCATGT	GGGGTTAGTT	TCACAACGTT	480
AATTCTAGGT	TTAATTGTTG	TGTTTATCTG	TTCATTAGTT	GGTTTTGTAT	ATTACGAAAA	540
TAAATAAAG	CATCCACTTG	TTGATTTTTTC	AATTTTTTAA	AATAGAGGAT	ACAGTGGTGC	600
AACTATTTCA	AACTTCTTAT	TAAATGGTGT	AGCAGGTGGT	GCACCTATCG	TTATTAACG	659

(2) INFORMATION FOR SEQ ID NO:722:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:722:

TGNAATAAAC	NTCAAAGCAG	TAAGAGAGGG	TCATAATACA	AGCCTCATAG	ATAAAGGCAC	60
GTATATGGAT	ATGATGTATA	TGGATGATGC	AATTGAAGCA	ATTATTAAAC	TTATGGAAGC	120
AGNCGACGCT	AAATTAAGAA	ACTAGAANCG	GTTATAATTT	GAGCCCAATG	AGTTTTGATC	180
CAGAGATGGT	AAAAGAAGCA	ATTCAAGAAT	ACTATCCAAA	TTTTACATTA	GATTATGATG	240
TTGATCCTAT	TAGACAAGGT	ATCGCTAATA	GTTGGCCGGA	TTCTATTGAT	ACAAGCTGTT	300
CACGTGGCGA	ATGGGGATTT	GATCCTAAAT	ATGATTTAGC	GAGCATGACT	AAATTAATGT	360
TAGAAGCTAT	TGAACAAAAA	GATACTGTTA	AAAATAATAA	CTAATCATTT	CCATTCAC TT	420
TAATACACGG	AATGATATTT	TAAATTACTC	TTTATTTTAA	TAAACTAGTG	CATGAATTCT	480
AATATTATTC	ATTATACATA	TT				502

(2) INFORMATION FOR SEQ ID NO:723:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1039 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:723:

TTGGCCCCAC	CAACCTGGCG	GTTATTAAAT	ACGGCGATGA	TTGTCCTGAT	AATGTCAGTG	60
ANCCACAATA	TACACATTGT	GTAAGAGCAT	CAGTCATAAA	CACTTAAAGC	CCNAATTAAA	120
CCAACGCACA	CGTTAATATA	ACNCGGCCAT	TTGGTGATTG	CNCTGGAAGA	TGGCCGCCAT	180
CGACCGTCAA	TCCACCCTGA	AAAGNTCATT	GGTAACAAC T	TCAACATCAT	CAAGCTGTCTG	240
GAGAGNCATT	TGGTGTATTT	ATTTTGAGAC	ACAAAGGTCA	AATTGTCCAT	AAGGNTAAAA	300
CAATTGGACT	TCAATTAGAA	GACNTGAAT	CNNNAGACTT	TATTTTTGCA	GTTGCAGGAG	360
GCAAATCGCN	AGGTGAAGCA	ATTAAAGCAT	ACTTGNCGAT	TGCACCCAAG	AATACAGTGT	420
TAATCACTGA	TGAAGCCGCA	NCANAGATAA	TACTTGAATA	AGAGATAAAA	AGTTTAATAC	480
TTTTTAAATA	TCATTTTAAA	GGAGNCCATT	ATAATGGCAG	TAAAAGTAGC	AATTAATGGT	540
TTTGGTAGAA	TTGGTCGTTT	AGCATT CAGA	AGAATTCAAG	AAGTAGAAGG	TCTTGAAGTT	600
GTAGCAGTAA	ACGACTTAAC	AGATGACGAC	ATGTTAGCGC	ATTTATTAAA	ATATGACACT	660
ATGCAAGGTC	GTTTCACAGG	TGAAGTAGAG	GTAGTTGATG	GTGGTTTCCG	CGTAAATGGT	720
AAAGAAGTTA	AATCATTCAG	TGAACCAGAT	GCAAGCAAAT	TACCTTGGAA	AGACTTAAAT	780
ATCGATGTAG	TGTTAGAATG	TACTGGTTTC	TACACTGATA	AAGATAAAGC	ACAAGCTCAT	840
ATTGAAGCAG	GCGCTAAAAA	AGTATTAATC	TCAGCANCAG	CTACTGGTGA	CTTAAAAACA	900
ATCCGTATT C	AACACTACAC	CACCAAGAGT	TAGACGGCTC	TGAAACAGGT	GGGNTCAGGG	960
TGCTTCCATG	TTCTACAAAC	TCAATAGCAC	CCAGGTGGNT	AAAAGGTTTT	ANACCGATGA	1020

CTTGGGTTTA GGTGGAGGG

1039

(2) INFORMATION FOR SEQ ID NO:724:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:724:

ATTTAAAGTN	GAAATTGCCC	AANATGGGTT	CCGGCCTTGT	AAAAAANCTN	TTGTTGTTTA	60
CCCATCGGAT	TTCCAGGACN	TTGCTAATTT	GTNTTAAAAA	TGGACCCTGT	TTGAGAAGCA	120
TGTGCNTCCA	AATGCCTTAA	TTTAAAGTTC	TTTAAATCT	GTAATATCAT	TTTGAATATC	180
AGGTTCTCCA	AGAGCTTCGG	TTGCATCATT	ACTGAACGCA	ACTAAAGTTA	AACGAGGGCG	240
TTCTTCTTTA	GGCATGCGTT	CAACCGTTCG	AATTACAGCG	TCTCCTGTTG	CTTCGTGATC	300
AGGATGTACT	GCATATCCAG	GATAAAATGA	AATAATCAAT	GATGGATTNG	TATCATCGAN	360
TAAAGATTTA	ATCATACCAT	CTAGATGTTT	GTAGGGCTCA	AATTCGACAG	TTTTGTGCACG	420
TAAACCCATT	TTTCTTAAAT	CAGTAATACC	AATAACTTTA	CAAGCTTCTT	CTAGTTCACG	480
CTCACGAATA	CTTGGGAACG	ATTCGCGTGT	TGCAAATGGG	GGATTACCTA	AATTTCTGCC	540
CATTTGTCCCT	AGGGTTAAAC	ATGCATATGT	TACAGGTATG	CCTTTGTGGA	TAGAACTTGC	600
TAATGTGCCT	GCAGATGAGA	AGGTTTCATC	ATCAGGATGT	GGAAATAGTA	CTGAAGAACA	660
TGTCCTTTTCG	NCCAGTCAGT	GTGATGCCT	CCTCTATAAA	NNNNATGGTC	GCTCCACTAA	720
TNTGAAGTGC	TGCAGCGAGN	TGACCNTCGT	AANTAAAACC	TGCAATTAAA	AATTCATCAT	780
GTTCAATTGAC	CTCCCNATGC	GTTAGACCTT	GTACATAAAC	CCANCCACCA	TTTGATAGTT	840
TAAGACCAAT	GCGATAAGGT	TCTTTATTAC	CACCTTTTAG	TTGTGCATGC	GTATATGTTA	900
CTTGTATGTT	TCNTAAAAAT	TGTACCAGCA	TTAAAAACAC	GTTGATCGAA	ATGGTTCCGA	960
TAGGCCCCAT	TTGTCGTTTC	AACATGCAGA	TACACAGGTT	TATGTTCCAA	AAGAAGCAAG	1020
TAAATCTATA	ACTTCTTGTT	CTTTAATTGG	TTCCAACACG	TTCACTCCTT	ACACTATCAA	1080
TGTGTTTATC	TTTCTATTTT	ACTAAAAACT	ATTCGATAAT	TGTATACGAT	TGCTCAATTA	1140
TTTATAAATT	AATTTTCATG	AAGGGTAATT	ACTCAGGATT	ACGTAATCAT	ACAGCATTAG	1200
TTTTTTACTT	TTAAAAATCA	AAAATTTGTT	GGAATTTGAA	AAGTGTTAAA	CATTAAAAAT	1260
GATGCTATAT	TAATGGTGTA	TGAAT				1285

(2) INFORMATION FOR SEQ ID NO:725:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 557 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:725:

```

AAGTTGCTTT CTTGCTCTAG AAATAGGATT AATATTGCAT GGTATCGCAT CATAAGTGAT      60
TAGAGTGTTT TCTTTTTTGC TAGTTTITAGG ATTGTAAGTT GCTACTTGTT CTAATTGAAA      120
AATAACTCTA TCTTCATATC TCAAAAGAAC ACAGCCCTTC CTTTTTTAGT TCTCGTTCTA      180
GCATTAAAGT AATTATCAAT AATAGCTTCA TACTCCTTGA AATCGTTCAA TTCATACGCA      240
TTGCTACGTC CGTCAACCGC TTCTGATGTC ATACCTTCAG CACCAATCCT GTTGTAGCGT      300
TTAACTGCAA CTCTCTTAAT CATGTAAC TAACCTTTCCG GTATTTGTTC AACTTCAATA      360
GGGTAACATT GATAACAAC TGGCTTTTAC AACTTTNNAT GGATTTCTTC TAATTGGTCA      420
NCTTTGCTTT TNCATCTTTA AAGACCAATA CGGTTTNNNT ACATCAAGCT AGCGTAGGTC      480
ATATTAACCA CCTACTCTT AGGTGACTCA AAAAGCATTG GATAATTCA GCTTTGGGTG      540
GGGTTTCAAC AACTTTG                                     557

```

(2) INFORMATION FOR SEQ ID NO:726:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1257 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:726:

```

GGTAATAGTT TAAANATATA TTTTGCTCCC NNNGGNTGGA TGATATATGC GTGTANCAAT      60
AATAGNCATG GGNCTGCTG GTGTAAGTGT ATTGAGAGAG TTAGTTAAGC NCCCGAAGTT      120
TAATCAATTA GATATAGATT TATACGATGA TAAAGTAAAN ATGGGACAGG GCGTACCNTT      180
TCAAAATGAT AGTTCTGAGC TGCTAATTAA TATGCCTTTC ANANAGATGA GTTTAAATTT      240
AGATGATGAG ACTGAATTTT GGAAGTGGTA TAANCAACAA NCTGATTTTA ATTTTGATGA      300
ACCTGCATAT TTACCGAGAT TTGTATTCGG ACATTATATG AAATCTTATT TATCTATGTT      360
CACGAAAAAA TATCCAAATA TATCAACTAA TTATAATAAA GTTCAAGAGA TTTATACAAA      420
TTCTAATATC GATGAANCGA ATTTAACTTA TTACATATGT ACTACAAATT CAGAACAATC      480
ATGGCAAGCG TACGATTATG TATTTTAAAC ATGTGGTACA TTTGCCCTACC ATGATCCATA      540
TAACTTAAAG GGTAATAAAG GATATATCGC TACGCCTTAT CCAACATATA ATACGTTAGA      600
CGAAGTAAAT GAACTGGACG ATATTGCGAT TATTGGTACA GGCCTTGCCA GTTTAGATGT      660
TGTCCGTTAT GTTGCTGCTC ATCATCCGAA ATTACCAATT ACTATGACGA GTCGNTCTGC      720
TCATTTACCA AGTGTAAGAG GTACAATGAT AGACGTGACA TTCAAGTACT TAACTAAAGA      780
CAAATTAAAT GACATTAAAA AACATCATTT CGGCAATGCA CCGCTTGATA CTATAGNTTC      840

```

TTTTATTTTT	AAAAGAATGT	GCTTGAATAT	GACATTGATT	TTTAAAAAAT	TAGTACATAG	900
ACGTACAAGG	AAATCATATT	GCAGATTGGA	AGTATTGATT	TAGCGCCGTC	CCAACAGAAA	960
TGGGCATTTT	CCAAAGTATG	ATTGAACATT	TGANAGAGAA	TTTAAATTGG	ATATGGAATA	1020
GCTTAAGTAT	TGAAGATCAA	CATCAATTTA	ATCCAAAAAT	ACNCAAAGAT	GATTCAATTA	1080
AATCCAAATC	CAATNCCTCC	AAGANCTGCT	GAACATAATTA	TTGAATTAAT	AGAAAAGAAG	1140
TCTTTAATTT	TGAAAAAAGA	TTTAGAAGAT	GTGAAACATG	ATGGCAAGTT	GTATTATTTT	1200
TCATACACAA	ACCAAGAATC	AGTAGACATG	TATAATGTTG	TCATTAACGC	TCGTGCC	1257

(2) INFORMATION FOR SEQ ID NO:727:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:727:

CTACTAGCAA	ATAATATCTT	TTAATTTTAA	AATTAACTT	ACAAGTTCTT	CATAGGTATG	60
TACATACATT	TCTTTTGTTT	CACCGTATGG	ATCTATAACT	TCTCCTGCTT	CTTTTACATA	120
TTCATGCAAT	GTGAAAACAT	GATTTTGCAA	ACCAAAGTGT	GCCTCTATTA	ATTCTTTGTG	180
CGAATACGAC	ATCGNCAAAA	TAATATCTGC	TTTCAAATCT	GCTTCAGTAA	ATTGTTGCGA	240
TAAGGTCGGN	TTTCACTAAA	TGATGTTCTT	CAACTAAGTC	TTCAACATAA	TTCGAAACAC	300
CTTGATTGTT	CACAGCGAAT	ATACCTCTTG	ATTCAAATTG	ATGATTTGCC	ATAACCNCTT	360
TTGGAATACT	TCCCGCTAAT	GGGNTACGAC	ATGTGTTACC	TGTACAAAAC	GAATAAAATC	420
TTCATAGTTC	ACATCCTTTA	ATAATGTGAT	TACCNCGAGN	TTTTAACATG	GGATCCATAA	480
CNGGTTCTTG	NNTTATCAAT	CAAGTCAAGG	CCGNTTA			517

(2) INFORMATION FOR SEQ ID NO:728:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:728:

AATTAGTATT	TGTGGATCGT	TTAATTAATA	ATTGCCGGGA	GTATTATAAG	ATGGATCTGA	60
------------	------------	------------	------------	------------	------------	----

TATTATTAAG	TTGATGTTTT	GTGATGTTTT	GATTGTTTGG	ATTATTTTGT	ATGCTATTAT	120
TAGGTGGATT	TTATCGTCNG	CTTTTTTCAN	ATTTTCTTTG	TTGCGNTTTT	GGTGNNTGCN	180
ANCNTTGTGT	TGGTGTGTAT	GAGACNTTTT	ATTTTCTTCT	TTTTNIGGGT	TTTCTTTTTTC	240
ACCACAAGCT	GTAAAGCTA	AAGTACTTAC	TAGTAATAAT	CCAATTATTT	TCCTCATATA	300
CATTTCTCCT	TTTTTATATC	TCTTTGTATC	GATAAACTCT	CACCGNTCA	AATGTAATAG	360
AATACTCGCC	ATAGTGAGTT	CCAATACCAT	ATATCTTTTT	ATATTGTTCT	ATTGCTTCTA	420
ATATGTATT	TTGCTTAAT	TGTAGATACT	CAGACAACCT	ATACAAGTTA	CGTACGCCAT	480
AATTATAAGC	TTCTACAATT	TCGCGTAGCG	GTACAGCTGA	GATAAAGCCG	TGTCGTCTTG	540
CGTAATTTTC	GAACTTGGCA	TTGTTGAATT	TCGAGTAATC	GGCTATATCA	CCGTATGTAA	600
GTTTATTATG	TGCTAATTCT	TCGAAGAGAA	TACCTCTAAT	TTGTTCTTTT	CGGATAGGGA	660
AGGTCTAATA	AAAATTTCTC	CTTCTTGATA	CCAACCATCG	AATCCTCGAG	GTCTCGTGCC	720

(2) INFORMATION FOR SEQ ID NO:729:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:729:

TCTGTATTAC	CTNCTTAATA	ATCCTTCANA	CATTTTCAAG	GCCAANCTAA	GCCATCGGAA	60
TTAAGATAAC	CTTTGTAATA	GCTGAAAATA	TCGTTTCATT	AAGTTTCCAA	GCGTATTANT	120
GATTACACCC	CCAANAAGAT	TTATTTGTTT	CAGGGGCTAN	AGTCATANAG	NCTTAGAAGC	180
TGACCTGATC	CAANCCAANT	GNCNATCGAA	TTTTTTTCGGT	ATGCGTGTGA	NNATATTCTC	240
NGNTGCGATA	ACATTCACCT	CCTTAACGCA	TTANATCTTT	NATACTAATA	AATNCNATGN	300
TTCTTTCACC	CTTGTCAGAA	ACNNCTTTAN	TCATAATATC	TGTATATGTG	TTTGAAAATG	360
CTGCAAAACC	ATCTATTTNA	CGATATCTGC	TTTGTTTAGA	TGGCAGCCAG	TTCCCATTTT	420
TGTCTAGTTT	CAGCTGAACA	TTATTGATAT	ACCATTTTCT	TAAAGGATTA	TTATTAAATA	480
TTATTTTCCC	ATCTAAAAAC	ATTTCTTTTA	GATCCTTCAA	TGCAGGGCTC	AAGGTCAAAG	540
CCCCTTGCT	TGTTTCTTCT	GTTTCAAAGC	CATAATCTTT	TAACTCTTGA	TTTAATTTAA	600
AAGCATTCGC	CCTATCATAA	GTGATTTTTT	CGACAACATA	ATGCTCATTC	ATCTTTATTA	660
TCCAANTTAA	AACATCTTGG	TAGTCTATAT	AAGGATTATC	TTGTATTGTT	AGTAATCCGT	720
CTTCTTCCCA	TTCTATATAG	GGTATCTTTT	CGGGTAGAAT	ATTCAACTTT	ATGCTTAGGA	780
ATCCAAGAAT	TGTGTTAAGA	CAGCAACTTT	GCCATTATCT	TNATGNAAAA	GTGGCACATG	840
CGGCTGTAAA	GGCCCCNGNN	NCTTGATNAA	ATCATAANCC	ATAGGGACAA	NGGTCTTNCC	900
NTCCAACCTCA	ACTAAGGAAA	TAATGTCATT	ATTTTTTTGA	AGTGTTGGAT	AATCAATAAA	960
ACTCATCTCA	TCATTATTAG	CAAAGATGTT	AAACCTTTTG	GTTATAAAAT	CCCCACGTT	1020
CATCTGGTGT	TGCTCTTAGC	CTTTTCCAC	TCTTCTTTCA	TTTCATCTAA	ATCGATAGAA	1080
ACACCTAGGT	TAGGATTTCG	TTTAATCCAA	TTGNCGAAT	CATTTATATC	ATCGTCATCA	1140

TCGAGAGAAG	CTAAATAGTA	AAAAGTTCTT	TCATCTTCGA	TGATTTCGATC	TAAGGTGTCT	1200
CTTCCCGCTT	CTACCATATT	AACAAGTGGT	CCATCTAGTT	GGTACCCTNC	TGTCGTAATG	1260
TAGATAAGAA	GGGGTTGTAA	CCTTGCCGCT	CTTGAGTTTT	TTATAACTGA	AATCAATTTA	1320
TG						1322

(2) INFORMATION FOR SEQ ID NO:730:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:730:

GATGTCAGAG	TTATTCTCTA	ACCGAAGATG	GTTTGAGTCT	AATGGTATAT	GCGATGNATC	60
TTGATATGTC	TNNATCATCA	TTTCTATTTA	ATATGTGCAT	GATGGCGNGT	ATAGTTAATA	120
ACAGTATTGC	CACGATATGC	ATTGCATAAA	TCATCAAGAA	AAATATCAAT	TTGACTATCA	180
TCGAAAATGG	ACACATGAAA	ATCTAATAGT	ATATATGCAG	CATCAGCGAA	CTGAAACAAT	240
TTAACTTTGA	ATAAAGGTGA	ATCATTAAAA	TGGTAAAGTAC	TTAATTCTTG	CTTAAAAAAA	300
GCTTCTAAAT	CATAGTTTGC	GGAAGAAGAT	GGAAC TTGTT	TTATCTCAAT	AAAAGGCAGA	360
AATTCATGAA	GTATCATTGT	TAAATTGTCA	TCGGTAGTAA	CATCAAAAAA	ATGTCTTATA	420
GATGCATGTT	GTTGCACAAT	TGTCGATAAT	GCATACATCA	TTTTAGTAGC	TTCAACATTT	480
TTAGCGAGTT	TAACCCAATA	CGCATTACGG	TGTGTCGTTG	ATTCTGTATT	ATTTTTGTAT	540
ATACGAAAAT	ATTCTGTGTTG	AAATCTCAAA	TTACCCATAA	TCATAAAAAG	TCCTTCTTTA	600
CATATCATAA	TACTCATTAC	TTACTAAAAAT	TGCATGATGA	TATTGATAAC	CGACGAAATG	660
TTAATTAAC	CCGGTATGTA	ATGATTAATA	TAAAACAACA	TCCGCAACAT	ATTGAGCGAT	720
ATATTCTACC	CTAAAATACA	TCTTGTGNTT	CACCCGNNAC	AAATGGGGAT	TATTTTCCAA	780
TGTAAATTAC	ATCAACTTTC	CGTAAATTGG	CACACTACAA	CTCCG		825

(2) INFORMATION FOR SEQ ID NO:731:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:731:

ATAAAAGTTA	TTTCCTATAT	ATACTTTGTG	TTATAAATCG	ATTTTGATAG	GTGTATCTAA	60
TGATTTGTCA	TTTCATCAATT	TAACAGATTG	TGGTGTCCAC	TTTAAAACAC	AAAGTTCTGG	120
GTCTTCTTNT	GAAGTAAAAA	AGCTTTTATC	TTGAGTCTCC	CATAACCAAT	CGATTACTTT	180
GTGATCAGTA	ACTACTTCTA	TCGTGGCTTC	CATTTCAACG	AAACTACGAT	TAGTTGTGTC	240
GNTATAGCCT	AACAAAACAT	ATGCTGCTGG	ATTATCTTTA	ATTTCTTTGA	CCTTAGCAGA	300
ATGGATATTC	CGGTTTTAGT	ATATAAAGTA	AGACCCATCA	TTATAAAAGA	CCATATATCT	360
ACTATTAGGT	TNGGTTATTA	TATGCAGTTG	ATAATACACC	AACTTTTGAC	GTTGGTAACA	420
CGTTTTCAAT	TGCTTGAATT	GCTTGTGAAG	TTACTCATT	CATATCATCT	CCTTATGATA	480
TAAATAGCCT	TTACGTAAGA	ACTAAACACA	AGAGGACTTG	TTAAGTATTT	AGCTTGGGTT	540
TAAAGCAAC						549

(2) INFORMATION FOR SEQ ID NO:732:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 905 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:732:

CGATTTAAAT	GATTTTGGTC	CTGCGTGGAT	TGAAAGATTT	GTTCGTGTTT	AAATCGAAGA	60
AGCATTTGCA	GTGGCGCTTG	AAACTGCGTT	CTTAAAAGGT	ACTGGTAAAG	ACCANCCAAT	120
CGGCTTAAAC	CGNCAAGTAC	AAAAAGGTGT	ATCGGTAACT	GAGGGTGCTT	ATCCAGAGAA	180
AGAAGAACAA	GGTACGCTTA	CATTTGCTAA	TCCGCGCGCT	ACGGGTAAAT	GAATTGACNC	240
AAGTGTTAAA	ATACCCACTC	ANCTAACGAG	AAAGGTAAAT	CAAGTAGCGG	GTAAGAGGTA	300
ATGTAACAAT	GTTTGTTAAC	CCGTCCGATG	CTTTTGTAGG	NTCAAGCACA	GTAATACACA	360
TTTAAATGCA	AATGGCGTAN	ATGTTACTGC	TTTACCATTT	AATTTGAATG	TTATCGAGTC	420
TACAGTCCAA	GAAGCAGGTA	AGGTTTTAAC	GTACGTTAAA	GGTTTATATG	ATGGTTATTT	480
AGCTGGTGGT	ATTAATGTTT	AGAAATTTAA	AGAAACACTT	GCGTTAGATG	ATATGGATTT	540
ATACACTGCA	AAACAATTTG	CTTACGGCAA	AGCGAAAGAT	AATAAGTTTG	CTGCTGTGTG	600
GAAATTAGAT	TTAAAAGGAC	ATAAGCCAGC	TTTAGAAGGT	CCCGAAGAAA	CACTATAAAA	660
TTTTATGAGG	TGATAAAATG	GTGAAATTTA	AAGTTGNTAG	AGCTTTTAN	AGACATAGAG	720
CACANTCAAC	ACAAGTACAA	NGTAGGGGAG	GTNGGTNTCC	AGCTGAAGGG	TATNACAACC	780
CTCGNGTGGG	ATTGGTGGAC	AAATCAAATC	AANAATNNGT	ACCGACAAAA	GNTTTATATC	840
NGCCCCCTTN	AGATAAGCTG	ACAAAACAAG	AATTATTAGA	ACTATGCGAN	TCATTACAAA	900
AAAAA						905

(2) INFORMATION FOR SEQ ID NO:733:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 559 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:733:

```

ACGAATCTTT CACGTCATAT TCATGAACA TCAATATCTG TCAGTTTATA ATTTGATTAT      60
AACAAATGATG AACTAAAATC AACTAATAAA AATGTGGGAA ATTGAATAAC AATTAATCTT     120
TATTAATTAT TATTGTATAC AAAGTTAAAG AAGTCAAAAA GGATTGGTGA AAAAATGTCT     180
TTTATGTTG TACTTATCAT TATCATGTGA GCATTAATTG GTATATTAGT TTAAATCAA      240
AGGTATAGTA ATAGTAAAT AGATACCGAA GTTTATGCAA GAAAGCAACT TATTAAAAAG     300
AATAAAGCAT TAAGTCAGA AAATGCTGAA TTAAGAAGCC AAATGCTGAG CNCTAATAAT     360
GATGTTGGCA CACCCATGCA ATACAAAAAA TGCTAACAAAG AGCATGACGC ANGATCTTAG     420
ATAGCTATCT CGAAAATGGN AAATTAAACT ATTACGATAT TATCCGCTAC AAGCAACTCA     480
GCTACTAAAN CATCCCGNNT TTCGGGTAT GCACGCCCTT TGGGTCPTTT CATGGTTCAG     540
ATTCGGGCTT CTAGCCTGG                                     559

```

(2) INFORMATION FOR SEQ ID NO:734:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 863 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:734:

```

CCTTAAGAAG CACCTTTACC AATCCGCCA AAATCTGTAA ANTCAAATGT AGTAGGTAAT      60
GTTTTTTTAG GTTGAACCAT TTCTTCTAAT TTAAGTAGTC TTGCATCTGN CACTTCNACA     120
ATACCCACAT TTGGGTCNAT AGTTGCGANC GGATAGTTTN CTCCAAGGC ACCCGCCTTT     180
GTAATGTCAT TAAATAATGT TGATTACCA ACGTTTGGTA AGCCAACGAT ACCTGCTGTT     240
AAAGCCATGA ATCATCTCTC TATCTTNGTG TATCATCCTG AGATACGATG ATTTTTTTTA     300
GTTTTTTTATC AAACGTTTGA CGTGGAATCA TAATGCTTCG TTGACAATTT TCACACTTAA     360
TTCTAATGTC AGCACCCATT CTAATAATTT TAAAACGATT GGTTCACAC GCATGTTGTT     420
TTTTCATTTT TACTATATCA TTTATTCAT ATTGNGACGC CATTAAATAT GACCTCCATG     480
TATTATAAAC TACTAAACAC CGNTTCACT ATGATTAAAA GGTGTCATTA TTGGNTGTGG     540
TGCTTTGATA CCTTCTTGTA AAAACATTTT GTGGACTTCT TTACGAATAA TACGCGCACC     600

```


AGAGAAACCN TCACCTGGTA TTGTTTCTGC TGAAACCCNT AATATTACTC TAGTATCTTC	660
AAAGGCATCA ATACCAATCA CAACAGGATC ACTTACAAAT AAATNNATAT TTACTACGCA	720
GAGGATGGTA AATAATGTGT TTAATTTCTT CTCAACATTA TCAATATTTT CATCTACAGA	780
TACTGGAATT TTAACAATTG CTGGTCCAC TCGGNAATTG AGTAANTCGG TATTCACCCC	840
NTNCTACTAT TTGGGAAGAT TGG	863

(2) INFORMATION FOR SEQ ID NO:735:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:735:

CCATAATCAA TCCCTAATAA GTTATCATCA GGGGAATTG ATACCTGCAT CGACAATGAC	60
AATTTCTGCT TTATACTCAA CTGCATAAGT ATTTTACCAG ATTTACACCTA GACCTCCAAG	120
TGCAAAATAC ACCTACTTCA TTTGGATGTA ATTGTTTCAT TATTTAGCAA TCTCCACATT	180
AAAGTGTTCT GAGTTTCTT TTTGTAATC TAAATGTGCG CCCTCTAATT TAGTGATAAA	240
TTGATATTA AAATTACGAT CTTTCAAGTA ACGACGTACT TGTCTTCTG TTTGAGCTTC	300
AACATAAAGT GATTGTGTAT TTTCACGCAC AATTACCTCG TCTCTGTTAT GTTGATAAAA	360
AACTTTAAAT ACTGCCATGT TAAAAATCC TCCTAAGAAT GTTTGTTTAA TTTATTGTTA	420
ACCCTAGTAG AATCGTATTG GAGTATATAT CGATAAATTC ATTCCAATCA TCTCTATAAT	480
TTAACTTAAT AACGATTTGG NTAATACTA GGTTCATCAT GTCGTTCAAT TTAATAAATT	540
AGTGAAATAA CACTAAAATT TCAGTTAAAT CTTATTTTAC ATGATGAATG ATAATAAATG	600

(2) INFORMATION FOR SEQ ID NO:736:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1020 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:736:

CCAACCCACC TTAATTGNCT ACATCGAAAT ATTGTTAAGC ATTAATGTTT CATNTCTTGA	60
CTAGTGTTCT TTTTANCTT TGGANAATTA AATAAANTCC CAATAAGNCC GCAAACNCCT	120

AATAANATAG	GATAAATCCT	GTATGGGAAT	AACATTANTG	NTGAAATACC	AGCTACACCA	180
NCCNCTGANA	TGACTTGCGG	GCTATATGGT	NATNAACCTT	GGAAGCAGCC	TCCCAAATAT	240
ATCAAGAATA	CTTGCTGATT	TCCTTGAATC	TACATCATAT	TCATCTGCAA	TATGTTTAGC	300
TAAAGGACCT	GACATACTAA	TAGAGATGGT	GTTGTTTGCC	GTGGCAATAT	CTGCGACACT	360
TACCAAACCTC	GCAATTCCTA	ATTCTGCGCC	ACGCTTTGAT	TTCACTTTAG	AGCGAACAAA	420
TTGCAACAAC	CATTCAATAC	CACCATGTG	TTGAATAATA	CCGACTAAAC	CACCAATTAG	480
CAACGCAATC	ATAGCAATAT	CTTCCATGCT	TATAATACCT	TTGGACACTG	CATCTAGTAG	540
TCCCATCCAA	CCGAATGAAC	CATCTATGAG	ACCAATGATT	CCAGCTAATA	ATGTTCCGCC	600
AATCAATACG	ATAATGACAT	TTACACCTAA	TAATGCTAAT	ACCAATACTA	AAATATACGG	660
ATACAACTTT	TAATTAGATT	ATAATCATAG	TTTTTTAGCA	TGATTTAAAG	AAATGCCATT	720
CCGGTTAAGA	AATACAGAAT	AATAATCCGG	CTTAAAATTA	GCAACCTGGC	AATACAATCT	780
TTAAAGGTCT	TACTNCTTGA	ATTTTATCTN	NTCAATTTCC	GGNTATGTTG	GTGGTTCTTT	840
AACCGCAGCA	AATTGGTTGG	CTTNTCTGAA	ATCAATTGGA	TAGGATTATC	GNCGAACATT	900
GCACCTCCAA	CANCTGTAGC	CATTGCTAGC	GCAGGTGGCA	CATCTGTCCG	TTGTGCAAAT	960
CCGTACACAA	CAGGGGTGCT	ATTGGAGAAC	AGNTCCTACA	GACGTCCCCA	TAGATTTTGA	1020

(2) INFORMATION FOR SEQ ID NO:737:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:737:

CCTGTTAATA	AATTACCATC	TTGATTTAGG	TAATGGTCTT	TATCTATTTA	TAGACAGAAA	60
AAATAAGGTT	GGAGAAGCAA	TTAAAAATGC	TAAAAATTAT	TTAGATAGAT	GGAAACCAAA	120
ATATGAGAAA	AAAATCATTG	CACAAATAGA	TATAAAAGTA	AAAGAGAATA	GATTGATGGA	180
TTTAGATGAT	CATGATAATC	AATATGAATT	TAATTCATTC	GNTGANGAAA	ATGAAGAAAC	240
AATATACAAT	GAATTAGATA	AGTNGATTAA	TAATAATACA	AAAAGTCGAG	GTAATATAGA	300
CGGCTTAATA	ATTGAGATTA	TGATTAGAGA	GTATTATCTT	GGAAATTGAT	GCTATCCAAA	360
AAGAACTTA	TTCTCAAATN	GGGTAAAAGN	AAAAAAAGAA	AAAGGATCTT	TACATACCCA	420
ACGGGTAAAG	AACTTTGGAT	TNAGACAGGA	ATGATATTAT	TAAGATAGTG	TATTTATTAT	480
GAAATGTGG	GNAACTTATA	TTAGGTAGAG	GGGTGAT			517

(2) INFORMATION FOR SEQ ID NO:738:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:738:

ATGACGATGA TTGAATATAA CCATCAACGT ATTGATAAAA TTATCTATTT TCATTACCA	60
CAAGCTGAAA ATAAAAAGTC ATCTGTAGCA ATCATTATGA ACCCTACAAC TGGCAATCAT	120
TTCCAAGCAT TTTATATCAT GATTAACGCT ATTAAATATC CATATCCAGA TTCAAATAAA	180
AAGTTTCAA TGATTAATGA TTGTGCTGAA AAATTCGACA TACCAATTTT AGGTATCGAT	240
GTACAGCCCC CTCAAGCATT TCATGATTTA TCGGTTATAT TATAATTATT TAATTAGTGT	300
GTTAAGGCTC CAAAAATGGA TACCAGAACT TCAATAATAT TAATTATATA TTNCGGGTTT	360
CTCTTTGTCG NAAGTTTCT TTAAGTATTT ATATGGTGAG CCATCAATGT GTCTAACGTA	420
TTTAAGTTGN ATTAGTTTAT GTACAATTTG GTCAACATCC TGCTCATTCA CATNCATAAT	480
TAA	483

(2) INFORMATION FOR SEQ ID NO:739:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1195 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:739:

TTCCCCGTCC TGTAATAACC TTCACTTGGC ATTCTGCGGA ATTTGACCAA CATCCTGTTC	60
ATTTTNATAG ACTTGCTTAA ATGGTACAGC TGAAAAATCC AAAGTAATGT CCGTTTTCGT	120
CTGGCCTGTG AAAATGGATC AATGAGGATT GCGGTGTATC TTACATAAAG CAGATATTCT	180
TGTAAGATAT CTGGCAAGAT TTCGAAATGC TCAATATCAC CTTTCATCAA AGTTTCAGGA	240
CGTACTGGAT AATTTTCCTT CACCATAAAT TGAAGCAGGT TGAATGACGG CACTCTAAAT	300
GCTTGTAATA TAGCCATCAT TTCCTTCCAC ATTAAACGCA TTTCACGGAT TAATGTCATC	360
GTTATCGGTC CTTTCAGGAA TAACTTATAC ACATAAACCG GTACATCCGT TCCTTCGAAA	420
ATGGCTTTCA ATGAAAAGTC ATTCATAAAT AGTGGCGGGT GCACATAAAG CGAACTGTTA	480
CGTGTTCAG CATGCACTGG CGACCCANCG AATCCGAATG TGAATCTTCA ATTGCTCAGC	540
TAAAGCAGAG ATTCGTTGAC ACATTGTTGA GTNTGAATGT GTCGATCCCA TGTACAATTT	600
CTTTTTTACA CCTGTTGTCA ACACATGATT AGGTGCTTCT TTATCAACAA TACGTGTATC	660
GCCAAGATAA GTTGAAAATG AAATCACTTC GATATCCTGA CTGAACTTAG ACATAAATTG	720
TTCCACGATC ATTTGCGAGC CAAATGTNGG TGANATTAAA ATGACATGTT TGACACCTTT	780
CCAAAGTTTC CTAACCGACN ATTGCTGTNG TGTGTCAATA ATAAGCATCC TTNCTGTGCA	840

TTGCCATGAC	CANCCGTTTC	GGTATTCCAC	CCTTAACGGT	TTTTAACATC	TTTAATACAA	900
ACGATTAAAT	TCCAAACTTA	CCTTCCAGAT	GTTGATGCGC	CTCGTTTTGG	ATTTTGACTT	960
CAAATGTGTT	CTCTTTTTTA	TACGCTTGAT	ATAAGCGTTT	TGATTTTTCT	GATGTTGAGG	1020
CACGTCCAAC	CATATCAATC	TCATAATCTG	ATTTTAAATA	GCAAATATTC	GCTAATTGGA	1080
TTGCGACCGG	ACCAGTGCCT	ATCATTAAATA	ATTTAGACAT	CCGTAATACC	TACCTTTATA	1140
GCTGCTTTTT	TATAAAGTGC	TATATCAAAA	ATTTGCTGTG	GTCTCATATG	TTTAG	1195

(2) INFORMATION FOR SEQ ID NO:740:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1044 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:740:

CTAATGGCTA	TGGTTATATC	AAGTTAAGAG	ATATTATCGT	TGAACGAATG	TCAAAGCAAG	60
GTATAAATGT	AGGTAGAGAA	AATGTAATGA	TCACCTCAGG	CGCTTTACAT	GCCATTCAAC	120
TTTTATCTAT	TGGGTTTTTA	GGTCAAGATG	CCATAATAAT	TTCGAATACA	CCATCATATA	180
TTCACTCTAC	AAATGTTTTG	GGAGCAATTG	AATTTTAGAC	ATATTGATGT	NCCTTATAAT	240
CAAATTAATG	AAATTAANAC	CATCATTGAT	AGATTTATTA	ATTNTAAAAA	TAAAGCGATN	300
TATATAGAAC	CTAGGTTTAA	TAACCCGACA	GGTCGNCTTT	TAACGAATGA	GCAAAAGAAA	360
AATATNATTA	CTTATAGNGA	AAGACATAAT	ATTCCTATCA	TTGANGATGA	TATCTTTAGA	420
GATATTTNCT	TTAGCGATCC	AACTCCTGCT	ATCAAACTTT	ATGATAAATT	GGGAAAAGTT	480
ATACATATAA	GCAGTTTTTC	AAAAACGATT	GCACCAGCAA	TAAGAATAGG	TGGATTGNTG	540
CTTCTGAAAA	AATAACAGAG	CANTTGGCAG	ATGTAAGAAT	GCAAATNGAC	TATGGNTCCA	600
GTATCNTGTC	ACAAATGGGN	GTATATTGAG	ATGTTGAGAA	AATAAGTCTT	ATGATAAACA	660
CTTAGNAANG	TTAAGGTATT	GTTTTAAAAG	ATAAACGAGA	CTTTATGGTT	AAACATCCTC	720
AATNANTTTA	TTTAAGGATA	TAGCACATTG	GGAGNTCCA	AGTGGAGGTT	ATTGCGNNTG	780
GNTAGNCTTT	AAAATAGATA	TAGATATTAA	ATATTTATTT	TACGAATTGT	TAAGTAAAGA	840
AAAAATATTA	ATCAANCCCG	GGTTACATTT	ATGGNAGNNA	AAGAAAAGAG	TATAAGGNTA	900
TCTTTTGGCT	TTGNATCAAA	TGAAAATATT	AAGCATGCGC	TCTATAAAAT	TTATACATAT	960
GTGAAAAAGG	TTTAATTAAA	ACAATAATTC	GAATCATTAT	GTGGNATGTT	AAACAGNTAA	1020
ATATAAGCTA	TGNACATTTA	ACAA				1044

(2) INFORMATION FOR SEQ ID NO:741:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:741:

```

AAAAGAAAAA TAAATATAG ATTGAGCACG AAGTGATTTG AAATAAGGTT GTGAAAGGGA      60
ATGACAAGGT CAGCATTAAA ACCATTTAAA AATAAACGCG TTATGGTTAC TGGACGTATA      120
CAACGTGTTN TGTTTAAAAA TTATTTAGAT AGACATAGCA CATTTANGCC GAATGTAAGG      180
ATATTATTAA AAGATGTATT TGTTTCAGGT GTATCAATAG ATCATTATG GTTATATGAG      240
ACAAATAAAT ACTATGCATT GGCAATGGAA CTTATTCATC AACGAGTAAA ATTTAGTGCG      300
AATGTTGGTA CCATATTTAC AAAATTAAAT AGAAATTAAT AATTTATTCC GCACAAAGAT      360
TATGGAATTA AGCCGTAAGG GTAGGTNTAA TTAAGAAGA AGCTTACAAT CAAAAACAAT      420
CAAGTATCAG GATAAGATAT ATTGAAAAAT NACCCGGTT      459

```

(2) INFORMATION FOR SEQ ID NO:742:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 857 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:742:

```

ACAACCCTNC AGTGCTTGCC CAATTAGGTA GAGAATTTNA CCTAGGTAAN TTAATGCGAT      60
AAAGCCCAAG TTTGTAAAT GTCCNTTGTG CGCCAATTTG TTCCTGTACN TANTGGGANC      120
TATTTTAGGA TTCTTATCAG GGATATTTCC CAAGGGTTTT GTTGACNCCT TAATCATGCG      180
TGCCTGTGAT GTTATGTTGG CAATCCCCCA AGTTATGTTG TAACGTTAGC ATTAATTTGC      240
ATTGTTTGGG ATGGGTGCCG AAAATATTAT CATGGCATT TTTTGACGC GTTGGGCATG      300
GTTCTGTCGT GTTATACGTA CAAGTGTTAT GCAGTACACT GCTTCTGACC ATGTCAGATT      360
TGCTAAAACA ATCGGTATGA ATGATATGAA AATTATTAC AAACATATTA TGCCGTAAAC      420
ATTAGCAGAT ATTGCTATCA TCTCTAGTAG TTCGATGTGT TCAATGATCT TGCAAATATC      480
TGGCTTTTCA TTTTATAGGAT TAGGTGTCAA AGCGCCTACT GCAGAGTGGG GCATGATGCT      540
TAACGAAGCT AGAAAAGTGA TGTTTACACA TCCTGAAATG ATGTTTGNGC CAGGTATTGC      600
CATAGGGATT ATAGTGATGG CATTTAACTT CTTATCCGAT GCTTTACAAA ATTGNTATTG      660
GATCCCCCGC ATCTCTTTCT TAAAGATAAA CTTCCGCNCC TTGTGAAAAA AGGGAGTGGN      720
GCAATCATGA CATTGTTAAC AAGCTAAGCA TTTGGCGATT ACAGATACCT GGACAGATCA      780
ACCACCGTGA GTGATGTGAN TTTNNCAATT AACTAAGGGG TGAAACTCTA GGCNTTATTG      840
GGGAAAGTGG TAGCGGT      857

```

(2) INFORMATION FOR SEQ ID NO:743:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:743:

```

GGCAGGAGCG GCATATCTTT TTTACTAATA CCTCTGCCAT AGTCTTTAAT ATATAACGAA      60
ACATGTTGAT CATTTAATTC TGTCCCAATT TCACTATTAA AATTCTCACT ATNTGATCAN      120
GGCGTATGAT AGAATCTGAC TCTNAANNAA ACGCAANCTT GTTGGCTGAA AGTTMNCATG      180
CTGGTGTGTA AACGGCATAT AAAGCTGTTA TGAAACCAGN TGAAGGNACA ATACTTACAG      240
GTGGAAAAGA TGCTGCGCAA GCTGCAATAG AAAAAGCAAA TAATACTGAA GATTGTATTA      300
GAATTAATGG AGNACATTAT TGGTAAAAGN CAATGAATCA CTTGGAAAAC ACAACCAAAC      360
TTATTAGCTG TACTTAAAGA AGTGGGTGT

```

(2) INFORMATION FOR SEQ ID NO:744:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 648 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:744:

```

AATTGCTCTA TTAATTGTGA TTTTTTAAAA ATAAGCTGCT TTATTAGTTA TTAATCTTGC      60
ATTGATATCA CTAATATGTT GCTTTTCAAC CAGTCCGTTT GCTTTTAGCG TAGTACCTGT      120
TTGAGCGATG TCGACAATTC CGTCTACCAT ATCTACGACA CAAGCTAATT CAACAGANCC      180
ATTCAATTTA ATCAATTCTGA CATCAATACC TTTTGATTTA AAATATGTTT CAGCAGTATG      240
AACATAACTC GTTGCGATTT TACGATAATT GGTCGTTTCA GGTTTCGCTG CAACCGCANA      300
ATGACATGCT CCAAAAGGCA TATTCAACAA ATTATTAACA TTATATTGGC GCTCATCTAA      360
TATGTCGCTA CCAACAATGC CTATGTCGGC CATTCCTTGT TCCACATAGA TTGGCACGTC      420
ACTTCCTTTT NCTAAAATGC ATTCAATATT ATCTACACTT AATAATAATT GGCGTTCTCT      480
ATTTTTTAAT GTTTCTGATA ATGTCGTATA TTCAATTACA TCTAAATAGT TAATTAAACT      540
ATCCATTAGA CGTCCTTTGG CTATGGCGAT TCTTAACATT GTGCATACTC CCTTACTTAA      600

```

AGTGTTAATC CTAATCCAAA CCCTTCGATG CTTCTTTTGT AATAACCG

648

(2) INFORMATION FOR SEQ ID NO:745:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1020 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:745:

```

ATTAGCGGAT GGNTAAAAAT ATGGTTTTAG TAAGCGGGCC ATATTCCCTT TTATTANTGC      60
GAGTGTTTTA TAGCTGACAC AACTTNCCTA CCTTGTTTCGT GGCAATCTAG TGATATTATA      120
TCTGCTGATT ATTTTCATGT AGGATTCGTT CGATATTTTA GTAGAATGAT TATACCTAAT      180
TTATTCCTCGC TTTTAGCAAG TATTATAGTA TTGTGGTTAT ATTTTAGAAA GGCGATACCT      240
AAAACGTTTG ATGATAATAA TATAAAGCAT CCTAAAGATG CCATTAATGA TTAAAGCTA      300
TTTAAATTT CAGGGATTGT CCAAGTAANA TTACNTTTCG GCCAACCTAA TCAAGTGAAT      360
TTNCCNAAAA TTCCGGGTAT CCAATTTTTC NCCTGGATCA TTGCTTTTAT TTTTCTAATG      420
TTGGCTCGTA AATCCAAATG CTGTAAATAT TAAGCAAGTC ATTAAGGGCG CACCTTGGAA      480
TATAGTATTA TTTTCAATTG GTATGTATAT CGTCGTATTC GGCTTAAGAA ATGCTGGCAT      540
TACTTTAATA TTGGCTAAAA TATTAGAATA TATTTCCAAT TACGGTCTAT TTAGCACCAT      600
TTTGGGAATG GGCTTCATTT CAGCGTTTTT ATCATCAATA ATGAATAATA TGCCTACAGT      660
TTTAATAGAT GCGATTGCTA TTGGTCAATC AAATGTCCAT GGCATGTTAA AAGAAGGCCT      720
AATTTATGCG NATGTTATCG GTTCTGATTT AGGTCCCNA AATTACACCG ATAGNCTCTT      780
TAGCTACATT NCTGTGGTTA CACGCTTTAA CACAAAAAGA TGTTAAGACT TCTTGGGGCA      840
CATACTTTAA AACTGGTATC ATCATTACAA TTCCAGTACT ATTTATAACC CTCATAGGGT      900
TGTATCTAAC ACTTATCATA TTTTAAGAAA TAAAAAGACG CTTTCTATTT ATTGCGATAG      960
AAAGCGTCTT TTTTACTTGT AGCAAGTTAT ATCATAACTT AACTCTATCA AATTACTTAG     1020

```

(2) INFORMATION FOR SEQ ID NO:746:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 587 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:746:

GTGATATCAC	CTATGGCCGG	ACATCATGGA	CGGAAAATTA	AAAGAAACCC	NACAATTAAT	60
GGAATGGGGC	GGAGTGTGCT	TCNACCNCAT	TTGTAAGTAT	TTATCCGTTA	ATAATTTCTA	120
AATTACCGAA	GAACNATTAT	CCAAATTCCA	TCCTTTCCCTA	ATAAAGTGGA	CNACGGAGGG	180
AATTAACAAA	GACAAAGATG	ATGAGGGTAG	CACTATCAAT	CCAACAATCA	CGGATAGAGG	240
CACAAAGATC	AAATANNAAA	GCGGTCATCA	GTCAATCTGA	TGTGTTAGCA	AGAATGACAA	300
TAGAAGAACA	TGAGCAAGAC	GGCGAAAAG	CTTATCAATA	TGTTCTTAAC	GCTGAACCAT	360
CAAACTTATT	CGAGACAAAG	ATAAGACACT	CAAGCAACAT	TAAAATTAAC	AACANACGTT	420
TCATTAATCC	AAGTATTAAC	GACGTAGTAC	AAGCAATCAG	AAATGGAAAC	TAATAAAAAA	480
ACTAAAAAGG	ACGGTATTTA	ATTATGAAAA	TCACAGGACA	AGCGCAATTT	ACTAAAGAAA	540
CAAATCAAGA	AAAGTTTTAT	AACGGCTCAG	CAGGGTTTCA	AGCTGGA		587

(2) INFORMATION FOR SEQ ID NO:747:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 770 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:747:

TCATAATATC	TTGTCACTCG	GTA CTGCTAA	AGTGGTTNTG	CNAAGTGAGA	TAGCNGTAGA	60
NTCAACTGGT	GAAGAAATAA	CGTCTTGCGG	AATACTAATG	ANACTTGCGC	CATNTTNTCC	120
TGNAGTAGCA	ATTCTGAATTG	CAGGTTGTCA	TAAC TTCTGA	TAATGATTCA	GGATCTTGTA	180
CTTCTTCACT	GTATTTTGAT	GAATATTTTA	ATAGCGCAGC	ATTATCAATA	CTTTGATGCG	240
CTAATCGTAA	TAAATCATT	CGTTTCACTT	GTCCACCTAA	CGCTAATACA	GGATCCCTTT	300
CAGATGTAGC	TGTTAATAGT	CCAGTCGTTA	AATTACTTAC	ACCAGGGNCA	CTTGTAACAA	360
GTA CTACACC	CGGTTTACCT	GTTAATCTTC	CAATACCTTG	TGCCATCATT	GCAGNATTTT	420
GTT CATGACG	AGTGACAATA	AGTTCAGGAC	CATCATCAAT	TAAAGCATT	AATAGATAGT	480
CTATCTTTGN	ACCCGGAATA	CCAAAAACAT	ATTCTNCCCC	ATTATTTTTC	AAAGTATCAA	540
ATAA CCCATA	TCGGNTGCAG	GGGTACTTTT	TATCAAGTCA	TTTATNTTCA	ATTTCTTTCC	600
CAATNGTGAT	GTATTTGATG	GTGGTNTTTA	CATGGTAATT	ACAATGGGGG	ATTGGGGGAA	660
TCTTATGATA	GGNTACGCAA	AAATTAATGA	TGGTTTATCA	AAATTTTACA	TTTTTCCGAT	720
TAGATTNGGG	GAATACAATA	AAATTTGCCT	CCCAANAAAT	TATTTT TACC		770

(2) INFORMATION FOR SEQ ID NO:748:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 695 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: lin ar

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:748:

```

GGCACGAGCG AAGGTGGACG TACTGTAGGA TCAGGCGTTG TTACTGAAAT CATTAAATAA    60
TTTCTAATTT CTTAGATTTT ATATAAAAAG AAGATCCCTC AATCGAGGGG TCTTTTTTTTA    120
ATGTGTAAAT TTTGTAATGG CTATTCGATT TAGAAGAACA ATAATTGATG AAAGACTGAC    180
TAATAAAACT TATAACTGAT AATACTGTTT AAATAAAATT GTTGAGTCTT GGACATTGTA    240
AAATGCTCCC TTCAAAGTTT TCATTTTTC AATGTC TACT TTGAAGGGAG CATTTTCATTA    300
GTTTATGTCC CAGACTCATA TCTTTCAATT AATTTAAATG CTTAATNTGN TTTAAATACT    360
TGCTCTAATT CAATGATTTT TAAAAATACA GCTACAGCGT ATTTTAATGA TTTTNCATCA    420
ATATCAAATT TGGGATTATG GTGTGGCGCT GTAATACCTT TACTTTCATT ACCACAACCA    480
GTCAGAAAGA ATGCACCTGG NCGGACTTNC AAATAATGTG AAAAATCTTC TCCAATCATC    540
ATTAAATCTG ATTCATTAAA GCGTACATGT AAGTCATGTG TTGCTTCTTT TAATAACTTG    600
ATATGCTTTC TCGTTATTAT GGACAGNGCA AATACCCTCT TAATATTAAT TCCAAAATCA    660
ATAGGNTAAT ATCAATTGCT ATTGTTAAAC CCTGG                                695

```

(2) INFORMATION FOR SEQ ID NO:749:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 823 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:749:

```

CGATTAAAAA ACTCTATCCC TTTGTGTTTA ACACACTTTN TGAAGCGATT GATAAATTAG    60
CAATTGATAC TGATATAGAG ATGAGCGAAG ATGAAATTGC ATTTTAAACA ATTCATTTTC    120
AAGCTGCCAT CGAGCGTCGT NCCAAAACAC AAGTAAATGT AGTNATTGNT TGTAAANTAT    180
GGTCCTAGGT GTGTGCAANT TTTTAGAAAC TNAATAAAT AACTTATCCG AAGAGTTGTC    240
AGTAATAAAT ACGAGTAAAC TAGAAAGTAT AACACACTAT CACTTTGACN ATGTAGATTT    300
ATTAATAACG ANCCATGATA TTCCAAAACA AACGCTAAAC ATACTTCCTA AGCACCTGAC    360
GACTATCAAG GTTGCACCAT TATTTTCTGA AGATGATCGT CACAAAATCA GACACGTTGT    420
GAAGCAAAAG CAAAATCCGG TTCAAGCACA TCATCATATG GACACTGTCA ATTTCCCTGT    480
CGGAAATACT GAACAAAAAT CACGGCATA C TGTGCAAATT TTGGAAGAAG CTCAAAAAAT    540
ATTACAAGCA CATCATGCGA TTGGTAGAAG GATATNTCGA ATCAGCTTTA GAGCGTGAGA    600
AATCATCTTC TACATACAAT AGGTAATTTN ATGGGCGATT CCTCAAGGAG GATCCCGGAA    660

```

AAAGGTTNAC	AAATCACATG	TGCTTATTTN	TCGCACAAAA	AGATTGTTTT	TCCCTNGGGC	720
GACAACAACG	ACNTGGCAAA	CTTGGCTTTN	NCTTAGGCGA	NTTCGGATTN	AGGCAAAGGT	780
TTTTCAAAAC	AAATTGNTGC	AANTNATTTG	GTACTTNGG	GTG		823

(2) INFORMATION FOR SEQ ID NO:750:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:750:

AATTCCGCAT	AAGTTTAATT	GGTTTGATAG	ATATCAAAAT	ACAATGCCGA	CCGGTAAAAA	60
TCCCTAAAAA	TTGTTGAAGG	TAATACACTA	GCTCCTAAAT	TCATATACCC	CCCATGTATT	120
TTTAAACCAA	TTCAAAGTGT	GAATCTNAAT	AANTATCTNC	CTGCATCTTN	AATATTTTTT	180
AATATGAACT	TTGAGATTGA	TTAAATGTTT	TAATCACTTC	AATGCCTTCG	ATAAACTCTA	240
CAATCGCGCT	ATTCATATAA	TTATTTGATT	TCATTTGTTC	AGCATATGTC	TCATTAAATC	300
CAGACATAAC	TTTTTTAAAA	GCGAAAATTG	AAATTGGTAT	CGTTACTAAT	AAGGCACTAG	360
CCATACGCCA	ATCAATGAGC	ATTATGTATA	AAAAGATAGC	AGCTGNCACG	NAAGTAAGTT	420
TCCTATAACT	TCAGGAATCA	TATGTGCTAA	AGGTNATTCT	ATTGTTTCCA	ACCTTAGCGA	480
CAAATATATT	TTTAAATTCA	CCTATTTTCT	TAGATTCCAC	TACGCCTAAN	GGGAGGCGCA	540
TTAATTTTTG	AGCTAATTTT	TTGCGAATTT	CAGATAAAAT	TTCATATNCC	GTAATATGTG	600
ATAGCATCGT	TGACGCTCCA	AAACAACACA	CTTGTGAAAT	ATAAGTGATT	AAAGCAATAA	660
AGATATAANC	CATAATCGAA	TTANTCGTAT	ATGCATTGTT	AATCATCNTT	AAAATAATTT	720
TAAAGACTGC	CCAATATGGA	ACTAATCCAG	AAAAGACNCT	GATGATAGAC	AACAANAG	778

(2) INFORMATION FOR SEQ ID NO:751:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 922 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:751:

CTGTCAATGA	ATATGATGAT	ACTGATAAAA	TTTTCTCTAA	CCCATCAAAC	AAGAAAACAG	60
------------	------------	------------	------------	------------	------------	----

AAGATTATAT	TTCAGGAAGG	TTTGGTTGAT	ATATAATGGC	AATAATTAGA	CAGCGATATC	120
AGGAGCAACT	TGATGATTTA	ATAAAGGAAT	TACGTCGGTT	AGGTGCAAAT	GTCTATGTGA	180
GTATTGAAAA	TGGTATAAAA	TCATTAAGTA	TTGACGATAG	AGGCTTTGNA	CGACAAACAG	240
TTAAAAACGA	TAAACATATC	AATCAATTAA	ATTATGATAT	TAATGAGCGA	GTTATCATGT	300
TAATTACAAA	GCAACAGNCC	ATTGCGAGTG	ATTTGCGTAT	GATGATTTCT	TCAANTAAAA	360
ATCGNCTCCG	ATTTAGAAAG	AATAGGAGAT	AATGCATCGA	GTATTGCCAA	TATTCGATTG	420
CGTACAAAGA	TTACAGATGA	TTATGTGTTA	ACCCGTTTAA	AGACAATGGG	TAAATTAGCT	480
ATGTTAATGC	TAAAGGACTT	AGATCAAGCA	TTTAAAAAGA	AAGATACCGT	ATTAATAAGA	540
GAAATAATTG	AGCGTGATGA	AGATATCGAT	GACTTATATA	GTCATATTAT	TAACGCAACG	600
TATCTTATTG	ATAACGATCC	ATTTGTCGCT	GCACAAGCTC	ATTTAGCAGC	AAGACATTTA	660
GAACGTATTG	GTGATCATAT	TATTAACATC	GCTGAAAGTG	TTTATTTTTA	TTTAACAGGT	720
ACACATTACG	AACAAATAAC	TTAAAGTTAT	TACTATAAAA	TCCCTTACGA	TAAATATATA	780
TTTCTATCAT	TCATAAACCC	TCAAAAAAAA	CCAAGATTCT	CACAAATTAG	NAATGNGTGA	840
AAANCTTNGN	GNTATATTTT	GGTTCTTACT	TATTAAATNG	GTCTCGCATC	TTAGGNTATT	900
TGGNTTGGTC	AATTTTCATCT	TG				922

(2) INFORMATION FOR SEQ ID NO:752:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 783 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:752:

TCACACTCAA	TTCTACATCT	AATATCAATT	TATTACCAAT	AGAATTAGCA	GCAACAAGAT	60
ATTACNTNAN	ATTACTCCCC	GAATTTAAAA	TATAAACAAT	GTAATAATTA	AGGGNATAAA	120
TTGATTTATC	CTGTAACATA	TTAAATGTGT	ATGGTATCTT	CTAACATCAT	GAAACGCATC	180
TTAATATAGA	TATGTACATT	TAAACCTTGA	GAGATAGATT	ATAGTAAACT	TTAGTACNAA	240
GTATGAATTG	CTGAACTCCA	ATGACTACTA	TTTGTCCGTT	ACAACTAAAG	TTTCAATCTA	300
TCTCTTTCTT	TTTGTGTTTA	AAACACGACT	TTGTAGTAAA	TATTGAACAT	CATATTTATT	360
AGCAAGTTCT	GCTAAAAAAT	CTAATAAAGT	TTGGGTGTCT	ATTTTACCAT	TAATAAAATC	420
AGCTGTAAGT	AGTNTTGAGT	GTTTCTTTTC	TTCTTCATTC	GCACATTTTT	TAAAAATATCC	480
CCACATATGA	GCAAAAGCAT	TACATACACT	TCCTATACTC	GGNTCAANTA	ACAAAGCATC	540
ATCAATCATT	TGTTGGACTT	GATGAAGTGA	TAAATCCGTT	TTTAAAGCAT	TCCTTATCAT	600
TTGGTAAGAC	TGTTGACTGT	GTAACAATAC	ATGATATTTT	TCCTCACGCC	AAAGCTGTTT	660
GATATGGCCA	CGTTCTTTCA	TAAAATTACC	TCCGATAATT	AATGTTAATA	TACATGCATA	720
TAGTATAGCA	ATAAAAAATGA	ATGCGCTATC	AAAAATGGTG	TAGGTGTTTA	TATAAAATGA	780
TAG						783

(2) INFORMATION FOR SEQ ID NO:753:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:753:

```

GGCGATGTAA AAAACGATGT AAGTGCCTG AGGATAAAAG AATCAATATC TTACCCTGTT      60
AGCCACGTGT TAATTAATGG TATTCGCTAC AAGATAATTG ATACAAAGAC ATACAGACAC      120
GAAACGTCAT ATTATATCGA AGAGGTCAAT TGATGAATAT AGACGGATTA GACGCACTGT      180
TAAACCAATT TCACGATATG AAAACAACA TCGATGATGA TGTAGATGAT ACTTTACAAG      240
AAAAAGCCAA AGAATATGTA GTACGAGCGA AATTGAAAGC TAGAGAAGTA ATGAATAAGG      300
GTTATTGGAC TGGTAATTTA TCACGCAATA TCAGATATTA AAAAAGTGGC GATTTGCAAA      360
TACACTATCA CATCGCATGC AGCTTATAGT GGGCTCCTTA GAGTTTGGGG ACTCGATACA      420
ATGGAGGCAG GACCCCTCCTA TGTGGCAGTA TATTGAGGGT AATAAGAA      468

```

(2) INFORMATION FOR SEQ ID NO:754:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:754:

```

CCAATTGATA TTACGGCGAT TGTAACNGTT GCTGATAATG GTGGGAGTAC NGGGNAAAAT      60
CAGAGATGAA ATGGTTATAC CAGCACCAGG AGACATCAGA AATGTGATTG CAGCTTTAAG      120
TGATTCTGAG TCAGTTTAA GCCAACTTTT TCAGTATCGC TTTGAAGAAA ATCAAATTAG      180
CGGTCACTCA TTAGGTAATT TATTAATCGC AGGTATGACT ANTATTACGA ATGATTTCCG      240
ACATGCCATT AAAGCATTAA GTAAAATTTT AAATATTAAA GGTAGAGTCA TTCCATCTAC      300
AAATACAAAG TGGTGCAATT AAATGCTTGT TATGGAACGA TGGAGAAATT TGTTTTTGGG      360
GAAACAAAAT ATTCCCTAAA AACATAAAA AATTGNTCCG CGTGTTTT      408

```

(2) INFORMATION FOR SEQ ID NO:755:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 747 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:755:

```

AATTGNCGGG NCGTCATTAN TTAACTCAG TANCAC TTGC ATTCATTCCG TCAAAGTTTT    60
CATTAGCTAT CTTCATCGCN TTANCCATTG CAATATCATT TGCACATTAA CTGTGCCACT    120
TCTAACGCCA TATTCTTGNC CACCACCATG GNCAGATGGG TCAACATTTT GNATGTGATT    180
TACAAGTAAG ACGCCTTGTC CTTTAAACC CATTAAACTT TGTGCCACN TAAACNTAAT    240
ACTATCTATG TTATTTGAGA TCCATTGAA ATTTTGGCCG GAATGCTTGT GAACCCGCAC    300
CTACATGAAA ATGTGCCTTA GGATAATTTT TTATAACTTT AGCCATTTTG TGGAAATAGGC    360
TGNATTTTGT CCAGTTACAT TATTTACAAT ACAATACATT GTNACTAAAC CCGACTTTGT    420
CTGACACCTA ATTCGGTTGA AGTGNCTTAA GTTAATACTG CCATCTTTCT TNACATCAAC    480
ANANTTAACN TTAAACCCTT CGTGTGCTCC CCAAANATCT TACCAACCCC TAATNCGGAC    540
GGATGCTCTA ACACGGATGT AATTATTTCC TTCGCTGNAC CAAATTTACG ATAGGCAATA    600
CCTTTTAAAG CAAGATTATT GGATTCAATT GCACCAC TAGAANACAAC AGCATAATTT    660
GTTTTTGAAT TAATCATTGC ATTAATTTGG GCTTTTGCTT GTTGTAGTAA TTGATTTGCC    720
TGCAAACCAG CTCGTGCCGC TCGTGCC    747

```

(2) INFORMATION FOR SEQ ID NO:756:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:756:

```

CTACATAAAG TCTGGATGAT TATATGTAAT AACCTTTGTT TCACATTGAC TATCTGTTTG    60
ACATAAAATA AGCTTTGCAA AATTAATCGC AACTTGTTTC ATCGTTTGTG CATCATCACC    120
TTCAAATAAA TAGGCATGCG ATAATTTATT TGAATGATAT GCATTGCTCA ATTGTTGCTG    180
TTCATCCATT CATTACAAAC TCCCTTTTGC TTTTATATAA AAAGGTTGCC AAAGAGCAAC    240
TAATTACTGC AACAAATAGC GACCATGATT TGGTGATTAT TTTTAGAACC ACAAAAAATC    300
AAAATCTTAT TGGNATCTTG AACTAGGTCG CAGGGCAAAG CNAACCCAAA ATTGGTTAAA    360
TAACTTTATT AATACACTAT TTNTANGTAT CTCTTAATTT GGATGGATNG NNTTTATTGG    420

```

AATTNNAAAT TGGATGGGAA TGNATCAACT TGGCATNACA AATNCAAGAG AACCGNCAAC 480
 TTCCAACTTT CAAACTTGAT TATTGGATTG TTCCGGATTG CC 522

(2) INFORMATION FOR SEQ ID NO:757:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1209 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:757:

CCAATCGGTC TTATCTTTCA ACACGTTTGA TTGTANCGGA TATCACCCGG TTCATAAATC 60
 CNAAATCGTT GTAATATATT TCTCTTTATA TTCATTATTT CTAGGAATCC ACCCCCNCCG 120
 TGCGGGCAAG TTTCTGGGAA ATTAAACAGC TATCCAGCCT TTCAACAAAT AAATCTGAAA 180
 TTCGATGTTT TAAAAATTTCT GCTTCTTGAT GTACTTCTTC CCAATTATAT TTCAATATTT 240
 CTATTAAAAA TAATTCTAAT AGTCGATGTC TCTTAATGAT ATCAAGCGTA TCGGTTAAAC 300
 CATCCTCTGT TAATCTAACA CCTTTGTATG GTTTTGTTC AACATAGCCT GCTTTTTCAA 360
 GACGTCCTAC CATTTCACTT ACAGATGGAG GCTTAATATT TAAAAATTGA GATAAGATTT 420
 TATTTGTCAC AAAGTTTTTA TCGCCATTAA TTCGTAAGGA TTTGCCTTTA AAATAAGTCC 480
 TCTTTTTCTT CAGNTAACAT ACTTTCACCT CAACAGACAT TGTCTATATT ATATCACGAA 540
 TTTACTTGAC ATGATAAATA TTCTCAGTTT ATTANACAA TAATTAGGTT AGCCTAAACT 600
 TTTAATTAGG AGGTATAAAC GTTTGTTAGA AACANAAGAT TTAAATCTGT TTTTAGGTAA 660
 TAAGCATGTA CTTAAAAACA TTTCTTATC GATACCAGCA CGAGCGGCGA AATAATTGGT 720
 ATCATGGGCC CGAATGGTGC TGGTAAATCT TCCCTTATCA AGTCTTTAAT TGGTGAATTT 780
 AATGCTACCG GTACTAAATN GTTNTATAAC AAACCTATAC AACAACAACN GCAACAGATT 840
 ACATATATTC CACAAAAAGC ACATATTGAT TTAGATTTTC CTATAAGTGT GGAACAAGTG 900
 ATTTTATCAG GTTGCTACAA AGAAATTGGA TGGTTTAGAC GACCTAATAA ATCAGCAAGG 960
 GATTAAACTC AAACAGTTAT TAAGCGATTT AGAATTAGAA TCTTTTACGT CATCGACAAA 1020
 ATTTCAAGAA TTAAGTGGGT GGGACAAATT ACAACGGTGG TGCTTANGTA GGAAAGAGCA 1080
 TTGGATGGTC CCGAAAAGTG AAGGTTTATT TTCTTTAGAT NGAGCCCGGT TGGTCGGGAA 1140
 TTTGGATTTT AGGGTAGCGA AAAAAATTAAT CAATGACAAA AAATCCGAGA ACTTTAAAC 1200
 AACAAAGGA 1209

(2) INFORMATION FOR SEQ ID NO:758:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 700 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:758:

ATCCATCACT AAAGCCATGG TAAAGCATT TAAGAATCGC CGAATATAGG TATGATTTTC	60
CACATTTTAA TTAGTTAAAC GTCAGTGTAT TCGAAATGTA CTAAGTGGAC GTGTAGGTTA	120
TCACCTCCTT GGAAAATGGT ATTAGGTTTA TTCCCAAAAG AAGACAAAAT TAAAGCAATG	180
GATGCACTAG NAACGCGTCA ATATCTTAGA TAAATATAAT CAACGCTCTG ATGAATTATC	240
AGGTGGCCAA CAACAACGTA TATCTATTGC ACGTGCCTA TGCCAAGAAT CCGAAATTAT	300
TCTTGAGAT GAACCAAGTTG CTTCAATTAGA CCCATTAACA ACGAAACAGG TTATGGATGA	360
TTTAAGAAAA ATCAACCAAG AATTAGGCAT CACAATTTTA ATTAATTTAC ATTTTGTGA	420
CTTGGCAAAA GAATATGGCA CACGCATCAT TGGTTTACGT GATGGTGAAG TTGGTCTATG	480
ATGGTCCCTG CATCTTGAAG CAACAGATGA CGTATTTTAG GTGAAATATA TTGGACGGTN	540
CAAATTAAAG AAAGGATGGA AAAAGCTTAG GAGGTGGAAC TTAACAATGC CTTNTAGGAA	600
ATACCTACAA AGGTATTGAC TCCCCNTNTA AAGAAAAGGT TTCTTTTAAA ACGAAGTTTN	660
ACCTCCANGT NATCAATGGT GCTTTATCAT TGGGAGTTCC	700

(2) INFORMATION FOR SEQ ID NO:759:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:759:

CTAAAAAGTT TTTCCTGGTT GGTAAAGAAG CCAGATTTGA ATGCGACCAA CCGACCTGCC	60
ACCAAAGAAT TTTTAGAAAC GCGTTAAAG NACGAAGAAA TATTCCNGCT ATTGAGAATA	120
TTACGGATTC AACTCAANCT AAAATGGATG CTTATAAAGA AGTTAGACAA TCAGCTACAG	180
CTAGAAAAGC GCACAATGCT ACAGTTTCAA ATGCAACTGA TGAAGAAGTA NCAGAGGCAA	240
ATGCAGCAGT AGATGCAGCT CAGACAGAAG GTTTACATGA CATCCAAGTT GTTAAATCAC	300
AACAAGAAGT GGCTGATACT AAAGCAAAAG TATTAGATAA AATCAATGCA ATTCAAACAC	360
AAGCAAAAGT TAANCCTGCA GCTGATACAG AAGTAGAAAA CGCATATTNA TACACGTAAA	420
CAAGAAATCC AAAATAGCAA TGCTTCANCT ACAGAAGAAA AAGAAGCT	468

(2) INFORMATION FOR SEQ ID NO:760:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:760:

GAATTCCTAT TTACCTTGCT GGACAGCNAC AATTTTCCCA TTAACCTTAC ATAGGATANC	60
NACGCCTTGA CCTACTTTTT CAATATGTGG CGCTCTTATA AAGACACCTA CAATATCTGT	120
AGNGATACCT TTAATATCTA ATTCTGTTTC AAAGNTGNCA ACTTGTCTAC CGAATGAGTT	180
TCGGTGACATA GGAATATNCA ACTTGTTAAG GTATCCTTCT TCACCAANTA TATCTTGGGN	240
TAGAACTATT AATCCTGCGC ATGTCCCAAA CATAGGTAAA GGTGANTTGT GGTGAAGNCT	300
CTTTANATCC ATATAAATTC ATTAATCGAC GNNACGGNGG GGNCTCGNC ACCAGGNAT	360
ATTANGCCNC GNNNNCTTCT	380

(2) INFORMATION FOR SEQ ID NO:761:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:761:

AGTTGGNCCC AATNAAGAAG AAATCGAGGG CCTTAAATAT TACCTGNTG GCCGAGTACC	60
ACACCGTNAC GTCGACTAAT GAATTTATAT GGAGTTAAAG AGNCTTTNCC AAAATTCAAC	120
TTTACCTATG TTTGGTACAT GCGCAGGAGT AATAGTTCTA GCGCAAGATA TAGNTGNTGA	180
AGNAGGATAC CNTAACAAGT TGAATATTAC TGTCANCGA NACTCATTCC GTAGACNAGT	240
TGACAGCTTT GAAACAGANT TAGATATTAA AGGTATCGCT ACAGATATTG ANGGTGTCTT	300
TATAAGAGCG CCACATATTG AAAAAGTAGG TCNNGGCGTA GATATCCTAT GTNAGGNTAA	360
TGAGAAAATT GTANCTGTCC ANCAAGGTAA ATATTTAGGC GTATCATTCC ATCCTGAATT	420
AACAGATGAC TATAGAGTAA CTGATTACTT TATTAATCAT ATTGTTANNA AAGCATAG	478

(2) INFORMATION FOR SEQ ID NO:762:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 535 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:762:

ACCAAGATTG GGANTNCCTG TAAATCCCCG GATAATTGAT CCAATGGGTC CAAGTACNCN	60
ACCCCNCTGA TGATNCCCA CATGTTTATG TAAGTGGTGA GNATANTCAN TAGTAGAAAA	120
TGATTTAATG AAGAATGTNC CATTAGCCN AANTANAAAT GTATNTNAAA TGATAGATAA	180
ACAAGAGTTT ATGNCTGTGT CTGGAATGAA TCGCATGGCT TATAATGATC AATATATTAT	240
AGGTCAAAGA GGAGACGAAT TTATTCCTTA TAAATTTGGA GATGAGTCAA TCGGTGTTTA	300
CAATACTGAA TTTGAAATGC AACAAGACTT AAATGAATTA GGGCAAAATT TACAATAAA	360
ACCCGAAAT GCTTATCAAT AGGAAATTAT TGCATAAGAA ATATATTTTA GTTATCCTGT	420
CACTAGAATA AATTTAAAAG GTTGGTGTAG TTCAAATGGC NGAACAATCN AAACNGAAAC	480
AAGCTAATGA ACAACAAAAG GCCCNGAAT TATTCGCACG TTGGAGACAA CTCA	535

(2) INFORMATION FOR SEQ ID NO:763:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 519 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:763:

GATCCAACGT TACCGTGATG AATAAAGCG CACAAGTTGG GCGCAGCCN CAACAATTAA	60
GATACAAGCG AGCCATTTTT GTGCTAATTT TTGCGCGTAA AAATGTAACG TCAAAGATNC	120
ACCGTATGTA CCAACAATAT GTTAAGAGAT ATTAAAAAAT ATGAGGCACA CACGGATCCC	180
AGCTGTTGAA CACAAATTCG ATGCATTCCA AACAGANTTC CATATTTCTG ATNATGATCC	240
NAGCCTTGTA TGNCTGGTCA AGTANACANA CGTATATCGC ATTAGGCAAT ATGATGNCGA	300
CAGCCGCANT GTTAGGTATT GATTCATATC CGATGGAAGG TTTTAGTCTG GATACAGTGA	360
CAGACANNIT AGCANATNAN GGTATCTTAG ATACTGAGCA ATTTGGTTTA TCAGTGATGG	420
TTGCATTGG CTACAGACAA CAAGATCCAC CGAAAAATAA AACACGCCAA GCATATGAAG	480
ATGTTAATGA AGGGGTTGGA CCAANAGAAT AAATAGNAG	519

(2) INFORMATION FOR SEQ ID NO:764:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 753 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:764:

```

CTGTTACTAG CGTCATTTGT ACTCATTACA CTTGGACAAT CTGTAGAACA ATTACGTGCT      60
GCAATTATTT ATGTTGTCTT GAATATTATT GGTTCATGGC TATTCTTATT AGGTATAGGT      120
TTACTTTATA AAACAGTAGG TACATTAAAC TTTTCACATA TTGCAATGCG TTTGAATGAC      180
ATGGGAGATA ATCGCACTGT TACAATGATT TCATTAATCT TCTTAGTCGC ATTTAGTGCG      240
AAAGCAGCGC TGGTCCTTTT TATGTGGCTA CCCAAAGCCT ACGCTGTGTT AAATACTGAG      300
CTTGCAGCAT TATTTGCAGC GTNAATGACC AANGTAGGGG CCTATGCATT AATTCGGATT      360
CTTCACTTTA CTATTTGGAT CAAACATAAT GATCTCATAC ATCCATTGCT AGCAACTATG      420
GCTGCTTATT AACTTATGGC CATCCGGCGC TATAGGGTGT CAATTGCTTA TTAAAGATAT      480
TAAAAAGATT GCAGCTTACC AAGTCATAAT CTCAATAGGA TTTATCATTT TAGGNTTTAG      540
GAACAAACAC GTTTGGAGGT ATTAANCGTG CAATATTTTA TTTGGGTAAA TGACAAATGGN      600
TGGTAAAAAC ATNGCTTATT CCTTTATTAT TGGGGAGGTT AGNTNTACAT TACAGGCTAT      660
CGACAATATC AATATTTGGG AATGGCTTAG CTAAAAAGA ACCTTTATTT GGGAGTTGCC      720
TTTATTATAA TGATTTTGG TANTTGGNCG GCG      753

```

(2) INFORMATION FOR SEQ ID NO:765:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:765:

```

GAAGAAGAAT CCGACATANC CGNAAGTTCC TNCATCTAAT TTGGGGAATG TTCCCCTCCC      60
CATGTTAGGG AACCACCACC ATCAGAATGC GCCTAATAAT TGTCNCCTCC GAATGCTTTT      120
TGTGTTACCC GTCGTCGATT GTTTTNCAG CCAAATAATT TAANCCGTCT AGATCATCAC      180
TATCTTTTTC AATAGTAATA TCATATTNG GATGATTAC TTTTACCNCT GTTTCGAATA      240
AGAAGCGCCG GCCTTCTTGT ACATATTGAC CTAAAGAATG TAAATCAGTT GTGTAGTTGG      300
CACTTGAAGG ATAGATACCT TTGAAGTCTT TACCTTCTGA TTCACCAAAT AATTGTTTCC      360
ACCATTCATT AAAGTATTGC ATAGATGGTT GCATAGTTAA TCAACATTTC TGTNGTATAA      420
CCTTTTGCAG ATAAATGTG TCGANTGTC GCATATTGGT ATNCAATGTT GTCTTCTAAT      480
TTATCTGAAG ATAATTCTTC ACGTGCTTTT GCAGCACCAA TCATCATAGC ATCGAG      536

```

(2) INFORMATION FOR SEQ ID NO:766:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 551 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:766:

```

GTCGTTACTA CTTNTAATTT GCCATTTGAC TTATCACTGC TTTGTTTACC ACCAGTACCA      60
CATGCAGCAA CTAGAAGTAN TAAGGCTAAT AATAAAGGTA CTAATTTTTT CATGTTAAAC      120
TTCCTCGTTT CTTTCTNTTC GTAAATTATT GTGAAAAATA ATGTGATGAT ATAAATTACA      180
AACGTACAAA GTACGATTGT CGNACCACTA GGAATGTTGT AATTNTAGCT GTAATAAAGT      240
CCGACAATTG AACTTATGAC ACTTATTAAAN CTTGCTATGA TCATCATTGA GTATAGTTTT      300
TTACTAATTA AAAATGCTGT NGATGCAGGT GTAATTAATA ATGCAACTAC AAGAATTAAT      360
ACCTACCNNA TGAATCACT TGCTACTGTT ACTACTGAGA GTAACAACCA TGCACAATGT      420
ATGTAATAAC GTCGGTTTTG AGACCACTCA TTCTTCTTAA ACGTTGCCCC GATTGTAGAC      480
TTCATTTAAT GCGGATAGAA AAATACAAAT TGGTTTNNGG CAGATGAACC AGCCACACGG      540
GTGGGTTTAC C                                     551

```

(2) INFORMATION FOR SEQ ID NO:767:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 764 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:767:

```

TNAATGNACC CNCGAATNAA CCTACACCTG TCGAATCCAA ATAAC TCACA TTTNCTNAAT      60
TAACATAAAT ATCCCCGAGT TCCATCTTGT CTCATAGTTG NTNNAACCTC TTCTAATTCA      120
GGCACAGTAT AAACATCTAA TTCTCCACCG ACTTTAACTT CGTAAAATTT ATCTTGAGTG      180
GTTGTTTCTA TATTAAGATT CATTTCATTA CACTCCTACT TATTANAAAT ATTTATCTTC      240
ATTTTAAGCN CTGTATCCAC CATATTTATA TTTCAAATTA TTATATACCC ATCGAAATAA      300
TTTCTAATCT TCTTTTTTAA ATTAATTTAC TCTTTTTATA ATCAAAATAG TCATATCATC      360
TTMTTTATTT GGGTTTIGAA GCCTTAAAT TGCTTCATAG ATAATTNGAA CAATATCTTG      420

```

TGGGTGCAGA	TGTTTATGTT	TTTTAATATA	TTCTAAAAGT	TTGTGTTTAT	CTATAAAGGT.	480
ACCTTCACTA	TTTCTAGCTT	CAGTCACACC	ATCCGTAAAA	ATGATAATTA	AATCATCAAG	540
GTATATAGGA	ATTTCTTGTT	GTGATATCG	TGTGTGTGAA	CTGATTCCCTA	ACACTCTACC	600
TCTAACTGAA	ATTTCTNCAA	ATTCTTCTTT	TACAGCGCGA	TAAATATATC	CAGGCTCATG	660
ACCAGCTGAA	CTACAATACA	ATAAATGGNT	CATCTCTTCA	TATAAACCAT	AAAACATGTG	720
ACGAACATAT	TGTGATTAAT	ATTCCTTTTC	ACAACACGAT	TTAA		764

(2) INFORMATION FOR SEQ ID NO:768:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 593 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:768:

CACAAGCTCT	AAACATTAGT	GTAAACCAAT	GCTTAGAGCT	TTCTAATTAT	TTTATGCTTT	60
AAAAGATAAT	GTGTTATCTN	CGATGNCCTT	ACCGTCTTTA	ATAACTTTTT	CCTGCGTGAT	120
TGATACCCAN	NATGATATGG	AATATATTCA	TGATTTGGTG	CATCCCAAAT	TACTAAATTA	180
GCCTTATCAC	CTGTGTTAAT	TGTACCCGCG	TTAATATCTA	TTGCTTTAGC	AGCGTTGACC	240
GTAACAGCAT	TCCACACTTC	ACTAGGCGAA	AGCTTTAATT	TTAATGCTGC	AATGGCCATA	300
ACAAGTTGCA	AGTTATTCGT	TACACTGCTG	CCTGGATTAT	AATCAGTAGC	TAACGCGATG	360
GCACCATTAT	TATCAAGCAT	ACCTCTCGCA	GCTGCATAAT	CTTCTTTACC	TAAATAGAAC	420
GTCGNTGCAG	GTAAGAGGAC	AGCTACAGTA	TCACTATTTT	GCAACTTTTC	TTTTCTTTTA	480
TCACTAGAAG	CTACTAAGTG	GTCTTGCTGA	TATTGCTTGT	TCATCAATTG	CTTAATTCCA	540
GTCCGCCTAA	CGGGATCAAT	TTCATCCCGC	ATGTATTTTC	ACTTTTAAAA	CCT	593

(2) INFORMATION FOR SEQ ID NO:769:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:769:

GGGGACCAGC	TTACNACCTG	TAGCTNCAGG	NNNAAGCATA	NATAGGATAN	GGAGCCNACC	60
------------	------------	------------	------------	------------	------------	----

AATGAATAAC	TTTAATAATG	ACAATCCTNA	TTGATACTTA	CCAACAATAT	TTGGNGNAGT	120
TTGAAGCGCA	TTNCGNGCGT	GTATTACAAG	ACGATCAATA	TATCGAAGCA	TTAGAAACAT	180
TGATGGATGN	CTATAGTGAA	TTTATTTTAA	ATCCTATTTA	TGAACAACAA	TTTAATGCCT	240
GGCGTGACGT	TGAAGAAAAA	GCACAATTAA	TAAAATCACT	GCAATATATT	ACAGCGCAGT	300
GTGTAAACA	AGTGAAGTC	ATTAGAGCTA	GACGTCTATT	AGACGGACAG	GCGTCTACCA	360
CAGGTTACTT	TGACAATATA	GAACATTGTA	TTGATGAAGA	GTGTGGACAA	TGTAGTATCA	420
CTAGCAATGA	CAAAATTATTG	TTAGNTGGCN	CAGGTGCATA	TCCAATGACG	TTAANNCAAG	480
TAGCAAAAGA	AACAGGTGCT	TCAGTTATCG	GTATTGATAT	TGATCCCACA	AGCCGGTGNA	540
CCTAGGGCGC	AGAATCCGNT	AACGTCTTTA	GCAACCAAAT	GAAGATATAA	CANATTACGG	600
CATCAAAAAG	GGTATCTTGA	ACTTAAAGAT	ATCAAAGATG	TGACGCATAT	CATNTTCCAA	660
GCTCCGACAA	ATCCCTTTAA	AGTACAGCAT	CTTAGAAGGA	ATTATATTGA	TTTAACAAAA	720
TGAAAATGTC	GNNGGGTTGC	AATGCGCTTT	GGGTGGATGG	CATCAAAGCA	ATATTTAATT	780
ATCCCGTCAC	AAAGAAACA					799

(2) INFORMATION FOR SEQ ID NO:770:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 686 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:770:

CTCNTTGCTC	TTTLAGTCGT	CTTCATTATA	TCCATCTCAT	GACAAGCAAT	GAAGTTTGTC	60
ATACCACAAT	GAAACTATAT	TCACATTTTG	AAATTGCTTT	CATATATGCA	AAACACATTA	120
CACTGGATAT	AGCATTCGGA	GGCGAACATA	AATTTAGCAA	TATTGTAAAA	ATATAACGAT	180
ATATTTATCA	TTTGGACAAA	ATATAGTGTG	ATCTACTAAT	TTATAACATC	TATACATAAT	240
GTGAAAAAAT	TTTTTAAATA	CAATTAAATA	TCGGTGTAAT	AAATCCCTTT	ATACATAGGA	300
GTTGTATACA	TGAAACTAAA	TAACTATTCT	TTAAAAAGTTA	AAAACAAACA	ACTAGNTGNC	360
AATTGTGATT	TAAATTCTTA	TCTTGGTCAG	ATCAATCACA	TTGNTGGTAA	AAATGGTGTA	420
GGAAAATCTT	TATTAGCTAA	AGATTTCTTA	CTAAATAATA	GTGGAAATAT	CCCTAAGTCC	480
ATTTCTCAAA	ATGGTAACCT	TAATATCAAG	NTCCATCAAA	TATTCCCTAA	TGGATATTAA	540
CAAAAAGATT	TTTTATTATC	ATTGTTAAAA	TCAAAATGTG	GGGAACAATC	GACAAAACAT	600
TCGATAAGAT	TTATTNACAA	TACTNAAACA	TCCGAAGCAA	TACCCGTCTT	TACGGTACTA	660
CTTAAAAAAA	CTTGAGTGG	ATGGGG				686

(2) INFORMATION FOR SEQ ID NO:771:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:771:

```

CTCCTAAGTC AATAAAATAT TTATGATTGA CATGCAACTT ATAATTATGT GACATATAAA      60
TGCATAAAAA ATATAATCCT AATNACTTGA TAGTGAGAAT CATTATCAAT TAGGTAACAC      120
ACAATATTCT AGAATTTTAA ATTTGAGGAG GAAGCGCTTT TGATTGAAAA AAGTCAAGCA      180
TGTCACGATT CATTGTTAGA TTCTGTAGGG GAAACACCTA TGGTTCAACT NCATCAACTA      240
TTTCCGAAAC ATGAAGTGTG TGNAAGGNTA GAGTATATGN ATCCTGGNGG GAGGATGAAA      300
GATCGACCTG CCAAGNACAT CAATGANCAT GGAATTAATC ATGGATTAAT CACTNAGAAT      360
ACACANNPAN TTGAAAGTAC TTCTGGCTAA TTTAGGCATT GAGTTGGCAA TGAATAGCTA      420
AATTCAAGGG ATTAATACTC ACGNGTGTG GTGGTCCCTA CCTTATCACC NACAAATTTG      480
GGAGATTATT AATAGTTATG GGTGGCAANG TNGGAAATNG GTGGAGGAAC CTGNTGCACA      540
A                                                                                   541

```

(2) INFORMATION FOR SEQ ID NO:772:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 659 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:772:

```

AATTGTGANA CCANATACAC ATGTGTCATT GNAAGTGAAN TANATGGTTT GNNAATACCA      60
CAATACATAT GCACTTCNAA ATAGTAATGA TTATTAAGAA ATTATGGAAG GAGGAATATC      120
ATATATAGTA CGTGNATCNA AAATAGATCC AGTCAATATA GTAGGTATTG GTATAGACTT      180
TACTTCATCT ACTATTATTT TTACCGACGA AAACCTTAAC CCGGTACATA ATTTAAAACA      240
ATTTAAAAAC AATCCACATG CGTATGTGAA ACTTTGGAAA CATCATGGTG CATATAAAGA      300
AGCAGAGAAA TTATATCAAC CTGCTATTGA AAATAATAAT ANGTGGNTAG GCCATTATGG      360
ATATAATGTT AGTAGTGAAT GGATGATTCC CAAAATAATG GAAGTCATGA ATCGAGCACC      420
AGATATTATG GAAAAAACGG CTTATATTAT GGAAGCGGGC GATNGGATTG TANTTAANTT      480
AACTAATAAA AATGTACGCT CGAATTGTGG ATTAGGGTTT CAAAGCATTG TGGGGAAGAA      540
GGAAACAGGG TCCTCAATTA TGGATTTATT TGGATAAAAT AGCACCCCCA CATTTATCAA      600
AAAGGTCATT CCAAAGATAA AAGTATCTTG CAACCNNGNT GGTTAATATT GGGGTGAAG      659

```

(2) INFORMATION FOR SEQ ID NO:773:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:773:

```

ATACACACAT GTNATCGGAA GATNTATTAA ATCGTGTAAC AGCTTTGGTA AGTAAAACGC      60
CAGAGGTTAA CATTGATATT GACGCAATAG CAAATAAAGT AATTGAAAAA ATAAATATGA      120
AAGAAAAGGA ATCAGAAATC GATGCTGCAG ATAGTAAAGT ATCAGCAAAT GGATTTTCAA      180
GATTCCTTTT TTAATACAAA AAATAGGAGG TCATAAAATG ACTATAAATT TATCGGAAAC      240
ATTTCGCAAAT GCGAAAAACG AATTTATTAA TGCAGTAAAC AACGGTGAAC CGCAAGAAAG      300
ACAAAATGAA TTGTNCGGNG ACATGATTAA CCANCTNTTT GGAGGAAACT AAATTACAAG      360
CAAAAGCAGA AGCTGAAAGA GTTCTNGT TACCTAAATC AGCACAATCT TTGGGTGCAA      420
ACCAAAGAAG TTTCTTCACG GGTTCANAA AAACGTTAAC TATTAAGAAG AAAAATTTT      480
GGC

```

(2) INFORMATION FOR SEQ ID NO:774:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 616 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:774:

```

GGTTGATAGT TATGNCCTAT GTGNACGTT ATATTGANCA GTTTTTGAGA CCCNNCAGTT      60
AAGAAATAAT ATCCAANCCC TACCTTTTAA TGCTAGATGA ANAANTGNNA AATTTAGATG      120
ATTATATGCG TTATTTAATT ACTAAAAAAG AACNACTTAG CAAGTTAATT GACAGTCTAA      180
TGCTAACATT AGAAAATAAA TATATTGATA TTGCTGAAGC ATTTCANATT CAATGTGCAA      240
GAGAAATCAA TAATCAAGAA ATTGAAAATA TTAANTCAGA GTTGAATAAA GTTGAAGCAT      300
ATTATGCACA AATTGAAACT CAAATTCAAC AAACCTCAAC TGAAAAAATA GCAACAGAAA      360
AAACATCGTA TCTAATAAAT TATATGAACG CTGTGGCATA GAAAGGCGGC GAAACATGAC      420
ACACANATAT ATATCAACGC AAATGTCGAC CAATTTTCAC TGCATTAATG ATNATTGCCA      480
ANTTTTACTA CATATTTTTT GAANAAATG GCTTTTACT CGTTCTATTA TTGGGATGTG      540

```

TATTAGTTTA TGTAGGATAT CTTTATTTTC ATAAAATACG TGGCCTTTTA GCGTTTGGGA	600
TAGGCGCGCT ATTAAG	616

(2) INFORMATION FOR SEQ ID NO:775:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:775:

CCATCGCTTT TAATTGATCC ACTTGATCNT TCATTAATGA TATTAGTGGA CTTATTACAA	60
TTGTTGTACC ACCTAACAAT AAACCTGGTA CTTGATAGCA TATAGACTTA CCTCCACCAG	120
TTGGTAAGAC ACCAAGCACA TTACGATGGT CTAATACTTT GCTAATAATT TCTTCTTGTC	180
CTGGTCGAAA TGTTTCATAC CCAAAGTAAT GCGATAATGT TTGTTCATC ATAAATTGAC	240
CCCTNATTGT TGTTCCTTAA TTTCTTCTAA CTCACTCCAT CTNGTGATGT CTAAATCATA	300
TTGGAATTNC AAGTNGGNCT TTTTCTTCGN TTAGTTCTTT AATTTTCCCA TAATCTGCAC	360
TTGCCTCAAT CATGAGCACA TCAATTTCTT CCATTCTTAC TTCCGCTTGT TCTATGCGTN	420
TCATCAATTG GTCAAATTCT AATTNNNCTT NATATTGATA AACATNTTNC TTACGGACAG	480
GTGTATTAGG ATTTAGGTG GTGGTTCAAN GNGGGTT	517

(2) INFORMATION FOR SEQ ID NO:776:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:776:

CGCAGTAGAT CCAAATGCTA TCAGACCACT TGTGTAGGT AAAATGAAAG ATGGTACNAT	60
ACACCNNTCC AAGTGAAACA TGTGCAATAG ATGTGTTAGG TGCCAGANTT TGTCCAAGAT	120
ATTGATGCAG NTGAATATGT CGTGATTANC CGATAAAGGT ATTACCAGTT AANTCTTAAT	180
ACACATCATA CGACAACTGC AATTTCTGCG ATGGAATATA TTTATTGTGC TAGACCAGAC	240
TCAACAATAG CTGGTAAAAA TGTCCATGCA GNACGTAAAG CTTCTGGTAA AAAATTAGCC	300
CAAGAAAGCC CTGTAAATGC TGATATGGTC ATCGGTGTAC CCAANTCATC GCTATCAGCT	360

GNGAGTGGGT	TATGCTGAAG	AAATAGGTNT	GCCATATTGA	AATGGGACTA	GNTTAANNAT	420
CAATATGTTG	CNAAGAACAT	TTATTCANNC	AACTCAAGAA	TTACGTGAGC	AAGGTGTGAG	480
AGTGAAGTTA	TCTGCGGTGG	AAGATATAGT	AGATGGGAAA	AACGTNCC		528

(2) INFORMATION FOR SEQ ID NO:777:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:777:

GAATTCCTTA	TAATAAATTT	TNGGATAACN	CNAAAGCNAT	TTTAAAAGAA	GTCATGGGAG	60
AGAATCGTGA	TTTCGAGCCA	ACTGAACAAA	AAATTGATAA	CTTCAAACAT	TCATACGGTA	120
CAATTTTGTT	TTATGAAGAT	CAAGATGTTG	TAAGTGGTTT	ACAAGAACAA	ATGCCAAACT	180
ACTATGATAA	TTTTGGAATA	TGGTCAACTC	AAACAAATGC	CATGCATCAA	TTTGGAATTT	240
GGGACTGGAT	TAGGTACTAA	AGGGATNGGT	GGTTCANTAC	AACAATATTA	TCCACTTGNC	300
GATGAGATTG	ACTTCAAATN	AATTTAATAT	TCCTAAAAGT	TGGNAACTTA	TTGNTCANAA	360
TGGCAAATGG	GGGGATNTTC	CG				382

(2) INFORMATION FOR SEQ ID NO:778:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:778:

GAATTCCTTA	NGTTAACGTG	TGCCATGTAG	TACTACACCT	CTTTTTTTAT	CGGATTATCT	60
AACTCAATAT	TTAAATATTG	CTTTACTTTA	TTTTCCATTC	TCATATTTAA	CAACGCTTTG	120
ACAGTAATTG	TTGGTCCAAA	CAAAATATCT	TTTAACTCAT	TTGNATGTGG	TAGTGTGGG	180
TTAATAGCAT	GCGCTACTAC	TTGCTGTACT	ATGTTAAATA	ATTCGGTTTC	TTCAACACAA	240
TCATACTGAT	TAAATGATG	GATTAATTCT	GCCATTTGAT	TTTGATAAC	AGCATGTTGG	300
GATTTTGGGA	AGCACTGCAT	CTATAGAATC	AGCTATTAAA	CTATCAATTG	GTAATTTTAA	360
TATCTGATAC	ACGAAGGTTG	GGATGTTTCT	TAATCAAATC	TTGGAACCAC	CCAATCTTTC	420

AACTAAAATT GGATGTCAAA AA

442

(2) INFORMATION FOR SEQ ID NO:779:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:779:

```

GGCACGAGAC CACNCCTCTT TTTTANCGG ANTATCCAAC TCAATATTTA AATATTGCTT      60
TACTTTATTT TCCATTCTCA TATTTAACAA CGCTGTTGAC AGTAATTGTT GGTCCAAACA      120
AAATATCTTT TANCTCATGT GCATGTGGTA GTGTTGGGTT AATAGCATGC GCTACTACTT      180
GCTGTACTAT GTTAAATAAT TCGGTTTCTA CAACACAATC ATACTGATTA AAATGATGGA      240
TPAANTCTGC CATGTGATTG TGAATAACAG CATGTTGGAA TTGTGGCAAT CACTGCATCT      300
ATAGAATCAG CTATTAAC TAAGTGGNN ATTTAATAT CTTGATACAA CGANGNGGG      360
NATGNTTCT TTAATCAAC TCCTTAGAAN CCACCNAANT CTCTTCAA      409

```

(2) INFORMATION FOR SEQ ID NO:780:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 675 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:780:

```

GTGATGTGGA NGAGCNTCAT TTGTTGTAAA TATTNATTGA TTTCAGGGGG AAATGGAATA      60
TGCNCGGTGG CGGGAACATC CACCAATGA TGAGCCAAAT CCGCAGATNC CGAAAGAGGA      120
TGGCTCCGAG NACCAAGNAA AACTTNAAGA AGGAGCGTAT TGTAGGAACA GCTGGCGGTG      180
GCATGGTTGC AGTTACTGTA ACTGGTCATA AAGAAGTTGT CGACGTTGAA ATCAAAGAAG      240
AANCTGTAGA CCCAGACGAT ATTGAAATGC TACCCAAGAC TTAGTGTTAG CANCTACTAA      300
TGAAGCGATG AATAAANCTG ATGAGCTTAC CCAAGAACGT TTAGGTAAAC AATACTCNAG      360
GCNTAAACAT CCCCTGGAAT GTGATCATAG ATGCATTATC CAGAACCCTAT ATCANAGCTT      420
ATTGATAGCT TTATGAAATT GCCAGGCATT GGGCCANAGA CAGCCCAACG TCTGGCTTTT      480
CATACCTTAG ATATGAAAGA AGACGATGTT GTTCAGTTTG CCAAAGCATT AGTAGATGTT      540

```

AAGAGAGAAG TAACATATTG TAGCGTATGT GGTCACATTA CTGAAAATGA TCCATGTTAT	600
ATTTGTGAAG ATAAACAAAG GGATCGTTCA GTTATTGNG TTGTGGAGGA TGACAANGNT	660
GTCNTNGCTC GTGCC	675

(2) INFORMATION FOR SEQ ID NO:781:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 628 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:781:

GTCGCATCAG ACGCACTTGC AATGTTACNA GTGACNAGCG AAATATAAAG AAATCCATGA	60
CCATGAAATC GTTATTGTTA AAAAAGATGA AGTTATTATT AAAGATGCAG ATGGAAACGT	120
TGTAGAACGT GATTCATATA TTGCTGAAAT TGATGCATCA GATGCTGAAA AAGGTGTTTA	180
TGCACACTAC ATGTTAAAAG AAATTCATGA ACAACCAGCA GTAATGCGTC GTATTATTCA	240
AGAATATCAA GATGCAGAAG GTAANTGNA AATTGGATCA AAGACATNAT CAATGANGTT	300
AANGAAGCAG GACCGCATTT ACGGTTATTG CAGCAGGGTA CAAAGCTACC CATGCAGGGT	360
TTAGGTAGGG TAAAGGAATT TTTTAGGAAA AAATGGGCTG NCGTACCAAC TGAAGGTACA	420
NNGTGTCATC AAGAGGTTGG GCTTACAAAC ATGCCATTAT TATCTTGAAA AACCATTGTT	480
CCGTTTATAT TTCTCAAATC AGGTGGAAAC AGGAGGTAGG CCGNGCAGGT ATTAGTTGGA	540
NACTTAATAA ATTAGGTCAT AAATCATTA CAATCACTTA ATGGTGGAGG TTCCAACTTT	600
ATCACGTGAA GGAGACCCAC ATTGGTTA	628

(2) INFORMATION FOR SEQ ID NO:782:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:782:

ANTTTCCCCT TGNCCACCNA AGANATAGTG GATAANAAGA NCCCTGAGAA GAATAAGAAT	60
GTTTCTMNNA AAAACACTCG CAACTCTGNC CATATATTGG TCGTATATCG AANCTTTCTT	120
TACCCACAG NTTGTGATAA TTAGCAACAA TTTTATCAGA GTTATATNTT AAATGGGGGT	180

CCTCTCAAAC	CCATTTCATCT	AATAGGTAGT	TTGTNTCACT	AAGATGGTAA	TAGTGTGTG	240
TNAATATGTG	NATAGGCTTT	ACGAGCGTGT	ATTTGCTCCA	TCATCGNCAT	AAATGAATAA	300
ACTGCTTTTT	TCCTTAAGTC	AGTCGTATGT	AGCATAACTA	AAGGCATGCC	ATCATCTCCT	360
NGATGGGTAT	CTAAGCCTGC	TAAACCAGCT	AATGCTTTTT	TAAAGGGGTC	TGGTTCAGCT	420
TCNGATAANG	NCTTCCAACG	GGCAATGTCT	TTTGATACTT	TAAATTCTGT	TTCAACCCAC	480
ATTTGAGATA	TATTTTGTCT	CCAAAACATA	TTCGTCATAT	CTTCTTGTGT	GTTCCAATTA	540
ACAGCTATCA	TGAATATTAA	TTTCCTCCTG	TAATGTTACT	CAAATAATTG	ACAAAATTAC	600
AGACATAGCA	AGGCTTAATC	ATCTGCTAAT	TCAAGACCCA	GATGATTAGC	TTGTTNGGCA	660
ATTTCAACAA	TTTAATNGGT	TAGATTAGAA	CAACTTGGTC	ATTCTTCTTA	CACTTAATAA	720
TTATTCTTAG	T					731

(2) INFORMATION FOR SEQ ID NO:783:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 535 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:783:

GGCACGAGAC	GTATGATGCC	GGCTCAAGAA	CCACCTTATA	CACGTTTAAT	CGATTCAGCT	60
AGAAGACAAC	CTGAACAAAC	TGAAACGTAT	GTCAAAGGTT	CAGTCGTTGG	TTTCTTTACA	120
CCAGAATTAT	TCCATGGTAT	CGGATCAGCA	GGATTTTCATG	TACACTTTGC	GAATGATGAT	180
CGTAACTTTG	GGTGGACATG	TCTTAGATTT	TGAAGTAGAA	GATGTTAAAG	TAGAAATCCA	240
AAATATAGAA	ACATTTGAAC	AGCATTTTCC	AATTCAAGAT	AAAGATTTCA	CTAAAGCAAA	300
TATTGACTAT	AAAGATATTG	CAGACGAAAT	TAGAGAAGCT	GAATAATGAA	TCCAGAAATA	360
TAATGACGGT	TTATGAAAAT	TGACTTTCAT	AATGCGCGAT	TTAGAAATGA	TAGTTTGGTA	420
AATATTGATT	AACCATGACT	ACAATAGACA	AATATTATTA	TTATTACGTC	TTAGGTAATA	480
AAATAAATCC	CTCACTATTA	GCAGTAGTGA	GGGGATTTAT	TAGGGTTCCA	GATAT	535

(2) INFORMATION FOR SEQ ID NO:784:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:784:

GAATTCGGCN CGAGCTTACN AAATAATTTA NNGACCTGAT TGGCGTTGAA AATCTCCAGA	60
TTTACCGCCA GACTTGCTTT CAAGGTAGGT TTCGCCAATA ATCATACCTT TATCAACTGC	120
TTTCGTCATG TCGTAAATGG TTAAAGCCGT TGCTGATGCA GCGGTTAAAG CTTCCATTTC	180
AACACCGGTT TTGGCAGTTG TAGAGACAGT TGTTTGAATG TTAAAGTAT AAAGGGTGC	240
ATTTGTTTCA TCCCAGCTGA AGTGAACATC TATGNCAGTC AATGGTAATG GATGGCACAT	300
CGGAATAATT GTTGATGTAT TTGTGGGAGG CATAATACCA GCGATTTGAG CAGTGNTCAA	360
CTACATAGNC CTNGGTATTG	380

(2) INFORMATION FOR SEQ ID NO:785:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:785:

GAATTCGACA AATAACAAC TTGAATGAGC TTGCTTTAAT GTTATGTTTT ACGTAATTTT	60
TACAATTGAT GAGGAAGCAT TCCCTTTAAT AATTAGGAGG TCAAGACATG ACAAATTTA	120
TTTGTTAAC AGGTGGCGTA GTTTCATCAT TAGGGAAGGG TATTACAGCA TCTTCTCTAG	180
GTAGATTATT AAAAGATAGA GGTCTAAATG TAACAANTCA AAANTTCGAN CCATACTTAA	240
ATGTTGACCC AGGTACAATG AGTCCTTATC AACATGGTGA AGTATTCCGT AACGGATGAT	300
GGTGCAGGAA ACTGACCTAG ACTTAGGACA TTACGAN	337

(2) INFORMATION FOR SEQ ID NO:786:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:786:

GAATTCCTAA CGAATTAAAT TTTTACCTGC TTTATCTTTT TGGCTTTGTA GTCTTAAAC	60
TTCTCCAAC TATCAAGCG AAGCAGGTAA GCCAATACGC ATTGAATTAA CCATTGTGCA	120

AATCCATTCT TCAGGTGGCA TCTGTTTATT AAAATGTTTA GCAAGACAAG TTCTTTTCGAA 180
ATTAGCATTG AATGCATACT TT 202

(2) INFORMATION FOR SEQ ID NO:787:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:787:

GGNACGAGGT GGCATTTCTA AGGAAGAAGC AACAGACGG TTATTAAACA ATGGTGACAT 60
TGTTAAACGA GCAATCAGAG ATAGACAACC TTAGGAGGGA TTAAATGAC CAAAGAACAA 120
CAACTTGNAG AACGAATTAT TGCTGCAGNA GGTGGTATGG ATAATATAGA TAGTGTCATG 180
AACTGCATGA CACGTGTGCG TATTAAAGTA TTAGATGAAA ATAAAGTAGA TGACCAAGAA 240
CTAAGGCATA TTGATGGTGT CATGGGTGTT ATACACGATG AACGCATTCA AGTTGTGGTT 300
GGCCCTGGNA CAGTCAATAA AGTGGCTAAT CATATGGCGG NATTAAGTGG TGTTAATCTA 360
GGTGACCCAA TCCACAACA TCACAAATGA TAGTGAAAAA ATGGNCTTAT AAATCATATT 420
GCAGGTTGAT AAAGCAANGG CGAATNNNNG AAGCACATTC 460

(2) INFORMATION FOR SEQ ID NO:788:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:788:

GGCACGAGCG GTAGGTTTCAT CCGCTAAAAT AATCGACGGA TTCGTATATA ACGCTTTGGG 60
CTATCGCCAC ACGTTGTTTC TGACCACCTG AAATTTCTGA AGGTAACCTA TTAAGCAATG 120
AAGTTAGACC TAATTGTGAC ATAAGTTGCT GATAGTCTTC ATTAGACATA ACATTCCTAT 180
TTTTCTTTTT CAATAATGTA AATTGTTGCT TTACCGTTAA AAATGGTACA AGGTTTGTAG 240
CTTGTAATAA AAAACCTATT TCAGACATTC TAACTTTTGG CAATGNTTTT TGCTTCATTC 300
TCGGTAATAT CTTGGGTTAT TGATTAAAAT TGTGCCCAGA TTGTCGGNGT TTGGTAAAGC 360
AACCTGCCAT AGGTTAGGAA ATTGTACTTT NNTACCAAGG AGGCCAGAAG GGTCCCAACC 420

CAATGCTTAT TAATATCAAC CTTTATTTAT CTCAAAAATT GGGTTTCTTT TAACCCGCTT. 480
CAAT 484

(2) INFORMATION FOR SEQ ID NO:789:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:789:

GAATTCATAG CTTGATTATT TTNTGTTATA GGACTAGAAT ATACACATAT TATTAGAGCA 60
TCTGTGNATT TTATCTCAAG AAGCGAGGTT AATGAACAAT GAATATGCAT ATTTTATATN 120
ACTTNCGANC TAAACATAAT TTAGAAATTG ACGANTTAGC ACAGCAATTA NNTGAGAAAT 180
ATGGCACTAA ATATGAAGCA CATCANATGG GGAATGGGA GAATCATCAT CATGACCCTA 240
AATTTANAGA TGCCATGCAT TTAGNTGACT TCTGTGGATG CACCATATGA AATGTTTNTA 300
GAAAGTAAGG TTAAAGAATA TCAGAAACAT TTAGAAGAAG TCG 343

(2) INFORMATION FOR SEQ ID NO:790:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:790:

GGCACGAGAC GTTGGGCGCA ATCTGGTTTT ATCTCTGCTA AAGGTAAGGA AACACCTAGN 60
AAATTTAATG GCATTTAAAG ATGGAACAAT TAATCCTAGA AAGAGTAATC AACTTAAAGA 120
TTATGTGTTT ATTGATGACG GATGGGCGAA ACATGGAAC TATTGTGTTG TCAGACGTAT 180
TCAATACAC ATTGAAACGT GGGATCGTAC TGCACGGA GAACAAGAGG CTACATTTGG 240
GTCGGGAAAC GACATAGTGG GTGCGCCGTT AACAGGTGGG AAAGAGTTTG GATGAAATTG 300
ACTTAAAAGC GAAAGATAGT CATGGCGAAG TATTATTATT GGATAAAAGA TGACCCATAC 360
GGAGACTTAG CGAAAGAAGC AAATTCGTCA ATTTTACGTT GGGAGCCTTT ACAATGTTGG 420
NTGGGACGGA TTTGACGCAC AGGGTTAACT TTCGGAACAG GCTTGGTGGG TCCAATGGCT 480
T 481

(2) INFORMATION FOR SEQ ID NO:791:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:791:

```

GAATTCCTAA TTGACTTACC TGAACCCGTT TCACCACTTA AACAGTTAA ACCATCAGAA      60
AATTGAATTT CTAATTCTTC AATAATAGCA AATTGCTTGA TTGATAAGGT TTGTAACATA      120
AACTCATCGC ATCCTTATAA CAAATTGAAA ATTCTTGACT TGATTTTCATC ACTTGCCTCT      180
TTGCTTCGAC AAATAATTAA ACAAGTATCA TCACCACAAA TTGTGCCTAG TACTTCTTCC      240
CAATTGATTT GGTCTAATAT AGCTCCAATA GATTGTGCAT TACCAGGTAA TGTTTTTAGA      300
ACAAGTAAAT TATCAGTACC ATCTATATTA ACAAAGGAAT CCATTAAATA ACGTCCCAAT      360
TTTTCTTAAA GGATGGAATT TTCTTATCAT TTGGGTAAAC TTATAAACAT ATTGGACTGA      420
AGGGTATTGG GTACTTTAAT AAGTGGTAGG TCTTTTAATA TCACGAGAAA CAGGTGGTTG      480
GAGTGACATT TAAATCATAT CGGNTAATCG GNNTACTAAT NCACTTGG      528

```

(2) INFORMATION FOR SEQ ID NO:792:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:792:

```

GAATTCCTTT TGNAGCAGNA TGGTTGATGA TGCTCTACAT ACCGAAATGA TTGTTGATGG      60
CACACATTCT CATCCGGCAT CGGTTGCAAT TGCTTACCGT ATGAAAGGTA ATGAACGTNT      120
TTATTTAATT ACCGATGCAA TCGTGCAAA AGGTATGCCT GAAGGAGAAT ATGATNTGGG      180
TGGACAAAAA GTAACGTTC ANTCGCAACA AGCACGTCTT GCAAATGGTG CGCTTGCTGG      240
TAGTATTTTA AAAATGAATC ATGGGTTACG TAACTTAATA TCATTTACAG GTGATACATT      300
AGNTCATTTA TGGCGAGTAA CAAGTTTAAA TCAAGCCATT GCATTAGGTA TTCGATGATA      360
GAAAAGGTAG TATTTAAAGG TAAATTAAGG ATGCAGGATC TTTGGTTATT CTTAGATGAT      420
GATATTGAAT TGTAATCTCT TACAAATAAA CAAAGCAAGG CTCACACATT TAGCTTAATA      480

```


AATTATCAAT AATTAAATCG TATTGCAAAT AGGATTTTAA TCTTTTGNTA CAATNAGCAC 540
T 541

(2) INFORMATION FOR SEQ ID NO:793:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:793:

GAATTCCTCT AGGGTATTAA ACATAGGTAA ATCAATTTTC TATCGCCAAT AGTATAAACA 60
TCATCCATAT TAATCTGAAG ATAGCTACAT AATTCTTTAA CAGCATAGCC TTTATTTGTA 120
TAAGGCGCCA TAAACTCTAT TAAATATGGT NTGTTGTGAG GTTCTATGT TTANTCATTT 180
AATTTNNCAT TATATAAATC GAATAATTAT AAAAAGTCAT CATACTTTTT ATTTTTTAAA 240
AATATNTGAA AATTTAATAG TAATCCAATT ATAAGATCAA ATATCATTAT CATTATAATC 300
AAGGCAACTA TAATCACTGG TGACACTCGG TTACATAACA AGCTAGGTAA TCTCCAGATA 360
AAATTGGACA TTTNCAACCA ANTCCATAA CTTTACAAT ATTTACAAAG GTAGGNAAAA 420
GAATTAATAA TACCTATACT TGTAATTAAT ATTGCAAGG GTATATT 467

(2) INFORMATION FOR SEQ ID NO:794:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:794:

GAATTCCTAA TTAATTAAAA TTTTANCGGA TTTCAAGAGG NCTTTTTTATA ATGACGCCTT 60
ATTTGNAAAA TGTCATATGT GGTTTAGCCT CTTTATAATA ATTTAATCTG TTCTCAAGTG 120
TGCCAGTATG TAATCTAGC TTATGACCAT CAGGGTCAGT AAAGTAAATT GATTGTCTAT 180
CTCTAATATC TCTAACTCTN CCNCCTAAAA TATTACGTT ATTATCTTTT ANCCTCTGAT 240
GCCAATATTT AAATTCGCTG TCATCTATAG TGAAAGCTAT ATGTGTATAT GAAAAGTGAA 300
TTTCATTACG TGGGTATATC TNCNTCTTCA CCATAAGCA AANCCATAGG GGCTGCAAAG 360
CTCAACAANA AGCAG 375

(2) INFORMATION FOR SEQ ID NO:795:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 535 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:795:

```

AATGTCTCAT AAGTACCTTG CACAATACCT TGAGNAACCA ATATATATCC AACTACCGGC      60
TGTCATCTGT CCATACATGA TTAAACCTTT TTTATCTAAT TCATTAAAAT GATCCCAGTT      120
TGCCCATTC A GGCATAATA CTGAATTTGA AATTAATACA CGTGGCGCTT CTTCATGTGT      180
TTTAAATACA GCAACTGGCT TTCCTGATTG TACTAACATT GTCTCATCTG ATTCTAATTC      240
TCGTAACGTT TTCTCTATTG CTTCAAAAGC TTCCAATTA CGTGCTGCTT TTCCAATACC      300
ACCATAAACA ACTAAATCTT CTGGTCTTTT CAGCAACTTC TGGGTCTTAA ATTGTTGGTA      360
TTAACATTCT TAAGTACTGC TTCTTGGTTC CCAACCCTTT AACTCAAAT ACTCAAACCC      420
TTTNTTTGGC TTGGAATTTT NTCTTCAATA AAATTCGCTC CTGGTCTTTT TAAGAAGGTT      480
AATTCCACTA AATTAAACG CTTACATTAT TATCTTCAAT ATTCAATATT GTATT          535

```

(2) INFORMATION FOR SEQ ID NO:796:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:796:

```

ATTAGTCCGA TTTGACATAG ATCCCGAAAA ATAATGGCTA ATAGCCACTT ATAGTCGAGA      60
TTATGAAC TA TATAATTTAT TTATTATTAA ATGGATTATA TACTTATTGT GTTTCTTAAT      120
ACCTTTTTAT ACTTTAATAT CTTGAATTTT TTCTAAATCA TTAATAATAT CTTTTAATTC      180
GTCTGTGGCA TTTTTCACCC AAGCCCCCTG TGCCGCATTT TTAATAATCAT CTTCAAAGTT      240
TGGGAAATGA CTTACCATTT GGTCAAGTAA TATTTTCTCA TCACTTTTC GCTTATTTGG      300
ATGATCATGA TGCATACGAA CATGTTTCAGG CGCAATAACC TACTAATCT GTTCTTTTCC      360
TTCATGTGGT CCAATACTGC TAAATCTGGT AAACCACTAA AATCAAGTCC CACGCTTATT      420
CATCTCCTTC AATCTGTGCA GATTGTTTTA GATATTCTCT TCTTAACTCA TCTTTATAAT      480

```

CTTCTAATTT	CATTTCCGGA	TGTCGGATAC	GTGGATTTCGT	TCTCTATCGA	AAGATTCTAT	540
AATACGTGTC	ATCCGGATCA	AAGCGGCTTC	ANTATNATTC	AATTTATGGT	NGGAGATATA	600
GGAATGATCA	AACATTGGGT	CAAAATTCCT	GGG			633

(2) INFORMATION FOR SEQ ID NO:797:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1493 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:797:

CTGTGATTTA	TCATTCGATT	GCATGATTAG	AGGGAGGGAT	TAAACGTGAC	ATATCATGAG	60
CGTGTTTTAG	CATTAAGAGC	AGANAGTAAN	AGNNCCGCAT	TGATTTTTCG	ATTCGGNAGA	120
TTTATTTACC	NAAGAAGAAT	GGCTAAGTAT	GTCTCTTGCA	GAAAGACNCA	AAGCTGANAA	180
AGCATTTTCG	CACGNAGTTA	AAAATATGGA	CGATGTAAGA	ATGCCCTTCT	CAAGTGTCCA	240
TGACGCCCCA	AGTAAATTA	TATAATGTTG	TATATTCTGA	TANCGGCATT	AAACGTAATT	300
TTAAACNAGC	TGAAAATGAA	GGATTCTAAT	ATCATTTTCGT	TTATATATAG	CAGACATGAT	360
AGAAATTTAT	ATGTAAATCT	TGTAGGTAAT	CGTTTTNNAA	ATAATATAAG	TATGACTAAA	420
NCCACATCCA	ATATAGGACG	GGGCTTTTAG	TATCGTTCCA	GATTTGTGGG	GAGTTAGGGT	480
TTACTTAATT	AAAGGGGTCT	GCCCTCAATT	GCTCACCAAC	GAGGGCAAGT	TACATCAATC	540
ACACTTCAAT	TGCCGCCGAC	TAGGGGTAGT	AATCATTTGGC	AATAAGAACT	AGTTAGTGAC	600
TAACGGATTT	ACGTTCCATA	AGCAAAGTGA	TACAAACGCT	CAGCATCAAT	GTAAGGCATA	660
GAATCAATAG	TTAGGTAACC	ATCTTTGATG	TCACCAATTA	ATCCTTGATT	TACACCAGTG	720
TTCACGTAAA	TATCATAGCT	ACTTACGTCT	GAGAAAATAA	GCGCTTCAAT	CTCTTTTCTC	780
ATAATCATCA	CTCCAATGTT	TATATATTAT	TTATATAAAC	TCTCTCGTCT	CTCTCTATTT	840
ATTAACTTCT	TACAAGTCTA	ATATTACATG	AATTTCCAAA	TAAATAAAGA	GGTTTGTGAT	900
GTATTTTACA	AATTTATCAC	TATTTTGGAA	AATTAAGAAA	TAGTTAATTA	TATAAAAAGTT	960
TAATAAGTCA	GAAAATATGA	TAAAATGTAG	ATGTTCTTTA	GACATTAAAA	GCTTCTAACA	1020
TGATACGGAA	TATGAGGTTT	CTGTATCACA	TTAGAAGCTT	TTTTGTTGCG	GTGCTTATAT	1080
TAATAATGGC	ATGAATGAAC	GCATGCTGTC	TTAGTTTCAG	GAATCGGCTA	GAATATTAAA	1140
CTTCCGTTCT	TTGAATATTT	NTTAATTTCT	TACTAATATC	ATCCAGTTCA	TTCTTCGCCT	1200
TTTTAACCCA	ATCTCCTTGA	GCTACATTAT	CAAATTCACC	TTTAAATTTT	TTGANATGGC	1260
TACCTATATT	TCACAGCTCA	CTTTAGATAT	CGAACTTGTT	TCTTCAGAGT	TACTTGTATT	1320
ATTACCAGGT	TTTATTTGAT	ATTCAGTTTG	ACTCATAACT	TGTATCCTCA	CTTGAAGTAT	1380
AGTGTACAGA	ATCTGTAAAA	TAAATGTTTT	CTTCTTTATT	TTCTACAAAG	GTAATTTCTA	1440
GATTTTTTGA	CCCTACAGAT	GAGCCTTTTA	AATCACCATC	NCCTTTTATT	AAG	1493

(2) INFORMATION FOR SEQ ID NO:798:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:798:

```

GAATTCCTGA TAGATATGGT TTTAAACGTG ACTTCAAGCT ATATGAATGC GATGACTGTT      60
CAGCATGTTC TTTGAGGCAA CAATGCATGA AACCAAATTC GAAATCCAAT AAGAAAATCA      120
TGAAGAATTA TAATTGGGAA TACTTTAAAG CCCAAATTAA TCAAAAAGCTT TCTGAACCAG      180
AAACGAAAAA AATCTATAGT CAAAGAAAAA TTGATGTAGA GCTTGTTTTT GGGATTTATG      240
AAGGNTATTT TGGGTTTCAC TCGAATGTCA GTTCGAGGAA TTAAATAATG TTAACGAGA      300
GCTAGGTTTT GGNTTTAATG GCACTTAATA TTAAGGAAAA TAGCAGGTCA ACGAGCTGGT      360
ACAATTATTA AAATACATAT CAAAAAGCT GGATTTCTTA TCAAANTTAA TTAATAGGAA      420
TCAACTT                                         427

```

(2) INFORMATION FOR SEQ ID NO:799:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 762 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:799:

```

AATATAATTT TGTTGGAATA TATTCGTAN AAAGTGGGGT NATTTAATTT AATTGATTAA      60
TTCTAATATA TGATAGTATA ATGAAATGTA GATAGGTATT TAATTTAACC AGAGGTGAAA      120
TTGAGATGTG GAATTTTATT AAATGTGTGT TTAAATTCGT ATTTAGCTTA GTTGCTATTA      180
CAACATTAGT TGCTGGTGTT GGTGTAGTAG CATTTGCTTA TATCTTTAAA AAAGATTTTG      240
AAGATATTGA AAGAAAAACT AAAGAAATTA TTTCTGATAT TGAAAGTAAA AATAACTAAT      300
AACATTTAGA GGCTGGGACA TAAATCCCTA AAAACAGCA GTAAGATAAT TTTCAATTAG      360
AAAAATCTT ACTGCTGTTT TCTATTTATA CAATACTTCG TAGTTGATGG CTTGCTTTTC      420
CTAGGTTGCC GTCTCAGCCT TGGTCGTCGN CTGGCNCCTG TCCCTCAGGA GTCTCGCCAT      480
TAATACNCG TATTNACATG TNATTTTACT NTTGANATNC TTTNAAAAAA TAAGACACTT      540
TGCCCAACTT GCACATAGAT GTAAAATTCA ATATGATGAA GTTCTGTGTG TGGGTCCCTT      600
CTTATAATTT AATAAATACC ACTAACTAA ATTAACGAGG TGCCTTATGT ATAAAAATTA      660

```

TAACATGACC CANCTACACT NCCAATAGAA ACTTCTGTGA GNATCCCTCA AAATGATATT	720
TCNCGATATG TTAATGAAAT TGTGAAACN ATACCTGATA GC	762

(2) INFORMATION FOR SEQ ID NO:800:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1028 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:800:

CGTAATTACA TTTTAGGCTT GATTTTCTAT CGCTTCTTAT CTGAAAAAGC GGAACAAGAA	60
TATGCAGATG CCTTGTTCAGG TGAAGATATT ACGTATCAAG AAGCATGGGC AGATGAAGAA	120
TATCGTGAAG ACTTAAAAGC TGAATTAATT GATCAAGTCG GTTACTTCAT TGAACCACAA	180
GATTTATTCA GTGCGATGAT TCGTGAAATT GAAACGCAAG ATTTCGATAT CGAACATCTC	240
GCAACGGCGA TTCGTAAAGT TGGAAACATC AACACTAGGT GAAGAAAGTG AAAATGACTT	300
TATCGGACTG TTCAGCGATA TGGACTTAAG TTCAACGCGA CTAGGTAACA ATGTCAAAGA	360
ACGTACTGCA CTAATTTCCA AAGTTATGGT TAATCCTTGA CGACTTACCA TTCGTTCA	420
GTGACATGGA AATTGATATG TTAGGTGATG CATACGAATT CCTAATCGGG CGCTTTGCGG	480
CGACAGCGGG TAAAAAAGCA GCGAGTTCT ATACACCACA ACAAGTATCT AAGATACTGG	540
CGAAGATTGT CACAGACGGT AAAGATAAAT TACGTCACGT GTACGACCCA ACATGTGGTT	600
CCGGTTCATT GTTGTTACGT GTTGGTAAAG AAACGCAAGT GTATCGTTAT TTCGGACAAG	660
AACGTAACAA TACTACATAC AACTTAGCAC GCATGAATAT GTTATTACAT GATGTGCGTT	720
ATGAGAACTT CGAGATCCGT AATGATGACA CATTGGAAAA TCCAGCCTTT TTAGGCAATA	780
CATTTGATGC GGTATTGCG AACCCACCAT ACAGGTGCGA AATGGACAGC AGATTCAAAA	840
TTTGAAAATG ATGAACGATC AAGTGGGTTA CGGGAAGCTT GCGCCAAAAT CCAAAGCAGG	900
CTTTGGCTTT ATTCAACACA TGGTACATTA CCTAGACGAT GAAGGGTACC ATGAGGCAGN	960
CTCCNCATN GCGTTATTNT TCCCTTNTGC CNCAGAAGGG GTGATTCNCN CGCCTTTT	1020
TTTGAAGG	1028

(2) INFORMATION FOR SEQ ID NO:801:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:801:

```

AGAAAAANCCN ACATCGTCAT CNCATAATTC NAGTTGTGNA AAACATCTTC AGGACAAGGC      60
GGAATCCATA CCAAGCATTT CGTAGACCCA TTTATCTTCG TTGGAANCGA TGACGCCTTT      120
AATCTCCGCT TTCATCTTCA TCACCACCTT TCAAAGTGTT TTCATCTTTT TCTTTTTCAT      180
CATTTTCACC NCTGTTAGCT TTTTCGTAGT TTTTAGTAAT CAGGTATTCG TCTAATTCAG      240
GATTGTCTGA TGGTCTTCA CCTAACATAA TCCGCACCTC ATTCCTTGTA AATGAACCAG      300
AACTTACAAG TTTGTCAATT GCTTCAGCAT ATTGAAGTGG GTCTTTTTTA TTCACACCGA      360
CAATTTCTAT TCTGTATCT TTCAAATACA TGCTTTGTGT TATTGAGTTT CGCGTTTAAT      420
TCGTCTGAA TCTTTTTTAA TAAAGGTGTT AAACAGAACT TCTCAAATA CAAGCGTGTT      480
TTTTTCCAAA TCAAGCTGTT TCTCCGTAAA TCCAAACCTG GAGGTAATAC CCAATCATCC      540
AAACGCAACA TTTTPTATTG CATCTCTCAT TAGCTCACTC AATTCAAGAA AAAGGCATGT      600
TACTATCTT ACCACCATTA GATAATTCCT CATAATCAAA ACCTTCTATC AAAGGCGCGA      660
TTGCTAGTTG ATTTTATTA AAAGTATTGA ATAATTTATT TGTAACGGC TTGTAATTTT      720
TCAATATTCT TTTCGTCATA TGCGCTAGAG GCAGATTTCA AAATCCCTCT TATTTGATAG      780
TTTTTTAATT GTGCACCTAT CATTCTCCG AATATTTTCC CGTAATCTTC GAATAGACTT      840
TCTACAAAGT GTGTCACTTT ATTGTTGTG TACTTTAAAT ATATGACCTC TTGCATTGTG      900
AAAGTACGTT GATAAGTATA ATCTTTAACC GTTACATCTT TGAATATATC ATCATACAAA      960
GCGTACTCTT CTCTGTAAAA GCTATCTGCG ATAAGTAATT CTTTGCTGTC ACTTACTACG     1020
ATTAAACCT CGTTATCATA AATTAGTTTA TATATAACTT GTTGCCAAAA ACTATCGCTT     1080
GATAAGTCAG TATTTGGTTT TATATTTAAC TTGTAGTAAA CATCATCTT TT              1132

```

(2) INFORMATION FOR SEQ ID NO:802:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 737 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:802:

```

AATTCAAGAA CGTACCATAC ATTTAACTGA GGATATCTCA ACATTGATTA CAACAGCACT      60
CCGGAACGAC AGTACAACGC AAAATAACAA CATTGGAGAG ACAGAAGATG TACTTAATAG      120
AACCGATTAG AAATGGAGAA TATATTACTG ATGGTGCGAT TGCACTGGCT ATGCAAGTTT      180
ATGTAAACCA GCATATCTTT TTAGATGAAG ATATTTTATT CCCTTATTAT TGTGATCCAA      240
AAGTGGAAAT TGGACGTTTT CAAAATACTG CTATAGAAGT GAATCAAGAT TATATAGATA      300
AACACAGTAT TCAAGTAGTT CGCCGAGATA CTGGTGGTGG CGCTGTGTAT GTTGATAAAG      360
GTGCCGNNA TATGTGTTGT ATTTTAGAAC AAGACACTTC AATTTATGGT GATTTTCACC      420
GATTTTATCA ACCAGCTATA AAGGCATTGC ATACATTAGG TGCAACAGAT GTGATACAAA      480

```

GCGGTAGAAA	TGATTTAACA	TTGAACGGCA	AAAAAGTGTC	AGGCGACNGA	AGNGTNGAAC	540
GGTGTTAAAA	CGGCGGTTTC	TGGTGGGATT	CAAGGTGTAG	TTGGCTGGTT	AACTGAATTG	600
TGGGGCANCA	TCCATTCTAC	NCTANATCCA	ATAATGGCAT	GCTCACCAGT	TATGGTGAAT	660
TATACACCCA	AGTTCATNAT	CGATAGGCAC	GTAGGTCACA	TCACATCACT	AATGACTATC	720
ATACAGCGTT	AGGTGGA					737

(2) INFORMATION FOR SEQ ID NO:803:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 982 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:803:

TCCTGCAATA	ATTTTGTGCG	GTACTACGAC	ATTTCTATAA	GTTTGAGAAA	TATCAGCGTT	60
TTTGAATACC	TCTTTAACTG	CTTGAATTTT	TTCTTTAGTT	GATATTTTCAT	TTGTATCTAC	120
GACATGTTTA	AGGAATCGAT	TCATTTTCT	CGGACGATAA	TACTTACGCT	TATTTAAAAA	180
TTTATCTTGT	TTTTCAGGAT	CCAGTTTCG	AATAATATGG	GCATATTTTC	TAAATAAACG	240
TTCTTCCGGT	AATTCACCTT	CAATAGATGT	TGGATTTACC	AACATAAGTG	ATGATGTAAA	300
TTCAGGATAA	CGTACTGAAA	TATCCGCACC	AATGATTTCCA	CCCATTTTCAT	GGCATACAAA	360
TGCAACTTCT	TCAATGTATT	AAATATTTAA	GTAATTTCAAC	AATGTCATCA	GAAAAATCTT	420
TTATTTCAAT	GTGACGAGGT	TTATCAAGAA	TAGCCATGTC	CACGGTAAAT	CAATTAACAC	480
AACTTGAAAT	GATTGTGGTA	ATTGTGCTGC	TAATNTATTA	AACACAGAAT	NATTATCAAG	540
TACAGTATGA	ATCAATACGA	TAGGATAGCC	TTACCTAAT	GTAATGTAAT	GTATCGATGT	600
TCCATCTTTT	TCTAGTAAAT	AGATCCATAA	TTTTCTCCTT	NGATTATCAT	TTTTTATTGG	660
TAAAATGGTT	AATAATTCTT	CCACTGTTGT	AATTGTAAAA	TCAACTTCTT	CTTCGAGTGG	720
CTCAATTTCA	GCATCTTCTT	GTTTATACCA	TACACTAACC	ATGCCCATAG	NTCGTGCTGG	780
AGNTACATCA	TTTAACGCAT	CATCGNCAAC	ATACATAATT	TGGTCAGGTA	ATACCCCNAG	840
GNGGATCAAT	CATNTCTTCA	AAAATTTTAG	GATGTGGNTT	TACGAAAACC	AACTGNNTCT	900
GATGNNGGAT	AAATNATTAA	TAACAAGCAT	CAANCCANGT	GAATGTAATC	GAAATTGGTT	960
AATCTTAGAT	TTACNTGTG	GG				982

(2) INFORMATION FOR SEQ ID NO:804:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:804:

ATGACGCCAC	CACCGAGTGT	ACTCAATGGA	CCTTTGAGAC	CACTAATGAC	TGTTGCAGCA	60
CTACTATAGC	CATTTTCCAT	AGAATGTGCA	GCTTTTTCAC	TACTGTAGTA	ATTTAATTGC	120
GCTATTTTTC	CAAAGTTTTG	AGCTATTTCA	TCATACTTTT	GACTAATGCT	TTCCAATTCT	180
TTTACAACAT	GTGCAATCGT	TTCAGCTTTA	ACACTAATTT	TTCCACTCAA	CGTCATTACT	240
CCTCTGCTTT	ATTAATATGA	TTTTCATCAG	TATCGAATCC	AAATAATTCT	CGTATAAATG	300
TATTAATGAC	ACCAATATGA	ACATTCAGCA	CTTTATCTTT	TAATGGGTAT	CGAATGAGTA	360
ACAAATCATN	TTGGTCATAA	ATGTTATATA	AACCTGGTTG	AGGGTCACCT	TGATGATTGG	420
TAGATTTCAA	TTTCTTAAAA	CAACGCCAAT	CGTATCGATA	CTTTCATTAT	TTAAGTTCTC	480
CAATATTTCA	TCGNCAATTT	GTTTAAAGTC	CCAATCATTG	GATTTTCTTT	GTCTCATCAA	540
TAAAGGATAT	GATTGTACAA	TCGCACCACC	ATGNAATGTC	TTTATTGATA	ATNCGNNTTG	600
GAAACCCATT	ATTTATAANC	CGGNTTAANA	AAATATATNC	ATCTTTTNCA	TAGCTAANTG	660
GTGNAANATA	CATATCATTA	TTCGGGATAT	TTACAATNGG	GNTAATATAC	TCTCTCACTA	720
ATGTGGCCAC	TNTNAGACCT	GCATCAGTTT	ATCTGGNCAT	CCTCTGCTAC	TACTCCTAGC	780
ACANTNAACG	CCACTTTAGC	TCCTCCAAAT	ATGG			814

(2) INFORMATION FOR SEQ ID NO:805:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 544 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:805:

AACAAGATTT	ACCCCTCGTT	TTTGAGACNA	NTGCGTTTAA	TNACAGCACC	GGAAGTCCTG	60
TTCTTAGAAT	GTCACGTCGC	CTTTAGCATA	AAGACTTAAT	ACNTTAATAT	CTCTTAAAAG	120
ACTATCTGAT	AGTAGTGCAT	TTTGCCAGT	CACCCAATTT	CGAATTGTAA	TTCCACCCGC	180
TACTTAACTC	AATAGCATCT	AAATCGGTTA	TATGATTATT	TGTTCTCATC	ATACTTTCCT	240
CCCTCGATGG	AAATTACATT	AGTATCCGAT	TTTAAACGGC	CATTTCATC	TACCATTGAC	300
GGGGAAACAT	CATCTTTATA	AACTGTACA	AATTTTGTGC	TAGGATATGA	TTGCATAATG	360
TCATTTATAG	ATTTTGAAG	GTTCCAAGCA	TAGTTTTTTA	CTGTTTCTCT	ATTTTPTTCT	420
TTATCATAAT	AAGCAATGAA	CTATGATTTT	ATATTTTTTT	GTATTTGTGG	ATATTTGTTA	480
ATCAAAGATT	GTAATGTTG	ATTGAATGCA	TCACCTTTTA	AGTGCATAAC	AGGTTTNNGA	540
AGTC						544

(2) INFORMATION FOR SEQ ID NO:806:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 995 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:806:

```

GGGGGGCCGC CCGAGGAGGG GNTTTCAGTT TNCAATACCG ANCCCATTTT TCCAAGATCC      60
GAAAGGANC GGAAGNAACCG ATTGAACCTT ACCGTAANCC CAACCCGTTT ACCCAATCTA     120
TAAGACCGTG CCAGTTGTTA AATACNATTT TCTGNCATTT CCAGGGGTCA AGATGATACC     180
NCTAAAAAGC CTAANNGGCC TTGTNACACC CTNGNCCAAC AACCTACTCT GAAATTTATG     240
ATTATCCAGT GGANTGAAAA GTTTGATACC CATATTGGCA AAGATTTTANC CTGAGTTTGC     300
CAAAGAGCA AGATGTAAAA ATTGCCATAG AGTTACATGC AGGATTTTTA GTTCATACAC     360
CATATACGAT GTTAAAGTTA CGTGAGGCTA CAAATGAATA TATCGGTGCT AACTTAGATC     420
CTAGTCATTT ATGGTGCAA GGTATTGATC CAATTGCTGC GATTTCGCATA TTAGGCCAAG     480
CAAATGCAAT TCATCACTTC CATGCTAAAG ATACGTATAT TAATCAAGAA AATGTAAATA     540
TGTATGGTCT AACTGATATG CAACCATATG GTAACGTTGC GACAAGAGCA TGGACATTCC     600
GNACAGTTGG TTATGGACAT AGTCCATATG TATGGGCAGA TATCATAAGT CAACTTATTA     660
TTAATGGATA TGATTATGTA TTAAGTATG AACATGAAGA TCCTATTATG TCAGTAGAAG     720
AAGGTTTCCA AAAAGCTTGN CAACTTTGA AATCTGTTAA TATTTACGAC AAGCCAGCAG     780
ACATGTGGTG GGCATAATAC GAACGAGG TTAGTCTGAA GTTTGCTGA AGTAAGACTG     840
GTGGCAGGGT TGAATGAATG CATATGTCGG CAAGNCATG CAAAAATNTC ACACTTAANT     900
CATGTCATGG GTGTAAAGAG GTGTACTTTA TATAAGTGT TAGCGATGGC ATCCCNTTCA     960
CAGGNACAAT CCCCAACCATG AAAGAGTATA TACCT

```

(2) INFORMATION FOR SEQ ID NO:807:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:807:

```

CCGGATAACC CTTCAATTGA TATATCCAAG AGGTTTGCCG AAAATAAANA TTGGTGGCCC      60

```

GTCAAAAGCA	TTTGCAGTTT	GTATTGAGCC	ATTGACCCCA	AAATTGATTTA	ATAGCCCAAT	120
ATCCAGTACA	ACTATATGGT	ACAAATGCAC	TTGATTGGGG	TCGTCAACGC	ATGTATCGTG	180
ACATTTAGCG	GACTIONTAAT	AGGTGTCAAA	GGTATGCCAA	CACCAATTGC	AGGTGCCATC	240
GTATTGTTTG	GCTTTAATAA	TGCAGTGACA	TCAATTGTAA	CAATCGCAAC	AGTGATTATT	300
GTCAGCATTG	TCTTAGCCTA	TATTATTGGA	ACACTAATTA	ATAAGTTTAA	TTTAATGAAT	360
ATCAACTTTA	AAATGCCGAG	CAAAAAGAAT	CATATTAAGG	AGAGTGTTTA	ATTATGGCAA	420
AGAGCTATGA	TTATCAAAGT	GCTTTTCGATA	TTATCGGACC	AGTTATGATG	GGCCCTTCAA	480
GTTCATAC	GGCTGGTGCA	GTAAAGATTG	GGAATNC			517

(2) INFORMATION FOR SEQ ID NO:808:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 665 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:808:

TCTTCATNTA	ACTTTTTCAC	TTACCATATC	TGATAATAAT	TCTTTTACGC	CAAGTAAGTT	60
TGTAGATCCA	CCAGTTACAA	TAAACCCACC	ATTTACTTGT	GTTAATCCTA	AATCTTGTA	120
AACATCAAAT	ACTTCGAAGA	ATATTTCTTC	TACACGCGCT	TCAATAAAGT	CACTCAAATC	180
TTTGTGAGTA	TACTGTACTG	TTTCATCACT	ATCAACCTGT	TCAACAGTGA	AGATATCTTG	240
ATCTGAAGCA	GAATCATAGA	ATGCATGACC	ATATTGGTGT	TTAACTTTTT	CAGCAGTTTC	300
ATAAGAAGTG	TTTAATCCTT	GTGCAATATC	GTCTTGTAAT	ATCAGCCCT	GCCATTTTCA	360
TAGAATCAGC	ATCTACTAAT	TCACCGCGTT	CATAAAAAGC	AACTTGGGGT	AACGTCTTCA	420
ACAATATCAA	TGACACATGC	ACCTAACTCT	TTNNCAAGTA	GCTTGTNAGG	ATTGGACCCA	480
TAGTTATATT	GCATCAGAGG	TAAACATCTT	TATACATCAA	CAACCACATG	CTTCTTCGGC	540
ATTTTATCAA	TATTAATTAA	AATCGATTG	TGGGATTAGA	AATTACGCCT	GCTTCCAACC	600
CTTAATGATT	GTCTTTGGAA	ATATTCCTTT	AGGGCTTTGA	AACCTCAATT	TCTTTTATCG	660
ATTTT						665

(2) INFORMATION FOR SEQ ID NO:809:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 775 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:809:

AATGGGAATA	GATATGACAG	AGAGCTTTAA	TGAAACAATG	GAAAAGTTTA	ATACAAGAGA	60
TAAAAATCGA	TTCGAAAGAA	AGTGAATTTA	AAAATATATG	CTTTATTTGG	ATTTGATTAA	120
GATTAAAAAC	ATAGACCAAT	GAATTGCATC	GCATGAAATT	ATATTATTTT	TAAAGTAAGT	180
AGAACTAGAT	AAATGATTAT	ATATACAACA	CCTGTTTTTT	AGATATTTGA	AATTATAAAC	240
TCAACATTAC	TATAAACTTA	AATTTAAACA	ATTATCTACG	CATCGAGAAT	AATAGAAAGA	300
GAAATAGAAA	GAAAGGATGG	GCAAGCGAAT	GAAGATAGGT	ATAACATGTT	ACCCCCCAT	360
GGGTGGCTCT	GGAATTATTG	CACAGAATTA	GGAATTAAAT	TAGCAGAGCG	AGGTCACGAA	420
GTACATTTTA	TCACCTCAAA	ATATCCCCGT	TTAGAATAAG	AAAACCATTG	CCGAATATGA	480
TTTTTCATCA	AGTTGAAGTG	AATCAATATG	CAGTATTTCA	ATATCCACCG	TATGATATTA	540
CGTTAAGTAC	TAAAATCGCT	GAAGTTATTA	AAGAATATGA	TCTTGATTTG	TTGCATATGC	600
ACTATGCTGT	ACCTCATGCA	ATTTGTGGAA	TTTTAGCTCG	TGAGATGTCA	GGTAAAGATA	660
TAAAAATTAT	GACAACGCTA	CACGGGTACT	GATATTACTG	TTNGGGCTAT	GATCATTAC	720
TCCAAGGTGC	AATTAANTTT	GGCATTNCAA	AAAAGTGATA	TTNGNGAAAA	GTGTG	775

(2) INFORMATION FOR SEQ ID NO:810:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 870 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:810:

TTGATTTTTTC	ATGGAAATGA	GATGTACTGT	ATCCCATTTC	ATTTAGTTGT	GCTTTATCAA	60
TTCTTAAACC	TTCAAAGTCT	CTAATATACA	TCGTGTCCAA	TAGACCATCT	TTCCGAAATG	120
TTGCAATAGC	ATTTTGCAAG	TGAGCCTCTA	ATGCAATGCC	ATATTTAGTA	ACTAGTGGGA	180
TTACGAGACC	AAGCAATGCT	TTACTATAAG	TTTCAATCCA	CGATTTGCCC	GATGATTCAA	240
AATCAGACAA	TGATGCAGCT	GATTGATAAC	GTTTAATCAA	TGTCACGATA	GGTGATTCAT	300
TGTTAAATGG	GTAGGTTGCA	ACTAAGCTTG	AAGGAATCAT	TGGTGTGACT	TCTTGTGGAA	360
TCATNTGGTA	TTTTGTTTNN	TCTTAAATAA	TGTACCTAAT	TGTTCACTTC	CGTCAAGNTG	420
ATAGTCTTAC	TTCCGNCCTG	CTCATTATAA	AAATGAATAC	CAGCAACTTC	AACAATAATT	480
GGTGGATGCA	CTAGGACTTA	ANTATGACAT	CTTTCTCCAA	AATATCAATT	AAAATACGTG	540
TCATAGGTGG	ACCATTTGTC	GTCGGTTGGT	CTGATAATGT	ACGAATNTCA	CCCTGTAATA	600
TGAACGGTNG	TCGACAAGTT	GATGTGTGGC	GACATAGCTG	GGTATTTAGG	AACTAATGTT	660
CTGAAAGATA	AACCGGCATA	ATAATCCAAC	GNNTGTGTTG	CTTCAATGAT	TANTTCTTCA	720
TCTACTTCTG	NTTGATAATC	AGAATGTAAT	ACGTCATCTA	ATNGCCATGG	ATGTACAATC	780
ATAATGTGAT	AATCATTTAA	GTNAAAGGTT	GGCGTANCCT	NCATCTNCTA	ATTGGTTTAA	840

TNANGTCCCG AAATAGNTGA TGGAACAGGC

870

(2) INFORMATION FOR SEQ ID NO:811:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:811:

```

ANCTATANNA TTTAGGTGGC GGNGCTNATN AANAAATNGC CATAGAGGTT CAATTGGCTA    60
ATNATAAANT CATCCAGAAA NAATACGTGA ATATTTTACC TAGTAAAGAA GGTACNTGT    120
TACCAATTAA TAAANATGTG TACGAAGCAA TTAGCAAAGA ACGATTGAGA ATNATGGTTA    180
TGAAGCTGAT CAGAAATGTAC GTATGACTCA TTATCATAAT GTAAGTCGCA AACAAACAGGA    240
AGTTNTATTA NAAGGTCAAA TCNACCCCN TAATACTTAT CATAATAAAG AAATTTATGC    300
ATTTGCAGGT TATCTAAACN ATTGATTTAA GAGGGTAGGT GTTTATTGCG AAATCTATCA    360
ACCCAATNTN AATGCAAATA NTGGCGGCAA NTACTATNAC ATATNACTTT ANGTINGNTCA    420
TGGCATCTTC TTTTGGNATA GGANCTTAAC                                450

```

(2) INFORMATION FOR SEQ ID NO:812:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:812:

```

GGCACGAGCT ACCCATTTCA AATTATTCAT GAGCCATATA TCCTTTTCCT ACTGTTGTTT    60
CGATTGCACT ATCCATACTA ATTTTCAGATA ATTTTTTTTCG TAAACGATTC ACATTTACTG    120
TTAACGTATT ATCACTAACA AATGCTTCAT CATCCATAA TGNAGTGATA ATTGTNTCTC    180
TCGACCCGAT TTGATTTTTT TTGCTAATAA GAATTTCTAA TATANTCATT TCTGTTTTGG    240
ATAGAAAAAT CGTATCGACA CCTTTGTGTA TACTATCTTG CGATAGATCA ACGACAGCAT    300
CTTGCCAAGT CAATGTACGT TTCTCTTCAG CTGTAAACTC ATAGACACGA CGATAAATCG    360
CTTGTAATTT AGCAATTAAT ACATTGGTAT AGAAAGGTTT TTGCATATTA ATCAATCTGC    420
GCCAAGTTCC ATACTCATCA CTTGGATCCA ATTGGATTAT CNCGAGATGA TANAAATAAT    480

```

ATTGGGNCGT	TGGAAACTTC	TCTCATTTTT	CCTGCACCAA	TAAAAACCCA	TCATATTTAG	540
GTAATTGAAC	AACCCAATAT	AACAATTTCA	GGNGTAAAAC	TNTCAAATGT	ATCCATTACT	600
TTGCCGAAAT	CTTCAATACC	AGCAACATTA	AAATCCCATT	GTGCTAATTC	TTTTTTTCAAT	660
TCTTGANACA	AAGTATTGTC	ATCTTCTACT	AGTAGTATTT	GCATCCATAT	CACCCAATAT	720
CATTTAGTAT	ATTTCATATT	TTCTCCTGAG	NTTAATCGAC	TCTGANAATC	TTTAATCCGG	780
CAGTCAACTT	CAAAGCCAGG	ANTCATCATT	TTTTGNATTG	GTGCTTGTAT	AAAGTAATAA	840
ATCGNNCNCA	ATAATCGAGG	GATATAATCG	TATAGATGTA	TATAAACGAC	TACCGACTCT	900
TTGATTAATC	TAAATTCTAA	CTTCCCTTGA	GTAAGTGTGT	ATTTTTTTCAC	CTAAACTCCC	960
ACTCCAATNA	AAGTAAAGTT	ATTATTCCGT	CAGCTGTTTC	TTCTATNNTA	AATACTGCGA	1020
GCGGTGCGAC	CTTATTCTTA	ATATATATCT	TAAATTGATC	ATGTGATTTT	TCTGTTTTCA	1080
CACAAGTTCC	TTTAGTGTA	CCCATCCATG	CAATAAAATG	GTTTACAACG	TTCTTTAATG	1140
TCCATCCCTT	TGGTAAAACT	ACCTTCATCG	TTGATCTAAC	ATCATCATAC	TTTGAAACTT	1200
GTAATTCTAC	ATTAACATAA	GAACGTTTAA	AACTAAATTT	TGTTGTTTCT	ACAGGTGTGC	1260
CATATGCACC	TAGGCGTTCA	ATTGTTTCAT	TATCATAACG	ACTCCCAGGT	ATGTAGATTA	1320
CTTTTTTTAC	TTGATTGATA	GCCGCTGCTC	GACCAAAATT	ATCTGCTGCG	ATTAATGTTA	1380
AATCTCTTGC	TGATGATTGT	GTTATTTTGG	CA			1412

(2) INFORMATION FOR SEQ ID NO:813:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:813:

TAGAAGACAT	AACAATTGGT	GTTTCTTCAT	TACTTTTCAT	CCATTGGCTG	ATATTATCAT	60
GAATATTATG	CGTCATCATG	TTGCACCTCA	CTCTCAGCTT	TTAGTGCTTT	AATTTTCATCT	120
CTAACAATGG	CTGCTTCCTC	AAAATCTTGG	ATTTCAATAA	GTTTTTTCAA	ATATTCATTC	180
TTTTCTTCGA	TTTTTCGCTT	TAAAGCTATC	TTTTTATGTG	AAGAATGTGG	TGTCTTTCCA	240
ACGTGCTCAA	ATTGTCCACC	TTGAACTCTG	CGGACGATAT	CAATGATGTC	ATCTTTAAAT	300
GTTGCATAAC	AATTAGCACA	CCCAAATTTA	CCAACATGTG	CAATATCTTT	CAAAGTCATA	360
TGACATGATG	GGCAACGTTT	TTCTTCCTTT	AAACGCTACT	TCTTGAAAAT	TAATGCCATG	420
TTTCGGAGCT	AAATGTTNGG	TAAAATTTGG	TTAACAACAA	ATGCTTCTTC	GAAATTATCT	480
TGATGTCCTT	GATATTCAAG	GCTGNTCCAA	TAGCTTGATT	CCACGGATTG	GTGCCCCCTCA	540
GCACAAGTGT	GACACACCAT	TTNCTCTTCT	NGTTNTATTT	NNACTTGGTA	ACTTTAACTT	600
TTAATTCGCG	TTCATTAAGT					620

(2) INFORMATION FOR SEQ ID NO:814:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1033 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:814:

```

CCGAAGTAAT ATAGAAAATA CATNCGNTGA TTTCTGGGCC TTCCTATCAG GTTGGGCGCA      60
ATCATTTATT NATTTTCCAG CTAACGTAGC AGCATTGTCT ATCGTATTTG CGACACAGCT      120
AATTAATTTA TTCCATTTAT CTATAGGTTT GTTAATACCA ATAGCAATCG CATCTGCGTT      180
ATCTATTGTG TTGATAAATT TCCTAGGTTT AAAAGCAGGC GGAATTTTAC AATCAGTTAC      240
TTTAGTAATT AAAGTATTTC CAATCATCGT TATTGTAATT TTTGGTATTT TTCAATCTGG      300
AGATATCACT TTTTCATTAA TTCCAACCTA CAGGTAATTC AGGAAATGGT TTCTTTACAC      360
CAATTGGTAG TGGTTTATTA GCAACTATGT TTGCATATGA TGGTTGGATT CATGTAGGAA      420
ATGTTGCGGG GGAAGTTAAA AATCCTAAAC GCGATTTACC TTTAGCGATT TCAGTTGGTA      480
TCGGTTGTAT TATGGCTGTG TATTTATTAA TTAACGCTAC ATTTTATTAA ACGTTGCCAA      540
TAGAACTACT TGCTGGTAAC TTAAATGCAG CTTCAGATA CATCAAAAAT ATTATTGGT      600
GAAAATGGCG GTAAAATTAT TACCAATCGG AATATTAATT TCTGTTTATG GTACGGATCC      660
AATGGCTATA CTATGACTGG TATGCGCGTA CCATATGCAA TGGCTGAAAG AAAATTATTG      720
CCATTTAGCC ACTTATTCGC AAAATTAACA AAATCTGGCG CACCATGGTT TGGCGCAATT      780
ATACAACTTA TAATCGCTAT CATCATGATG TCAATGGGAG CATTGATAC AATAACAAAC      840
ATGTTAATCT TTGTTATTTG GTTGTCTTAT TGTATGTCAT TTGTTGCTGT AATAATTTTA      900
AGAAAACGTG AACCAAATAT GGAGCGTCCA TATAAGTAC CGTTATATCC GATCATACCT      960
TTAATTGCTA TTTTGGCAGG ATCATTGTA TTGATTAATA CACTGTTTAC ACAATTTATA     1020
TTAGCAATCA TTG                                     1033

```

(2) INFORMATION FOR SEQ ID NO:815:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1009 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:815:

```

CAAATCACTT AACATAGCAT CTTGTACCAG CTAAATATTC ATCACTTACA GGTAATGCCG      60
GTCTGACATT TGCCAAGCCT CGATATAATT ACCACAAATC TTCAAATGAA GATGGCATT      120

```

CCAATACGTC	ATTGTCATTT	CTCTCTCGAC	GCATATCATT	GATTAAATAT	TCAAGTCTCG	180
CTTTATTTGA	TTTAAACGTT	TCCATTTAAG	CCTCCGGTAA	TGCTAGGAAT	GCTTCTTTAT	240
CGACATCATC	CAATTTGAAC	AACCAATTTT	CTTCTGGGTT	TTCAGAGTTT	AAAATTGTCG	300
GTTCTTCTTC	CGCTTTTGTA	TTTCGCTCAA	TAATCGTTCC	TGACAAATGGC	GTTTGACAT	360
CAATGACCGT	TTTCGATGCT	TCGATACTCA	CAATTTTCATC	ATCCACTTTA	ACTTCATCTG	420
GACTTACGAA	TTCAACATAA	CCTACTGTCC	CAATATCATC	TTGCAATTCA	GGTGTCTATC	480
TAAACACATA	CAAATCTCCT	ACTTTTCTTA	CCCATAAATA	ATTGGCTAAC	TTTTTCATCT	540
TATCTTCATC	CTTCTCTTTC	TATTTAAAT	GCTACAAATA	AATTTCCGCG	AGTAATTTTA	600
ATGTTTTTACA	ACGCTGTTCA	ATACCTGGAA	TAAGCGGTGC	TACTAACACC	TCATCAACTT	660
CAAACGTAGC	AATGAAATCA	TCTAATGTG	CTTTAACCTG	TTCTTGTTG	CCTGCAATGA	720
TGCGTGCTTG	ATGTACTTGA	ATCATCTCTT	TGCTCTGATC	ATTAAGCTTA	TACTTTTGTG	780
CTGTGTCTAC	TGAAGGAAAA	TGTTCAAATT	CTGCAAATTG	GTAATTTACC	TAATAACCAA	840
ACATCTAAGG	GATGTTGGAA	TGNTGGTACT	TCCGCTTCCG	GTATCTGGTA	CAAATGACAA	900
ATACAGGATG	CCATCAACCT	TGGGGGTCCA	TTTTTATCCG	NTGGATGTTG	GNAATGTTTT	960
TGGGAATATC	AAAGTNATCC	CTCGNTGGAT	GTATCGGATT	ATATCTGGG		1009

(2) INFORMATION FOR SEQ ID NO:816:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 569 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:816:

GAATTCAACA	TAACCTACTG	TCCCAATATC	ATCTNGCAAT	TCAGGTGTCA	TACTAAACAC	60
ATACAAATCT	CCTACTTTCT	CTACCCATAA	ATAATTGGNT	AACTTTCACA	TCTTATCTTC	120
ATCCTTTCTC	TTCTATTTAA	AATGCTACAA	ATAAATNTCC	GNGAGTAATT	TTAATGTTTT	180
ACAACGCTGN	ACAATACCTG	GAATAAGNGG	TGCTACTAAC	ACCTCATCAA	CTNCAANCGN	240
AGCAATGAAA	TCATCTAATT	GTGCTTTACC	CTGNTCTTGT	GTGCCTGCAA	TGATGCGTGC	300
TTGATGTACT	TGAATCATCT	CTGTGTCTCG	ANCATTAAGC	TTATACTTGT	GGTGCTGTGT	360
CTTACTTGAA	GGAAAATGTA	CAAATTCTGC	AAAATTGGTA	ATTTACCCTA	ATACCCANAC	420
ATCTTAAGGC	ATTGGTTGCA	ATGCTGTCTAC	TTCCGCTTCC	GGTATCTTGC	TACAAATGAC	480
AAATACAAGG	TGGCCATCAC	CGTGGGGGTC	CAATTTTCTC	CGGTGGATGN	TTGGGAAATT	540
GTTTNGTGGG	GAATATCAAT	GGTCATCCC				569

(2) INFORMATION FOR SEQ ID NO:817:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 915 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:817:

```

GANTTCAGCA CGCGCAATAT TGGGAGATAT TCCTAAAAAT ATTGAAATAC ATTATTATGA      60
ATCATTTGCT CAAACACACC AAGGACATGG TACAGATGTC GCTATTGTGG GTGGAGCAAT      120
GGGATATTCA ACATTTGATA ACCGAATTAA ATCTTCATTA GAAATTGCAG CTGATGATGG      180
TATTTAAATA GATATCATCG AAGAAGAAGG CGATAGTATT GGTCAACATC CAAACTGTGC      240
TTATATTAAA TCATCTCGTA ATGATGGTCG CTATATTGAA ATTATCGGTA TTTCAATCGG      300
TGGTGGTACA ATTTAAATTA AAGGTATTCA ATATAAATGG ACTAGAAGTA GATTTAAATC      360
ATGGATTACC AATTTTAGGT GGTGGACGG AAATATTGAC TTAAAGCACA AGTTAAATCA      420
ATTTCAITTA TGATATCAAC GATATGGAAA TTAGACTTGT AAGGATTGAT TTATTAAGAT      480
AGATGAAGAT AAATGCTGGG TTGGGATACC CATAAATTAA GCAATCTCAA GATCGGACAT      540
TAAATCAAAT TAAAGGAGAA ATACAAGTGA CGTAAACGCT TCCTATATAA ATTAGAGGGG      600
GAATAAACAT GTTTGATTCA ATTAGAGAGA CTATAGATTA TGCCGCAGAA AATAATATGT      660
CATTTGCGGA TATCATGGTT AAAGAAGAAA TGAATTAAG CGGTAAATCA CGTGATGAAG      720
TGCGAGCGCA AATGAAACAA AATTTAGATG TCATGCGAGA CGCAGTAATC AAAGGGACGA      780
CAGGTGATGG CGTTGAAGTG TAACGGGCTA CACTGGTCAT GACGCTGCTA AACTACGTGA      840
CTATNATGAA ACACATCANG CTTTGGCTGG ATATGAAATG ANTGACGCAG NCAAGGTGC      900
CATTGCAACA AATGA                                         915
  
```

(2) INFORMATION FOR SEQ ID NO:818:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 767 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:818:

```

GTAAGTGGTC GCTATGAATA ATACCTCATC GTCATGATGG GTTGTAATCC CTAGGATATG      60
ATTTATGTCC AAATAGACAT ATCTTGATA TCAATTCAAC ATATATATAT GTATTATCAC      120
GTACTCATTG TGATATATTC CAAAGATTTT TAAACCTATA CCCTGCACCC ATTAATAANC      180
TATTATCGTT GTTGACCTGC CCTTTAATAT GTATACAGGT TCTGACGTAA GAACTGTCGG      240
AGATTTAGGG AGTATTAAAC AACCTTTACC TCACTTTTAA ATCCCTAATG TGCCCTTTAA      300
  
```


TTTAGAAACA	CTTCACATTA	TTTTCCCTTA	CTCTTTATCT	ATGGCTATTG	TAGGTTTAGT	360
AGAAAGCTTA	CTTACAGCTA	AAATTGTAGA	TGACGCTACA	GATACTTATA	GTAGTAAAAA	420
TAGAGAGTCA	CGTGGTCAAG	GTATCGCTAA	CATGATCACC	GGTTTATTTG	GTGGTATGGG	480
TGGTTGTGCC	ATGATTGGTC	AATCGGTCAT	CAATGTAAAA	TCAGGAGCAC	ACAGTAGATT	540
GTCTACATTT	ACAGCCGGTA	TCGTACTTAT	ATTTATGATT	ATTGTACTTG	GAGGACTCGT	600
AGTGCAGGTT	CCAATGCCAA	TTTTCAGCAGG	TATTATGGTT	ATGGTTTCTG	TTGGTACATT	660
TGATTGGAAT	TCTTTTAAAT	ATATTAAAAA	AGCACCCNAA	AACAGATGCA	GTTGTTATGC	720
TCATTACGGT	GATTATCGTT	TTAATGACTC	ATAACTTAGC	TCGTGCC		767

(2) INFORMATION FOR SEQ ID NO:819:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1017 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:819:

TCAACAATAA	ATAATCGTCT	TTATTAAACA	ATTCTACTGT	CACTTTGTGA	CCGTTTGAAT	60
GACGCAATGT	ATTCGAAATT	GCTTCCTGTG	TAATTCTGAA	CAAATGATCT	TCAATACCTT	120
TAGGCACTTT	AAAATCTTGT	ATTCATGCA	CAACTTTCAT	TGGCACTTT	TTGTGTAAAT	180
CAATAACTAA	ATCTTTAATA	CCCTCACCTA	AAGATTGTG	TTTTAAACCA	AGCGGTCTTA	240
AATGTAACAG	CAAAGCACGC	ATTTCTAACT	GCGAATCTTG	AACCATTTTC	TCTAAAATCG	300
GAATTTGTTG	GTCTAATGGT	GGTTCTAACT	TCCGTTTCTT	TGATAGCAGA	AAGCATCATA	360
CTTGCCGCAA	AAAGTTGCTG	ACTAACAGAA	TCGNGAAGTT	CTCGAGCTAG	TCTTTGACGN	420
CCATCTTCAA	TAATCTTTTT	AACTCACACA	TCATTAATAT	TATAATTTTC	ATTGGNTAAG	480
TTTTGAGTTT	TAAGTCGCAA	CTTATGCAAT	TCTTGATTTA	AAGGTACGAG	TGTATGGTAT	540
AAATCTAACG	TTTCACTATA	TATTTCTATA	TTTGGATCAT	TAATGCCAAC	TGTTTCGCCT	600
TCCATTGAAC	GCTCAATTTG	CGTCTTAATC	CAATCATTTT	GCTGATTGAT	TTTGTATGCC	660
AGTACCGAAC	CAACAATAAT	ACACAATAAT	ATGATGATGA	GATTTAAAAA	TAAAAAGACT	720
GGNATTCCGA	ATATTGGTGT	ATAAAACATA	CCTTGGAAAA	TAGATGATAT	TTACAAAAAC	780
TTTATCGATG	AATAGAAATG	CAGCTAGCAT	GCTATATACT	AAGATGAGCA	TGGAACCAAT	840
TGTTCTAATG	TAGGGGTTCA	TCGATAAATC	ACCTCTACGT	CTCCGATAAA	CGTTGATACG	900
TAGATATTAA	CTGTATAGTT	ATCCGGTTTC	ATCATTTCTT	CAATATGAAT	ATTGTTATTT	960
TCAACTTTAT	ATGATTTTTC	ATTCACGTAA	GTACTTCCAT	AAAAAGCAGC	TCGTGCC	1017

(2) INFORMATION FOR SEQ ID NO:820:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1318 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:820:

```

ATTAAAAAGG TAGGGATAGA TGTGAAGAAA ATCATTAGTA TCGCAATTAT AGTTTTAGCG      60
TTGGTATTAA GTGGTTGTGG TGTCCCTACG AAATCAGAAG TGGCTCAAAA GTCATCGAAA      120
GTTGAAGTGA AAGGCGAGCG ACCAACAATA CATTTCCTAG GACAAGCAAG TTATGAAAAT      180
GATATGAATA TCGTTAAAGA TCAATTGGAA AATGCAGGAT TTAACGTGAA GATGAATATC      240
CACCCAGATT ATGGTAGCTA TCGCACACAA CGTCAAGCCG GCAATTATGA TATCCAAATT      300
GATGACTGGA TGACAGTGTT TGGGTGACCC GAACTATGCT ATGACCGNAT TATTTAGCTC      360
TACAGGATCA AATAGTTTAT TGANAGATAA ACATGTAGAC CAGGTGGTTA AATAAAGCTT      420
CTACTCAAAA TGAAGCAGGT TGTAAACAA ACATATTATG CAANTTGANG ATGANGTTGG      480
TTTTGGTAAA GGTATATGG CGCCTTTATA TGGATCAAAA AAGAATTTNG TATATGACAA      540
TAAAGNGTCA GATAAAAATA GTGTGGATT GCCAAATTCA CGTGCATTAA TATGGCAACA      600
ATTTGATTAC AACAAATAGTA GAGAACGACN CGATNCGCGG CCACTTGTGA TGACACAACA      660
AGATGGTGAA ATTCCTACAT TGGATCCAAT ACGTTCAATT GCGCCGNCAG TATATTCAAT      720
TAATATGAAT ATGTACACAA GGTATTATT ATTAGATGAA AATGATCACT TAACAACGAA      780
AGGTTTCGTT AGTCGTGATT ATGCTGTGAA TAAGAGACAA TAAAGCATTT TATTTCTTGT      840
TAAGAGATGA TGATTATTTT GCGAAAGTGG TCAATGGACA AGCACGTCAA TACTGGAGAG      900
CGTGTATCGG CTGAAGATGT TAAGTTTCT TTAGATAGAG CACGTGATAA AAAGTCTTGT      960
GCCTAACAAT AATACTTACA ATATTGCACA AANCATATTA AATTGACATC AAAGATATTA     1020
ANAGATGNNG ACATCGATCA AGTTGCGTTN AAAGAGAAAAG ACAAAGGATT GATAAATCAA     1080
TCTTATGATA AGTTNGGANT AANGCTTATT AACGTCAAAT CCGGNNAGCG ACAGATNGNC     1140
TCAAAAANGG AAATAATAAA GGCGGTATTT ATCACATTGT TAAATTACG ACAGATCAAT     1200
CGATGCCTCG AGAGGTAAAT TACTTAACAC ACTCTTCGGC AGGCATTTTA TCTAAAAAAT     1260
TTGTTAATCA AGTAAATCAA GAATATCCCA CAGGATATGG GGATAGCAGT CTCGTGCC      1318

```

(2) INFORMATION FOR SEQ ID NO:821:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:821:

TTAAATTACA	AGTTGCGGAT	CAAGTCAGCA	CGCTAAATCG	AATTACAAGT	GCTTTTGTTC	60
GCCTACAATA	TAATATCGAT	ACATTACATG	TTACACATTTC	TGAACAACCT	GGGATTTCTA	120
ACATGGAAAT	TCAAGTCGAT	ATTCAAGATG	ATACATCACT	TCATATATTA	ATTAAAAAAT	180
TAAAAACAAC	AATTAATGTT	TTAACGGTTG	AATGCTACGA	CCTTGTTGAT	AACGAAGCTT	240
AATTTTAAGA	CAAAGGCAAT	GATGCGCTAA	TTAGTTATAG	ATATATCATA	GGCTGCTAGT	300
TAACATCTGC	CACTATTACA	AAGTTATATT	TCAGAAATTTT	CGAAAAACAA	AACATTTAAT	360
TATTTGGAGG	AATTTATTAT	GACAACAGTT	TATTATGATC	AAGACGTAAA	AACGGACGCT	420
TTACAAGGCA	AAAAAATTGC	AGTAGTAGGT	TATGGATCAC	AAGGNCACGC	GCATGCACAA	480
AACTTANAAG	ACAAATGGAT	ATTGATGTAG	GCATCGGTCT	TCGCCCAGGT	CGGTTCTTTT	540
GACAAAGGCT	TAAAAGAAGA	TGGATTTGAT	GTCGTTCCC			579

(2) INFORMATION FOR SEQ ID NO:822:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1442 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:822:

CTATGATAGN	ATCGGAAAGA	TGTATAAAGT	TATCTAAAAG	TTATACGACA	CAAGTACACG	60
AGGCACATCG	CTATGCGGTG	TGCTTTNTGG	TATGCAATCA	AAGAGGTGTA	AGAGATGACC	120
AAGCATAATA	ACATTTATTA	GCATGGNCGT	AAGTCATATC	AATACGATTG	GTTCTATCAT	180
TCAAAAGCAT	GGAAGAAGTT	AAGAGAGATA	GCATTAGATA	GGGATAATCA	TCTTTGTCAA	240
ATGTGTTTAC	GTGAAGACAT	NGTAACAGAT	GCAAACATAG	TGCATCATAT	TATTTATGTT	300
GATGAAGATT	TTAATAAAGC	TTTAGACTTA	GATAATTTGA	TGTCAGTTTG	TTATAGCTGT	360
CATAACAAAA	TTCATGCAAA	TGATAATGAC	AAAAGTAATC	TTAAGAAAAT	TAGAGTATTA	420
AAAATTTAAA	TAAAAAATA	ATTTATTTT	ATAGCCCCCT	ACCCATCGGC	TTAAAATGTT	480
TTTTCGACGG	GTACCGGCGG	GGGCCCTTCG	CTTGCAACGC	GGATAAACTT	TTATGAAAGG	540
GGGTCTTTAT	ATGAAATTAA	CAAAAAACA	GCTGAAAGAA	TATATAGAGG	ATTATAAAAA	600
ATCTGATGAC	ATATTAATTA	ATTTGTATAT	AGAAACGTAT	GAATTTTATT	GTCGGTTAAG	660
AGATGAACCT	AAAAATAGTG	ATTTGGATGA	TAGAGCATAC	AAACAAGGCT	GGTGCCGAGC	720
AATATTGTTA	AGAATCCATT	AAGCATAGAA	CTGACAAAAA	CAGNTCAAAC	ACTAAATAAC	780
TTACTCAAGT	CTATGGGTTT	ANCTGCAGCA	CAAAGAAAAA	AGATAGCNCA	AGAAGAAGGT	840
GGATTTCGGT	ACTATTAAAG	TTTTAAATGA	ACCTTCACCA	AAACTATTAA	CAACATGGTA	900
TGCAGAGCAA	GTCACTCAAG	GGAAATAAAA	AACAAGCAAA	TATGTTAAAA	AAGAATGTGA	960
GAGACACCTT	AGATATCTAG	AAAATGGAGG	TAAATGGGTA	TTTGATGAAG	AATTAGCGCA	1020
CCGCCCTATT	CGATTTCATG	AAAAGTTTTG	TAAACNTCC	AAAGGATCTA	AACGTCAACT	1080
TGCATTACAA	CATGGCAAC	ATTTTATTAT	TGGCAGTTTG	TTTGTTGGG	TTCATAAAGA	1140
AACAAAACCT	GCGAGGTTTA	AAGAAGCTTT	GATATTTATG	GGGCGAAAAA	AATGGTAAAA	1200

CAACTACTAT ATCTGGTGTT GCTAACTATG CTGTTTCTCA AGATGGAGAA AACGGCGCTG	1260
AAATCCATCT NTTAGCAAAC GTAATGAAAC AAGCTAGGAT TCTATTTGAT GAATCTAAGG	1320
CGATGATTAA AGCTAGCCCA NAGCTTAGAG AAAATTTTAG ACCTTTGAGA GATGAAATTC	1380
ATTACGATGC ACTATATCTT AAAATATGCA CAGGCTTCAG ACAGTGATAA GTGGTTGGTT	1440
AA	1442

(2) INFORMATION FOR SEQ ID NO:823:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 554 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:823:

AAGCCGACCG ATGAAGGTTA TTTGAAATTA CATAAGACGT GGTTTTGTA ATCAAAGCTA	60
TGTCCAGTTT GTAATTGGAG GCGTGCTATG AAAAATAGTT ATCAAGCTCA AAAAGTGATT	120
GAAGAAGTAA TTAAGGAAAA GCCAAAAGCA CGTTGGTTGT TTTTAACACT TCCAACAAAA	180
AATGCGATAG ATGGAGATAC TTTAGAACAA AGTTTGAAGC ATCTAACTAA AGCATTTGAT	240
AGGTTGAGTA GATATAAAAA GGTAAACAA AATCTTGTG GATTTATGCG TTCAACAGAA	300
GTTACCGCTA ATAAAAATGA CCGTAGTTAT NATCAGCATA TGCACGTNTT GGTATGTGTT	360
GAAAATGCAT ATTTTAGAAA AAAAGAGAAT TATTTAACTC AAAGAAGAAT GGGTTAATTT	420
ATGGCAAAAA GCATTACAAG TTGATTATCG ACCTGTNGGT ATTATTAANG CAATTACCCC	480
ACCAAAAAGG CGATAAAGAT ATTTGGATTC CGGCAACAAN GAGACATCAA ANTATCCGGT	540
CAGTCATCTT ATTT	554

(2) INFORMATION FOR SEQ ID NO:824:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 918 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:824:

CTGTGCTTCA TCAAAAACAA TATAATCAAA TTCATTTTCA TCAAATTGCT TAAAATTATC	60
ATCCCAAGAT AATGTTGGAA GGGTTCCAAA TAAAAATTG CCACCGACAN CTCCATGTTT	120

TCCTTGCCAN	CCAACCCAAA	ATCACTATCA	TTTTTAATNG	GTAAATACTT	TNTNGAAATT	180
CTTCCCTTAG	CTCTAATTGN	AAAATCCCCCT	CATTATGGGG	CAATAAATAA	AAATTTATTA	240
GGGTTTACCT	TCTCTAACAA	TCTAATGCAC	ATAAAATCGT	TTTACCCTGT	ACCCAGTTGC	300
AAGATATTAT	TAACGCCCTTA	TCTTTGGNTT	TATCCCTAAT	AGCTTTTAAT	GACCTTAATG	360
CTTCTGCTTG	CATTAAATTG	GGGACAATTT	CCACTGATTT	TTTCACCTTA	TCAGCTAGCA	420
GCATTTGAGT	TTGTTCAACC	TCCGCTAATT	TTTCTAAGGA	GCGGTACTCA	NATGATTCTT	480
TATATGAATT	AATCCATTGC	TCAGTCAGTG	GGGTACTCTT	TTGCCATAAC	AATTCAAATT	540
CATTTTTTAC	ACTATCAACT	AAATCACCAT	TTTTCATAGT	AGACAGTAAA	ACATTATGCT	600
CAGAATTAAC	CTTTAACGCA	TTAGATGTTA	AATTAGAGCT	TCCTATTACC	ATAGAACTAT	660
AATCCTTATG	TTCAAAAATA	TATCCTTTGG	CATGGAATCC	AGCAATATCA	GTAAATCTTA	720
CCTCTACATT	TTTTAATTTA	AGTAATTCTC	CATACATTTT	AGGACTATTA	AATCCTAAGT	780
AATTAGATGT	TAATATTTTC	CCTTTAACAN	CCTTATTGCT	TAATCTAATA	GGTGAGCCTT	840
TAGCTGGCTA	ATCCGCTTCT	TGTATTAAAG	CTACAGAAAA	TAGACGTTCA	CATTNGAGG	900
TCACTATATG	GTGGAAGG					918

(2) INFORMATION FOR SEQ ID NO:825:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1642 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:825:

CCATTTAAAA	GTATTGTAAA	ATCATCCACN	TTNTATAAAC	CAACCACNTT	AACNTTTTTT	60
ACATTTGTTA	TCCGATGAGA	TTAAAAGATA	TCAATNAATA	CAATTTTTAN	AATTAATGTC	120
ACTATGTTTT	CCGATAATAT	NACCCAATCA	TCGNAATGTT	ACCCATTTAT	AAAATGANAA	180
ATCNTTGACA	TAGGTANAGG	GAATGTATAT	TGGTCNCGGA	TCACTTAAAT	TAAACCCANA	240
TCATGTCATC	TGGTAATGTN	TCAATGTTAA	TTGCTCCTGA	AGCGGCGTAN	ACTTTAATCT	300
TCCATGTTAA	ATGAGTAAAT	TGATGCGTCA	ACTCNAAAAT	AGGTGTTTCT	NCTGGNTGAA	360
TGTCATGACC	GATTTTTTCA	NTCATTTTAC	GTCTANCATG	CTCACTATCN	AACATAGGAN	420
ATTGCCACAT	ACCATACNAT	AATTNTTCCC	TACGCTTTTG	CAACAGATAT	TGACCTTGAT	480
TATTTCTAAT	TAANAAGACG	GATTGCTCAA	TTACNTTTTT	ACTTACATTT	TTAGATTTAA	540
CAGGTAACTT	TTCAAATGGA	CCTTTATCAA	ATGCCTCACA	GTTTTCTTGN	ACTGGACNAA	600
ATAAGCATAA	TGGATTTTTT	GGTGNACAAA	TTAATGCCCC	TAATTCCATC	ATAGCTTGAT	660
TAAACGTTCC	AGCTTCTGTA	GTAACATACG	GTAACAATTC	TTGTTCTGTAC	GATTTCTCTG	720
TCGATTGTAA	TTTAATATCT	CGATAGTCAT	CATTCAATCT	AGACCATACG	CGAAAAACAT	780
TTCCGCTCTAC	AGTTGCTAGT	GGTACATTAT	ATGCAATGCT	CATTACTGCA	GCTTGTGTGT	840
ATGGGCCAAC	ACCTTTTAAAC	GCTTTAAATT	GATCAGGATC	TTTGGGAACT	AAGCCTTCAT	900
ATTTATCANA	AACCTCTTTA	ATCGCCGTAT	GAAAATTTCTG	AGCTCTACTA	TAATATCCTA	960

AGCCTTCCCA	ATACTTTAAC	ACTTCATCTT	CCGAAGCTTG	ACTCAAAACT	TCCACAGTTG	1020
GAAATCGGNC	ACCAAAACGA	TGATAATAGT	CAATAACTGT	TTTAACTTGT	GTCTGTTGTA	1080
ACATGACCTC	ACTTAACCAA	ATATAGTACG	GATTGGTCGT	TTGTCGCCAT	GGCATTTCCTC	1140
TTTGATTTTC	ATCAAACCAG	TGTATCAAAT	TTTCTTTAAA	ACTAGACTGC	TGATACATTT	1200
ATAAAACCTT	TTCCTCACCA	AAATTAATTG	TCTTTACTCA	TAATGTTTTT	ATTGTACATT	1260
AAAATCATGG	TTAGTATGTA	AGTTAATTTA	GTTATNTGCG	AAATTGGATT	ATAATAGTAT	1320
ATATAATATT	ATGAAATGAG	TGAACTGATA	TGGACACTGC	AACACATATC	GCAATTGGGG	1380
TGGGCCTTAC	AGCACTTGCA	ACTCAAGATC	CAGCAATGGC	TTCTACGTTT	GGTGCAACAG	1440
CTACAACCTT	TATCGTTGGT	TCATTAATTC	CTGATGGGGA	TANTGTNCTT	AAATTANAGG	1500
ACANTGCAAC	ATATATTTTCG	NATCATAGAG	GNATNACGTC	ATNCCATCCC	CTCCCACAA	1560
NNTATGNCCA	GTNCNMTTA	CANTTTNTAT	NTNTTCACGT	CACNTNGCT	GGTANGCATC	1620
CCNCCTCACG	TATGGCTTGT	GG				1642

(2) INFORMATION FOR SEQ ID NO:826:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 961 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:826:

CTAATCGCTT	ATGCAACAGC	TCAAACAGAA	TTATCGATGA	GGCAATATTT	CGAATCAACA	60
GCTTATCGTG	TGTTCACTGA	TCAAGCAGGT	ATTTTAGGTG	AAGGTGTACA	AGTAGCTAAA	120
GAAGTTATAG	ATACAATTAT	AGATACACAA	TTTCATGGTG	TCGTTTGGTC	AGAGCGATTA	180
TGGACTAATA	CCGAAGCAAT	GAAGCAAGAA	ATAGAAGAAA	TAATTGCCAA	TGTAGTTATT	240
AGAGGTCGAC	ATCCTAACGA	ATACGTTAAA	GATATGCGTA	AGCACCTAAA	TAAATTCGAA	300
GGCACAGCAC	GACAAAAGGC	CGCAGCAATC	AAATCATTGG	TTTATACAGA	ATCAGCACGT	360
GTTCAACGCAC	AATCAAGTAT	TGACAGGATG	AAAGAAATCT	CTCCAGAAGG	ATATTATATG	420
TATATTGCAA	AAATCGATAA	TAGAACAAC	AAAGTATGTA	AAGGGCTTAA	TGGAGAAGTA	480
TTCAAAGTTT	AAAGACGCTA	AAATTGGTGT	TAATTTCTAT	CCTATGCATA	TCAATTGTCTG	540
CTCAGATTGC	GCTTTATTAC	CTAAATCCAT	GTGGCCGAAA	AAAACAAGAA	CAATAANCCG	600
AAAAACAAAA	TACTTTGGAG	GGAAAGTGAA	AAGCGGTGAT	TGATTTGAAA	GTGAAGGTTT	660
TTAGAGGCAA	AAAAGGTAAG	TTAGCTTTGT	ATGACAGTGA	ATTAAAAATT	TGGAGGATAC	720
TAATATGAGC	AATACTGACA	AATACCTTAG	AGACATAGCA	AGAGAGTTAA	AAGGTATACG	780
TAAAGAGTTA	CAAAAGCGAA	ACGAAACAGT	TATTATTGAT	GCAAACCTAG	ACAGCGTAAG	840
GTCGGCAGTA	TTANCCAATA	AAGANAAACC	GAAATATAAC	GAACCACTCT	TTTAATAGTC	900
GTAGCACTTA	ATTGTGTTGG	CTATTTTTTA	TGTCCAACAC	GTGCTGATGA	CATAAAAAGC	960
A						961

(2) INFORMATION FOR SEQ ID NO:827:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:827:

```

ACGATATTGT TCTGTTTGTA TCGGTTCTAT CACGATTTC AATTGTTTCA TTCATTTCAA      60
TCCTCTATGT TAATTGTGTA TCACAATCAT TTTTAATTTT ATTTAATAAC CATTGCTCAA      120
ATGCTGTAAA ATCTTCATGC TCCCTTACAT TAATGCTATA ACAAACATTC GACAATTGTT      180
GTAATACTTG CAACTCTTCT TCATCTCGAT AGACTACGAC TTTTTCAAAA TCAGCATTTT      240
TAAAGCCTTC AACTAATACG ATATTGGTGT CAATTGTAAC AGATTCTCTA ATAATTTGAG      300
TAAGATTGTT GGATTATCTA CACGTGTTAC AGTTTGCTGA TATTGAAAAC CTTGTACAAT      360
ACTTTGGTCT GCCCCGCTT CAAAATGCTT CATGTGATCC GACGGTCTTG AATCCTGTAA      420
TTGAATATCT TCCTTAGCAT GCCCATGATG TTTAATAGTA GCAACTGTAT TACCATGTTG      480
TCTTTAAGAA AGAGAAATAT GGCCTCATCA ATGTNGNCTT ACCAGACTTT GTGGTNACCT      540
ACAATTGGGA AATCATAAAG AAGTCCCCTT CAAGAGGGTC AGTCAAGTCA ATTTATTCTC      600
T

```

(2) INFORMATION FOR SEQ ID NO:828:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:828:

```

TTGAACTCGT CAAGCGTTTG AATCAATTTA NTTGAANTTT NACAAGAACC CAATACTTTG      60
TCCCGANCCG ATTGGATTAA CTATTGTTGC CCCGTGACCC ACCACCTAGC ATTGATAGAT      120
CCCNACATTA ACNTTAAAAA TATTGAATCA CNTCAGTGAA AATTGCCAC CGATAACTAA      180
CAATTGCNTG TATCNTTGGG CACAATATAC CAAACCAATA TTCAATAAGT AAGTAGGGAA      240
AGTTATGACA GTATTGTGTA TGCAATTACA GAGTAAC TTG AATAGTATTG AAGAATTAAT      300
ATCACAAAGT CGTTGGTCAT ATAGGNAAAA NCCGCGTACA GTCAACTATN GATACAATCA      360
AGATAAACTC ATGCACAGNT TGGGAGATAT TTTNGCGCAA TATGGAATNC AACATGACAC      420

```

AGGTTTATNA	CCACATGAAT	GGNATTATCA	CATCGCGCCA	CGAGGTANGG	CAGATATTGC	480
NCAACACAAT	CGTGATGGAC	AGCCCATCTA	TGTGAGCTTA	TCATATAGTT	ATCCTTATAT	540
CGTGTGTGTT	GTCGATAAAG	ANCCAGGTGG	TATAGATATC	GAAAAGATAT	CACANCGTTT	600
AGNCTGGCGN	AATCGTTAGT	GACGTGTCTC	TCTACAANCG	AAGCACATCA	NATATGTAGG	660
CTTACGTGAT	TTNTCTCAAN	TCTGGACACA	NAAAGACGTT	TTACAACCTT	GATTGGGCGA	720
ANGGTTTACT	TGGCAAGCGA	ATCATACTTC	TTTTAATAAG	GTGCTTGNTA	GAAAAGGTGA	780
CCTNGATGAC	ATTACATTAC	AGCTTTATAC	AGAAGCTGAT	TATGNATCAN	TTTG	834

(2) INFORMATION FOR SEQ ID NO:829:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1825 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:829:

TTCCATATCT	TGTATTTCTT	ACCATTACGT	TGATGCTTCA	TAATTTTCGT	ATNACAAATN	60
CCGCTTCATC	ACGTTCTGTC	ATTGCTTCAT	AGTAATGAAT	TTTCTCACCA	TTCGTATTTG	120
CAGTCCACAG	TCCTTTTGGC	TTACGTTTCA	AATTATTTT	AATCACTTCG	TTACCCNCAN	180
ANAAATCGT	TCTCGTCGAN	CGATAATGTN	GCTCTAAAA	GATTGTATTC	GCTTCTGGGT	240
AGTCTTTTTC	AAATGATAAG	ATATTTTGAA	TATCAGCACC	ACGCCAACCA	TAAATTGACT	300
GATCTGAGTC	ACCTACAACA	CATAAGTTT	TAAACTTACT	TGCTAATAAT	TTAACTAATG	360
TATATTGTGC	TTTATTAGTA	TCTTGATACT	CATCTACATG	AATATATTGG	AATNTGTTCT	420
GATAATATTC	TAGAACTTCT	GGTACACGCT	CAAATAAGTT	AATCGTTGTC	ATAATAAGGT	480
CATCANAATC	TAACGCTTCA	TTACGCGACA	ATTGGCGTTG	ATATCCACTA	TAAACCGTTG	540
CTACCATTTG	CGAGTGATAA	TCTGTGGCTT	CTTTTGTAGC	ATCTGCAGGT	GTTTAAAGTT	600
CANTTTTCAA	ATTACTGATC	GCACCGATAA	ACATACGAGG	NTCANACTTT	TTACTATCNA	660
TATTTTCATT	TTTTAAGACG	TCTTTAATAA	CAGATTTTTC	GTCTGTAGGA	TCAATTATCG	720
TAAAATTGCG	TTCTATACCT	ATTGATCTG	CATCAGCAGC	TNAAAATACG	AACACACATT	780
GAGTGGAATG	TTGACATCCG	CATAACTTCT	GCTTGATCAC	CTACTAATTT	TTGNACACGT	840
TCTTTTCATT	CTCTTGACG	TTTATTTGTA	AAAGTAATAG	CCAAAACATT	GTATGGTGAG	900
ACATCTTTTT	CGTCTAATAA	ATAAGCAATT	CTATGTGTTA	AAACACGTGT	CTTCCCTGAA	960
CCAGCACCTG	CCATAANTAN	CAATGGTCCT	TCTGTTGTCT	TTACAGCTTC	ACNTTGCTCT	1020
GTATTCATAT	GATTTAATAA	CGCATTCAAT	TACTAGACTC	CTTTATTTTT	NCTGNNTNTA	1080
NAGCTTTNIT	AATATCTTAA	TAAATAATAT	CNCCGCCGAT	AATTGTATCT	CCAATAGCTG	1140
CCATCTCTGT	CGCTTGTGTT	TCTGAGGAAA	TACCGCCACC	ATAAAAAAGT	TGCGTTTCTG	1200
TTAGATGGTC	TGAGACAGCT	TGAACCTTTG	AGACGTCGCC	ATAAATGCCA	CTATACTCTA	1260
TATACATAAC	CGGTAATCGA	CACATATGAT	TGACCAGTTG	GGCATATGCT	TCTAAATCTN	1320
CTGTTGTAA	ATCTGTATTT	GCTTTGGTAT	GTNTNGNCAC	TGNGCTATCA	GCATTGCACA	1380

CGACATACCC	NACANATATT	ACTTCTACAA	AATCTATACT	ATGTCCATAN	GTTTTAAGCG	1440
CTTCTAATAA	AGTCTCGTNC	CANTGTGAAA	TGCAACATCT	GTA CTGCACA	GNA CTGNAGG	1500
TACAAAATAA	AANTCAANAC	CAGGCATTAC	ACTNGCGATA	TGTGATATNA	CAAGTACTAA	1560
AGGCAATGGG	TATCTTCTTA	TTCTGCTCAT	TAAATGAATG	ACATTATCTT	CAGTAACGNC	1620
ATCAGNTCCA	CCANTCATAA	TTGNATCTGT	GTGGAGACAT	ACAAACTCGC	ATCTAAATCA	1680
ACATCTTGAA	ATATGTNTAG	CTGGGGTCTT	AATTTAAAAA	TATGGCGCCA	TTTTTTAATG	1740
TCATACATTN	NCCGAACTC	CTTTTNTAAC	ATACATATGA	TTATAGCATT	TNNAAGTGTC	1800
GAGTTCTAAA	GACTTAATAT	GAATT				1825

(2) INFORMATION FOR SEQ ID NO:830:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:830:

GAATTCGCAT	CATTTTTATA	TTGTCTTACG	TATAATTTGT	TTTTAATTTT	AACCAAAGAT	60
AGAAAGAGGG	TTGTTTATGA	AAATAGCAAT	TGTAGGATCA	GGAAATGGCG	CAGTTACGGC	120
AGCAGTAGAT	ATGGTGAGCA	AAGGCCACGA	TGTTAAATTA	TATTGTCGTA	ATCAATCTAT	180
AAGTAAGTTT	CAAAACGCAA	TCGAAAAGGG	CGGATTTGTA	GCGCGTAAAA	TGACATTACT	240
TAAAGATTGC	GGAATATCCT	TACGTACATC	TGTTGTCACA	TTTGGCACAG	AATCCTGAAT	300
ATGTTTAATC	GCAATGCTAA	CTGCAGNTTC	TCCATTAAAG	GGTGGTTCAC	CAACAAGCAT	360
TTCATATAAC	ACAAATACCN	ATAGAATAAA	TATCTTGTAC	ATTCAACCCG		410

(2) INFORMATION FOR SEQ ID NO:831:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 551 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:831:

GCATCATTTT	TATATTGTCT	TACGTATAAT	TTGTTTTTAA	TTTTAACCAA	AGATAGAAAG	60
AGGGTTGTTT	ATGAAAATAG	CAATTGTAGG	ATCAGGAAAT	GGCGCAGTTA	CGGCAGCAGT	120

AGATATGGTG	AGCAAAGGCC	ACGATGTTAA	ATTATATTGT	CGTAATCAAT	CTATAAGTAA	180
GTTTCAAAAC	GCAATCGAAA	AGGGCGGATT	TGATTTTAAT	AATGAAGGTG	ATGAACGTTT	240
CGTAAAATTC	ACTGATATTA	GTGATGATAT	GGAATATGTT	TTAAAAGATG	CTGAAAATTGN	300
TCAAGTGATT	ATTCCATCTT	CATACATAGA	GTATTATGCT	GATGGTAATG	GCAGAGCATG	360
TAACTGATAA	TCAGTTGATA	TTCCTTCAAC	ATGGNTGCAG	CAATGGGGTC	AATTCCGNTT	420
TATGAATTGT	TTTAGAAGAT	AGACATATTG	GAACAACACC	ACAACTAGCG	GGAAGCTAAT	480
ACGGTGACGT	ATGGTACGCT	CGTGCCGATT	GTGAAATGCA	GCAAGGTGAT	TATCTCTTAA	540
ATTGTACGCC	G					551

(2) INFORMATION FOR SEQ ID NO:832:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:832:

AAAAANCCGCC	TCCTTCTCCT	TCCTTCTCGG	CTTCATGTTG	TTTGCCAAGT	GCACCCACCC	60
TGTCCNCTTG	AGCACACGAA	AGAGGGNGCC	AATAATAGGA	TANCTAACNC	TGTTCTAGCA	120
CATTGCCCCCT	TCTTTTTAGG	TANAAATGCA	CAAGCTTTAA	ATCCTTTTTT	ACGTATAGGT	180
GTTTCAATAA	AGCGATACGA	AATTTCAGCC	ATTAACGCTG	TTAACACAAT	TTCTATAATA	240
TAAACGTATA	CCGGTATTTG	TCCTTGTCNG	TAATAACTGT	TCACAAAAAC	AATGATAGGA	300
TAATGCCATA	AATATAAGCT	ATATGATCGT	TTACCTATAA	TTAGTAAAGG	GTTCATACTT	360
AAAAATTTAG	CANATAAACT	AGAAGGATGT	NCCGCAATTG	CANTAATGAA	TAAAGTTGCA	420
AATGATATAA	TNTAAAATCC	TCCATTATAG	ATCCATTGAT	CTTGGNCGNC	AACTATAAAC	480
GNNCAAAGGT	CANNAGANCC	CGNAAAACCC	AGATATCCCC	NNNCCCCCCT	CTNATCNATA	540
CCGCCAANCC	CCNC					555

(2) INFORMATION FOR SEQ ID NO:833:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 922 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:833:

GGCACGAGAC	TTTGAAAGCT	ACTGCAACAA	TTATTCCAAG	CTCAATTAAAC	ACTAAAAACG	60
AAGCACGTGA	TAACCACTTA	AAATCTGGTG	ATTTCTNTGG	GACGAGACTG	ATGAATGTGA	120
TAAATCACG	TGTGAAACAA	AATCAGTTAC	TGAAAACAAA	GNTGTTGGTG	ATTTAACAAAT	180
TAAAGGTATC	ACTAACGAAG	AAACATTCTGA	CGNTGGAATT	CAACGGAGTA	AGTAAGAATC	240
CTATGGATGG	NTCTCAAGTA	ACAGGTGTTA	TTGTTACTGG	NACANTCAAT	AGAGAAAACT	300
ACGGCATTAN	CTTTACCCAA	GCACCTGAAA	CTGGTGGCGT	NATGCTAGGC	AAAGATGGTT	360
AANTTCCGAN	GCATCAGCTG	AATTCTCAAT	CTCAGAATAA	TCTCATTACA	CAATCCTCAT	420
TGTTTTAATA	TATATATACG	AAATGCCAAC	TATATCATCC	CTAGGTATAG	TTGGCATTTT	480
TCGTTTAACT	CATGTGTAAC	AAGCACTAAC	TGTTTACCCT	AATTTAAGAC	GCCTTTTCATT	540
CAGGTAGGTC	TTATTGAAAC	TGAAAACGTG	GATGACCTTG	TGCAAAGCCA	TTAACTGTAT	600
AAAGCATAGA	TCCTCCGCCC	ATTTCTATAT	CATTGGAACA	AATGATGAGT	TGATGTGTTT	660
CAGGTATAAA	TTGCGGATGA	GTAGAACGTA	ACATATGCCC	TTCATCTCGG	NCTGGTATCA	720
ATATNTGTCC	TATTTGATAA	CCCCTCTTAT	TAACAACTA	ACACTCGACC	CTGACCANAC	780
ATTGCTACGT	ATAAATTATC	GNCACTATCA	ATACAACATG	AGTCTGGTCC	TTCATGAACC	840
TGTAAATAG	NACGGNATAG	TAGCTCCAAA	TGGGTGTGTC	GCACACCATC	ATCTTCAAGT	900
GCAATGCGAN	GTNATCGACN	GG				922

(2) INFORMATION FOR SEQ ID NO:834:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:834:

AATACCCATC	GTGATTACCT	ATCATTAAAA	CCNTCCTNGG	ATANACNTTG	ATATGCTACT	60
TGCTTCTTTC	CCACCCATTG	CTTAATTTCAT	TAGAAAACCC	CTTTGCTATC	GCTGTGTTGA	120
TTTTCTTATT	NTTAATTCTT	GTATCTATAA	TGACGAGTTC	AATAACATCC	TGTGCTTTGT	180
TTTTCAATAT	ATNTAAAAAT	GCTGAACCAG	CCTGTTGACC	TAACATTCTGA	GGCTTGATGT	240
CAATACAGGN	TTGAGGTGGT	GACGCAATTT	CGGNTAAATA	AGAATCATTG	AACGTTGCTG	300
TCATTACATC	TTTCGGGAAT	TCAATATTAA	GTTTCATATAG	GACACTTAAA	ATCGCTAAAT	360
GTAACATAGC	ATCTAACGAA	ATGATTGCCT	GTTTAATATT	TGGGTCCTTC	AAACGCGTAT	420
GTAGATTTTG	CATGTAATTT	AAAATAACTT	CTCTTTTCATT	ACTAGTCTCA	ATAATTTGAT	480
AATCCAGATT	AAATGGGGAG	GCAACCGTTT	CAAATCCTGG	AATTCTATCT	TTTGAAACTT	540
CAAAATTTCC	TTTTTCTGTA	ATAAATATTA	ATTTCATCTAC	ACCTTGTTCA	ATAACATGTC	600
GTGTCAAATT	TNCAGAAGCT	AATATATTAT	CATTATCTAT	GTGTGTAAAT	TGATGATCTA	660
TATCCGATGT	AGGCTTACCA	ATCACAATAA	ATGGCATGCT	TTCATCAATT	AACATTTGGT	720
TAATTGGATN	CANTTTCTTT	TGAATAAAGC	AGGATAAAGC	CATCAACCAT	NCGTTGTTTA	780

ATCAATTTTA TAANCTTCCA ACCCAT

806

(2) INFORMATION FOR SEQ ID NO:835:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:835:

GAATTCTGGA TCAACCANAT TCCATTTCATC TTGNATTGCA TCAACAAATT CCCATGTTGA	60
TTNTAANTCT CCCCGTGGC TGAAGTTAGT GGNATCANCN NCACGACATT CGANTNNNNG	120
ATTTTCATNT GCATCTNCAG NTATTCANTC ATATCTTGAG CGGCTCANTG ACTTTGACAA	180
TCGATCAGGT NCAGCCATCG NNNGCCNAGC GTATTNNTCT TNAGTAANTA GATGTAAAGA	240
TACACCATCA TNAGGTNGGN TGATTGTTTG ACTAANTAGG TGTGGTNTGC TTTTTGTTN	300
ATCAGNTANC ATTGATATTC NTTATTGNT AGCTCCTTCT ATTTCAACCC ATAATTAGTT	360
TNGGGTNGTG CGNCTTGTCN NTCCNTTTNT CAGTCTGGAC TGTTGANTNN NTTCAATNNA	420
CCCTCCTTAA CGTNACAATC CGTTNCTTA ACCCGCNATA AA	462

(2) INFORMATION FOR SEQ ID NO:836:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1246 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:836:

GAACAANTGG TAAAACCACG ACTTCNAACT TAATTGGACN TACTTTAAAA GCAAATAATA	60
TNCNAATTAT ACNCAATAAT GAAGGTGCTA ATATGGCTGC AGGTATAACT TCTGCATNCA	120
TCATGCAATC AACACCTAAG ACTAAAATTG CGGTAATCGA AATTGATGAA GGTTCGANTC	180
CACGTGTGTT AANAGAAAGT ACACCTNCAN TGATGGTATT TACTAATTTT TTNAGAGATC	240
AAATGGATCG CTTCCGTGAA ATTGATATTA TGGTTAATNA CATNGNAGAG ACAATTAGTA	300
ATANAGGCAT CAANTTATTG CTAAATGCTG ATGATCCATG TGNGAGTCGG GTGAAAATCG	360
CAAGTGANAC GATTGTGTAC TATGGTATGA AAGCACATGC CCATGAATTT GNACAAATGT	420
ACGATGAATG AAAGTAGATA TTGNCCAANC TGTGGTCGCT TATTGCAATA CGATTATATT	480

CATTATAATC	AAATNGGTCA	TTATCACTGT	CAGNGTGGTT	TCANACGAGA	GCAAGCAA	540
TATGAAATAT	CANGTTTTGA	TGTGGCACCG	TTTCTATATC	TANATATCAA	TGATGAAAAAN	600
TNTGATATGA	AAATTGCAGG	TGACTTGAAC	GCTTATAACG	CGTTAGNAGC	ATATACTGTT	660
TNAAGAGAGC	TAGGGTTAAA	TGAACAANCA	AATTAANAAT	GGCTTTGAAT	ACGTATACAT	720
CAGACAATGG	TCGCTATGCA	GTACTTTTAA	NANAGAACGA	AAAGAAGCGA	TGACTCAANT	780
TTAGCTAAAA	ATCCTGCAGG	AATGAATGCA	NAGTCTATCA	AGTGGGTGAA	CAATTAGAAG	840
GCGAAAAAGT	GTATGTTATT	TCGCTAAATG	ATAACGCTGC	AGATGGTCGA	GATACTTCAT	900
GGATTTATGA	TGCAGATTTT	GGAAAAATTA	TCTAAGCAAC	AAATTGAAGC	TATCATCGTG	960
ACAGGTACAC	GAGCAGAAGA	ACTTCAATTG	CGATTGAAGT	TAGCAGAGGT	TGAAGTACCA	1020
ATTATTGTTG	AGCGTGATAT	TTATAAAGCA	ACGGCAAAGA	CTATGGATTA	TAAGGTTTCA	1080
CAGTTGCAAT	ACCAAATAT	ACATCAATTA	GCGCCTATGC	TTGACAATTA	AACCGTCCGT	1140
TTGAAGGAGG	GCAATCATAA	TATGCATGAA	TTGACTATTT	ATCATTTNAT	GTCAGATAAA	1200
TTGAATTTAT	NCAGTGATAT	AGGAAATATT	ATTGCTTTAA	GACAAC		1246

(2) INFORMATION FOR SEQ ID NO:837:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 586 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:837:

AAAGATAAAA	GGAGGAAATA	GACATGACAG	ATGGTCCAAT	TAAAGTAAAT	AGCGAAATTG	60
GAGCTTTAAA	AACTGTGTTA	CTTAAGCGTC	CTGGAAAAGA	ATTAGAAAAT	TTAGTACCTG	120
ATTATTTAGA	TGGATTACTA	TTTGATGATA	TTCCATATTT	AGAAGTAGCT	CAAAAAGAGC	180
ATGACCATTT	TGCGCAGGTG	CTAAGAGAAG	AGGGTGTTGA	AGTACTTTAC	CTTGAGAAGT	240
TAGCAGCTGA	AAGTATTGAA	AATCCTCAAG	TAAGAAGTGA	ATTTATTGAT	GATGTATTAG	300
CAGAGTCTAA	AAAAACAATA	TTAGGTCATG	AAGAAGAAAT	TAAGACATTA	TTTGCGACAC	360
TTTCTTAATC	AAAGAACTTG	TAGGATAAAA	TAATGTCAGG	GGGTACCGTA	AGGAAGAAAT	420
TAATCCCGAA	ATGTACACAT	CTNGTGGGAG	TACAATGATG	GATAAGTTTC	CATTCTTATC	480
TAGGATCCCA	ATGNCAAAAC	CNTTTATTTT	ACTTAGAGGA	ATCCACAAAG	CC'TCAATTAG	540
GNNACCGGAT	TTACCAATCA	ATCCNGNTTG	TTCTTGGA	AGCACG		586

(2) INFORMATION FOR SEQ ID NO:838:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 901 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:838:

```

CAAGAAGTCC ATTTTCAAGT CCNNACCATT AAGCGCAAAG ACNAGTTCNA AGATAGTTGC      60
CCAATCCCAA TNATNGANNA AGTCAAGAAA CCCNACAATA ATTTATTANC CAAGNAGGGT      120
AAAAGNAAAA GATTACCACC NNNAAAATAC GGTGAAGAA GCTTTTGTGAA GTCGTAATTG      180
GAAGCAATTA NAGGGTGACC ACAAAGCAT TTGTAAGTGA AGTAGCAGAT GAACTTTATC      240
ATTTATTTGT CTGATGCAT GCGCTAGNCG TCGATTTTTC AAGAAATTGA GCGGGAATTA      300
GCGCGTAGAC ATCATAAGCG CAATAACTTT AAAGGTGNAC GACACAATAT CGANCAGTGG      360
TAAANCAAGT ATGGACTAAG ATATAAGGAA AAGGATCATG GCTTATACAC TTACANATAT      420
TGTGGNTGAC GTGACATTTT CAAGNTTAAA ATACGACACC AACATATTTT AACTATGNAT      480
GCTGTGATGG TACTAAAGTT GCGAACTCGT TATAGATAAG TAGTGGATAA TCACAATACG      540
AACCACAAA TAATTATGAA AAGTAAATTG AGCAACTCAG GAATAGATGT CACTGTTAAA      600
GATGTCGAAA AGTATATGAA TCGATATAAT GAAGTTATGA TGGGAAAAAN TGGCGAAAAA      660
GCTAAAGAGT TATGTTTGTC GTTACTACCN TATTAATNTC ATAGCTGTCT TTACATTCTT      720
TGNATGTATA CTATAANTAC AAATATATCT AGCCTGAAAT AGAAATGTCA NAGCCTATTT      780
AAAAGACAAT CTCCATCAGG AACTAGATCG TGCATCCCGA ANGTNAGACT ANANAACNA      840
CTNNATGGGG NGGTNTTCNT ATGCTTAATC ANCATNAATT CGAGGATTAC CGNTNANAGG      900
T                                                                    901

```

(2) INFORMATION FOR SEQ ID NO:839:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1109 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:839:

```

CTAGCATATA TGCAACATGA TGATCATGAT CCACATGCAT TTCAAGAGCT ATTACCTGTA      60
TTGANAGAAC ACCAAGCAAG AGTGATGANT CACAGAATCC CNGGGCGACA TAATGATGAT      120
TCACCTACCA TTGNAAGTNG GTTGTGTAAT TNCNACAACA TTATTTAGGA AGACCAAGAT      180
TGGGAGGAGG TCCAACATNC TGNAANCCN AAACAATTTA AAGTGACTTG GAATTAATAT      240
TTCACCANCC TACATTTATG TATGGCCCTA AAGTATCATT TTCCANATGG TGAAGTGAAT      300
TTTATAAATC CTTTGATGCC CTCTGGATTA CCGATTCATG AGTGGTTGAT GTTAAAGCAA      360
TTTTCAAAAT ATAAAAGTGC GCCAAGTTTA CCAATTTTGC GTAGAGGACA GCATTATAAA      420
TTGCATTTTG ATTTTGATGC AACGCCTGCT GGTTCACTGT ATTTTATCAT CATTTTTTAT      480

```

AATAAAATG GCACAACTA AGTACTGAGA TTGTAAAGTC AAATAGTATT ACGATTCAAT	540
ATCCTGATGA AGCCTATGCT TATAAAATAA AAATGATGAA TGCAGCATCG ACGAGTCTAA	600
TATTTAGATG TTTAACAATT ACAGAGATGA CGCATCAAGA TGATTTAGAG TATAAAAGCA	660
TGCGGGTGAC GAAGATAGAC GATAACCAAT ATGGAAATGA TAGGATCAAT GTCATTATTG	720
CAGAACCATC TGACACCTAT CCAACTATTT CGAATGATTT TTTGAACTG TTTGGTCATG	780
TTTGGCTCGT TGAACGTTGG ATGGACGACG ATATCAAGGA AAATATTAAG CAACTAAAGG	840
ATGATTTGCA AAGTCAAGAT ACCCTAACGG CTATTAATTT GATTAGTTAT GGGTCAAAGT	900
CAAATGTTTC TGCAACTTAT GTCGCTCAGC ATTTAGATTG CAAAGTATAT CGTACAAGCC	960
ATGAAGATGA TGATTTAAAA GAATGGCTTA CAGAACATGT CCCCAGGAAA TAATGAACTA	1020
AAAGATCAAA TTGTCGAGTT TCTATTTTAA AGAAGAGCAA GACAACCATC TAAATTATAT	1080
GTCACGTTTA ATGAATCCAG TCTCGTGCC	1109

(2) INFORMATION FOR SEQ ID NO:840:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 691 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:840:

CTGAAGCAAA ATCAGCATGA ATATGTGTTT CTGTAGCTTG TGTAATTGTT AAACCTTCAG	60
AATCTGCAAC TTCTATATAT TTCGATAAAT CACGAACAGG GTCTATTATT ATTGCCTCTC	120
CTGTACGTTG ACAACCCACT AAATATGATG CTTGAGATAA ATGATTATCG TAAAACTGTT	180
TAAAAAACAT GATAACAACT CCTTTTATTA ATAGATTTAA TTAGATAAAT AAATTATGAT	240
TGCGATTTTC AGTAGACCA ATATAAGTGC CTACACCACC GTACTCAACT TCATCTCTAA	300
GTTCTTCTCT CTGAATACCC ATGACATCCA TACTCATCGN ACAAGCGATT AATTTGATAT	360
GTGGCTCAAT AGCTTGATTG ATAAGTGTG GTAATGAATC AACATTTTTC TTTTTCATTA	420
CGTAGCGCAT CATCATATTN CCTAAACCAA ACATATTCAT TNGGGGAAAG AGGCATTCTG	480
ATTTTCTTTN GGGGGGNAAC ATTAAATCAA ACATTTGNGG NAATACCTTG CTTTNTTACA	540
ATAACTGGNT GGACTTTTTT TAATGCATTA AGCCCCAAA AGGTAAGGAA GATAGTTACA	600
TCTTTTCCAG GAGTCTTAG CGCCATTGGG AATACCAATG CTGTACAGGT TTGGCTTTAT	660
TCTCCACTAA TTAATACAAA TGGTCGGTCC C	691

(2) INFORMATION FOR SEQ ID NO:841:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 815 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:841:

```

GAAGATACGT TGTCTAATGT TCTTGCACTC ANAATACGAG AAGAAAGAAA TTATTATCAT      60
TAATGATGGA AGTTCAGATA ATACAGCAGA NCTCATCTAT AAAATCANAG AAAATNATGA      120
CTTTATTTTC GTCGATTNAC AAGAAAACAG AGTGTAAGC CAACGCACTC AATCAAGGCA      180
TTAAACAGGC TTCATATGAT AATGTAATGT GCTTGGATGC AGATACTATC GTTGATGCAA      240
GATGCACCAT ATTATATGAT TGAGAATTC AAACATGAGC CCAAACTTG GTGCAGTTAC      300
AGGTAATCCT AGAATTCGAA ATAAGAGTTC TATTTTAGGT AAAATTCAAA CGATAGAATA      360
TGCAAGTTTA ATTGGCTGTA TTAAGCGAAG TCAGACACTT GCTGGCGCAG TCAATACTAT      420
TTCGGGTGTC TTCACTCTAT TTAATAAAAG TGCAGTTGTC GACGTTGGCT ACTGGGATAC      480
TGATATGATT ACCGAAGATA TTGCAGTTTC TTGGAAATTG CATTTACGTG GATATCGTAT      540
TAAGTATGAA CCGCTTGCCA TGTGTTGGAT GTTGGNTCCA GAAACATTGG GAGGCTTTTG      600
GAAGCAACGC GTGAGATGGG CTCAAAGGGG GGACACGAAG TATTACTACG AGACTTTTNT      660
TAGCACAANG ACGAAAACGA AAGGGTTTCC TTTATATATT GTGATTGTGT GAGCAAATCA      720
TCTCAATTTT ATGGGTATTA TATTAGGTGC TTCTATATTT AGGCTATTTG GCTCCAATAC      780
AAGAACTTC CTTAGACTTA TACAATTATG ACAAT                                     815

```

(2) INFORMATION FOR SEQ ID NO:842:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 880 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:842:

```

CCAAATCCTA AAATCGATGG AGAANCGGCT GAGAAAGATT GGGATTTC TC CAAGTTGAAG      60
AGGTTGAAGG TGAGNCACTT TTCCCTTTAA GTTGATAATA AAAAGTCAGT ACCGTAAGTA      120
ATATCTTTGA TTCAGCTAAC ATGACAAATC ATGATGGAGA CGGTGAAAAA GGCGAAGAGN      180
CTTTCTTAAA GAAAATTTTA GGCGAAGAAT ATACTGGAAA CGTGNCAGAG GGTAAACGGAA      240
GAACTTTGT AACACAACCG GCTTCATCGG ANACTGCGGT AAAGTCGGTT AATATACCAG      300
ATAGCATTA AACTTTAAA GTTGGCGACA CAATACGATT TAAATGTTGT AGTAGAGCCA      360
TCTAATCANA GTAAGTTATT GNAATACACA ACAAGATCAN ACGAATATTG TATCAATCAA      420
TAGTGATGGT CAAGTTACTG CGGAAGCACA AGGCATTGCT ACGGTAAAG CAACAGTTGG      480
TAATATGAGT GACACTATAA CAATAAATGT AGAAGCATAA GAGGGGGCAA CCCCTCTATT      540
TTATTTGTAA ATAAGGAGAG TATTATAAAA TGGCANAATT AAAACGTAAC ATTATTCAAT      600

```


TAGTAGAAGA CCCGAAAGCA AATGAACTA AATCACATAC GTACTTAACA CCACACTTCA	660
TTTCATTGGA AATTGTATAC GAGGCAATGG ATTTAATCGA TGATATTGAG GACGNAAATA	720
GCACGATGAA ACCAAGAGAA ATCGCTGACA GATTGATGGA TATGGTTGTA AAAATTTACG	780
ATAACCAATT CACAGTTAAA GACCTAAAAG AACGTATGCA TGCACCTGAT GGAATGAATG	840
CAC'TTCGTGA ACAAGTGATT TTCATTACTC AAGGTCAGCG	880

(2) INFORMATION FOR SEQ ID NO:843:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:843:

GGCACGAGCT AACGTTAAAT GAATTTATGA TTGGCGAAGG ACATTATGAT GTCAGACTTA	60
AATTACATCA CGAAACAAGA AGCACACAAT GTATGTACCT TTAAGTGTCA ATGCGAATAA	120
ACAATATCGT TTTAACATTA TGTTAGAAGA TATTAAAGCG TATTTACCTA AAGAAAAAAT	180
NTGGGATGTT TTCTTAGAAG TCCAAATAGG TACGGAAGTA TTTGANGTGC GTGTTGGGTA	240
ATCAACGTAA TAAATATGCA TANTNCTGCA GGAAACAAGT GCATTAANTC AMNNACATAA	300
TGATTNTAT TAGATTAACA ACCGTATTTT CACAAAAAAG ACTTNNANTA ACATCTCCGG	360
TATTCCTTNN CAGGTTATTT ACAATNAACG GGTTCANTCT CA	402

(2) INFORMATION FOR SEQ ID NO:844:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 809 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:844:

CGGCTCTTCG TAATATTGAT AATGTGCAAT ATTTNAAGAA TAATCAATTT ATTGAAGAAG	60
AAACCGTAGT GACCGTGAGC GAATATCGAA NCGGCTATTG ATAGAATACG TACTGAAATG	120
GACCCGAATG AATATCGAAG NCGATATAAA TGGTAGACCT AAACATATTT ACAGTATTTA	180
TCGGNAAATG ATGAAGCAGA AAAAACAATT TGATCAAATT TTTGATTGTG TGGCGATACG	240
TGTTATTGTC AATTCTATTA ATGATTGTTA TGCGATACTT GGGTTGGTGC ATACGTTATG	300

GAAACCGATG	CCAGGACGTT	TTAAAGATTA	TATTGCAATG	CCTAAACAAA	ATTGTATCA	360
GTCATTGCAT	ACTACAGTAG	TAGGTCCAAA	TGGAGACCCG	CTCGAAATCC	AAATACGAAC	420
GTTTGATATG	CACGAAATTG	CTGAGCATGG	TGTTGCAGCA	CACTGGGCTT	ACAAAAGAAGG	480
TAAAAAAGTA	AGTGAAAAAG	ATCAAACCTA	TCAAAATAAG	TTAAATTGGT	TAAAAGAATT	540
AGCTGAAGCG	GATCATACAT	CGTCTGACGC	TCAAGAATTT	ATGGAAACCT	TATAATATGA	600
CTTACAGAGT	GACAAAGTAT	ACGCATTTAC	CCCAGGGAGT	GATGTTATTG	AGTNGGCATA	660
TGGTGCTGTG	CCGATTGGAT	TTTGGCTTAT	GCGAATCACA	GGGAANGTAG	GTAATAAGAT	720
GATTGGCGCC	CAGGTGGAAT	GGCAAAATTG	TACCANATTG	ACTTATNTTT	TCACAAAACA	780
GGCGGATATT	GTTGGAAATA	CCGTTCTAG				809

(2) INFORMATION FOR SEQ ID NO:845:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 590 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:845:

ATTGGGATTG	TTTTCCTAAA	GAAGCCCCAA	ATAGGTNNGG	GAAGTAATTT	GGAAGTGCGT	60
TGTTGGTCAA	TCCCCNCGTA	ATAAAATATG	CATAATCCCT	GCAGAAACCA	AGTGCATTAA	120
ATTCAATTTA	AAATNATGAT	TTTTATAGAT	TAACCCCGT	ATTCACCAN	AAGACTTTAA	180
TAACATTTTCG	TAATACTTTA	CAGCTATTAC	ATTANCGGAT	TCAATCTCAA	TGAAGTTAAA	240
AGGTAAAAAC	ANAATCATTT	TAAGTGGTCT	GGATCGTGGT	TATGTATTTG	AAGAAGGTAT	300
GGCTAGTGTC	GTGCTAAAAG	ACGACATGAT	TATGGGAATG	TTAAGCCCAN	ACGTCAGAAA	360
ACGAAGTGGA	AATCGTACTT	AGTAAAGATA	TTAAGAAGCG	AGACTTCANA	AATATTGTTA	420
AGTTAAACAC	TGCACATATG	ACTTACTCGC	GAAAATAAAT	AATAAATGCC	CTCAAATCTA	480
TGTGAACTAA	CATAATTTGA	GGGTTTTATT	TTGCTATTTA	TGAAATGATT	ATGACATTTT	540
CCTGATTTTC	ATTTTCATAT	ACATTAAATT	GTATACACTG	AAAATGAGGG		590

(2) INFORMATION FOR SEQ ID NO:846:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:846:

ATAAGTGANT	ANNCCGNCCTT	AANACAATCT	GATAGTAGTA	TCCANATCTC	CACCTATAAT	60
AAATGTTAAT	GGAATCTTGA	CTAAATAATT	CTTACTCACA	TAGCGTTTGN	CNATATACGG	120
NNCGATTAA	CCACCANATC	CAATTGGTCC	TCCCNCTGAC	ACCGACATAC	CTGTAAGAAT	180
AATGNCTAAT	AGNCCAATGA	TAATTCTAAC	TTTATTTATA	TTTTGACCCA	ATCCCTAANC	240
AATGTCATCN	CCTAGTTCCA	TAATCGTTAG	TTGACGTCCA	ATAAAAATCG	TGACAATTAA	300
AGCNCCCAAT	AATCCATGGT	AAAATGGGTA	AAATTTCATC	CCACTTCNTA	CTGGNTAANG	360
ATGCCGACAA	GCCCCNANAA	CATCNCTGGT	NCGTGTGAAT	TCTCACTCAA	AATAATAATA	420
CCTTCAGTCA	TACTACTAAA	AAACANATGG	NTGGCCATAC	CAGCCAATGC	TAATTTAATG	480
GGTGTCATAC	CTTTCGTAGC	ACCTGTNAGT	GTATAAACAG	NTAAACCACC	TATAAATGCA	540
CCTATCACAC	CTAAATATAA	TGCATAATAT	TCTAATGATG	GANTGATAAT	CGTCACAAAT	600
ACAATGTGAA	ACGGATGCAC	CCAAGAGCTT	GACACCAAAA	ATTTTAGGTG	ATGCTAGCGG	660
GATTGCGTGT	CATTGCTTGC	ATTAACCCAA	ACCAGATACC	GCTAATGCAC	CGCCAATAAA	720
TAACCCTGCA	ATCATCCTTG	GCATACGTAC	ATTATGCAAT	AAAAACGTTG	CTTTCGTATC	780
TGTNTGACCA	GTAACATAGT	GANTGATATC	GCTAAAATTA	ATTTTCGAAG	ANCCAATCGC	840
CATATTTAAA	TATATACAAA	TAAAAAGAAA	GCACANACTC	ACTATATACG	TGAGTGTGTG	900
GCGTCTTTTT	CTTTTATGAT	CTATGGCAGA	TTGGCTACTT	ATTTCTTTTA	TAGCCATTTA	960
CTTCCACCTT	ACTTTTGTTT	TTTTTTTGAT	AATTCAACAA	GTTCTTTAGC	CATTTCTTCA	1020
GAAGAAATTA	AGCCACGAGA	TCTTGCCCAA	ACATCACGGT	CAACAATATC	CACGCTCGTG	1080
CCTTTAACTG	CATTCAACTT	TTTCCATGTT	GCATCTTCTT	GTAACCTTCTT		1130

(2) INFORMATION FOR SEQ ID NO:847:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 637 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:847:

TCATTGGGAA	GATTAATTAA	TCCTCAATTG	GACTANCCAT	TGGAGGTCAT	TCAACCCAAT	60
TGGGCCTNCT	TGAAAATAAT	TCGCGCCAGC	AACACGCNCG	ATTGACNAAA	GTATCATGAN	120
ACGGCACAAAG	TATTTACGCA	TGAAAATCAA	TATTGGCGTG	AAGGTGATTG	GATTGTACAA	180
CCCGAATTAG	GTAAGACATT	TCAAATATTA	AGAGAACAAG	GGTTTAATGC	ATTTTATAAA	240
GGTGACATTG	CGAAACAATT	AGTCAATGTT	GTTAAAGCAT	GTGGTGGGAC	AATCATTTTA	300
GAGGATCTAG	CCAATTATGA	CATTCAAGTT	AAAGCGCCAA	TCAGTGCGAC	ATTTAAAGAC	360
TATGACATTT	ATTCAATGGG	ACCATCTAGT	TCTGGCGGTA	TCACGGTCAT	TCAAATATTG	420
AAGTTATTAG	AACATGTCGA	TTTACCATCT	ATGGGTCCAA	GATCTGTCTGA	TTACTTGCAT	480
CATTTGATAC	AAGCGATGCA	TTTAGCATAT	AGTGATCGCG	CGCAATACTT	GGCGGATGAT	540

AATTTTCATG AGGAATGCCG GTACAGTCAT TAATTGATGA CGATTATTTA AAAGCACGCA 600
 GTACGCTCAT TAATAGCAAT AAAGCAAATA TTGATAG 637

(2) INFORMATION FOR SEQ ID NO:848:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 804 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:848:

CAGCGTGATG TNTTGGANNT TTCATTGTGC GGANTCCTCC AAAGTCAATT GGATTTGATT 60
 CCTCAGGGGA CTCAGTGTAT CCCCCAACG TGANCNGNTT CACAANCCAC AGCAGTATGG 120
 TAATCGATAT CAATAGCTGA TGAATCCGTT TCTTCTATTG TTTCAATATA CCCATCAACA 180
 TAACCACCCT CACCAGCTAC GAGCTGTGTG GTAATCAATG TCAAGCGGTG TATTGTCTTG 240
 ATTTTCTTCT GTTTCATAA TTTGCTTGGC ATCGTACTGC CCGCTCATAG TTCCTGNTGC 300
 AGTATCTTCT TTATATTCAN AATCATTATC TTGAATAATT TGTCCATTTT TACCATTGCC 360
 GTCAGCTTTA TTGCTATAGA AAACATAACC ATTATCCCNA GGNAAGCGAN ATCCCCCATA 420
 ACATAGTAAG ATTTATATGC TCGTCTGGA TACCCATATA ATTCACTTCT AAAATTAACC 480
 TGANCTGACC CTTGCAAATA TTCACCTGTA TAATGAATGA CATACGTTTT ATCCAACCTA 540
 TCTAAATTCA ATGAGTAACT ACCATTGTCT TGCACACTCA ATTTTCCATT CATTTCCCTT 600
 GTTACATCTT TGAATTTGTT AGTATCTGAT GTATTTGCAT AAACACTTTG TGGCAATTCA 660
 TCTTTTTTCC CTAGATATTC ATATACTTTA ACAGTAGGTT GTCCACCAGC TAAATTACCA 720
 CCTTCAGTCA ACGTCCCTGT TACTGATACA GTGTTTGACT GGTTTCCATT CATTTGGCTTA 780
 ATATAAGCTA TATGTGTAAT TTTG 804

(2) INFORMATION FOR SEQ ID NO:849:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1053 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:849:

ACATATGCCA AGTCGTTAGC AGGTATAAAG TCCCAAGAAT GTATGTACCC AGTGACACAA 60

ATGCCGTTAT	ACAGTACGCA	GAGACCAGAT	AAACTTGCGA	TTCGACAATG	ATGAATGCCG	120
AAGTCTCACA	AACACTTTAA	AGNTGAGGGA	GATTTTGTGAC	ATTTAGTGTA	AGCGTTGACA	180
AATAAAGCGT	GTTGTTTTTG	AATTAGATGC	ATTTACACATT	AGTATTCATA	TTATTTTGTAG	240
GAGGAATTTA	TATGACATTT	GAAAAAGAAN	CGGTCCTAGA	AACATTATTT	CCTGAAGATG	300
TACTTAGTAT	TGCTAAAGGT	TTAACAGACG	GTGAAGTCGA	ATTTTACAA	CAAGTAGATT	360
CATTGCTAGA	AAGTAAGTAC	CGTGAAAATA	TTAATCANCA	TTGGATAGAC	GCTACTGTAC	420
CCGAGGACTA	TTTTAAAGAT	CTGGGAGAAT	TAAATTATTT	TAACAATCCA	TTACTTTACA	480
AGGATCGTCC	AAACGCCAAA	ATGCCTAGTC	AACATTTTCA	GTTTTTCATG	TCTTACCTAC	540
TCGCGCGATT	TGATATTTCC	TTAGCTACCC	TACTCGGTGT	TCACCAAGGT	TTAGGGCATA	600
ACACTTTCTA	TTTCGGAGGT	AGCAAAGAAC	AAATTGCGAA	ATATGTACCT	AAATTACAGT	660
CACATGAAGT	GCGTACATGC	TTTGCTTTAA	CTGAACCAGA	ACACGGTTCG	GACGTTGCCG	720
GAGGTCCTGA	AACAGTCNCT	GAACGCCAAG	GCGATACTTG	GGTTATCAAT	GGTGAAAAGA	780
AATGGATTGG	TGGTGACAT	GTATCTGATG	TCATTCCAGT	ATTGCGAGTA	AATAAAAAAA	840
CTGGCAAACC	CCATTGCTTT	GTAGTCAGAC	CAGAACAAGA	TGGCGTCGAT	ATTGAAGTCA	900
ATTGATAATA	AAATCGCACT	TCGCATTGTT	CCTAACGCAC	TAATTAATTA	CTAATGTCAA	960
GTAGATGAGC	GGTCCGCTTA	CAAACATACA	GCTTTAAGAT	ATTGCCAAAT	TCCTTATCAA	1020
CGAGAGCAGG	CGTTGCTATA	TGGTACAGGT	GGG			1053

(2) INFORMATION FOR SEQ ID NO:850:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 717 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:850:

ATATTAGCAG	CTGTGCTTGC	TTGTATTTTA	GCTGGTGTAC	CCTATCAAAG	CAATTATTGA	60
TAGTTTAACT	ACATTTTCAG	GAATAGAGCA	TAGATTGCAA	TATGTTGGTA	CTAATAGAAC	120
TAATAAATAT	TATAATGATT	CCNAAGCAAC	AAACACGCTA	GCAACACAGT	TTGCCTTAAA	180
TTCATTTAAT	CAACCAATCA	TTTGGTTATT	GTGGTGGTAT	TGGATCGAGG	GAGATGAATT	240
TGACGAACTC	ATTCTTTATA	TGGAAAATGT	TNCGCACGAT	GGTTGTATTC	GGACAAACGA	300
AAGCTNAGTT	TGCTAAACTA	GGTAATAGTC	AAGGGAAATC	GGTCANTGAA	GCGAACAATG	360
TCGAAGACGC	TGTTGATAAA	GTACAAGATA	TTATAGANCC	AAATGATGTT	GTATTATTGT	420
CACCTGCTTG	TGCGAGTTGG	GATCAATATA	GTACTTTTGA	AGAGCGTGGA	GAGAAATTTA	480
TTGAAAGATT	CCGTNCCCAT	TTACCATCTT	ATTAAAGGGT	GTGAGTATTG	ATGGATGATG	540
AAACGAAGAN	CGATCAACAA	GAATCAAATG	AAGATAAAGA	TGAATTAGAA	TTATTTACGA	600
GGAATACATC	TAAGAAAAGN	CGGCAAAGGA	GAAAGGTCAA	AGGCTACACA	TTTTTCTACN	660
TCAAAATAAA	GATGATACAT	CTCAACAAGC	TGATTTTGAT	GAAGAAATTT	ACTTGAG	717

(2) INFORMATION FOR SEQ ID NO:851:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1063 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:851:

```

ACTTTACCCC TTCCCAACTC TGCTCAAGTT TACCCTAAAT GTCTTAATGT CGGCGTTAAT      60
GCTGCGGNAG AAGAATCCTT CTTTTAACTT GCGAACTTGT GNCGAATATG GTGTGTACGC      120
TCTTTGAACC CACCATTGCC GACAGAAGCT TGATTTACAT CTAACAATAA ATAGCCAATG      180
TCCTTCTTCA ATGATATTAA TTCACTTAAA TGTGAAGTTA AGTTACCGTC ATCTAATATT      240
GCATAATATT CCTCTCTAAG TTGNCGATAA CGTTTTTTTAA AAGCTNCAAC ATCATACTCT      300
AAATATTGAT TTATTCCGTT TTGCGCATTT GAAAATGCAT CAATTAACTC TAAAGAACTT      360
NTAATTGAGC CTAATCCTAT TGGAATTTGG TAAGCAATAA ATTGCGGGCG AATAAGTTGC      420
CGCAAAC TGG CTTTCGCATCA TCGGTGATGA TTTGTGATTG TGGCACTACG ACTTGATTCA      480
ATGTGATNTG ATACGTTGCT GACCCGTTGA CCCCTAAAAA ATTGGTTTTT TCAACGAGAG      540
TGATACCATC TTGATTGGCA CGTAGAATGA ACATGACAAA TTCATCTGAT GAATCATGTT      600
TCGAAATCGC ACCAAAATAA TGGTCTTCTT GAATATTAGG CTTACGAGCT GGCATACGTC      660
CACTGACAAC CAATTGTCCA TCAACATAAG TGTGTTCAAG GTTCANCTTT TCTAAATCAG      720
TAAATGACTT CATCGGATTA GACAATCCGG TAGCACCTAA TATTTCTCCA GATAACAATT      780
GCTGTTGTAA GTCATTATTT AAATGTGGCT GCGTGGCATT TTCTAAATAC GTTGAAAAAG      840
CTAATTGGCA CCATAACAA AATCCTGTTG TCAACAAGA CTGCGATACA GCTTCGATTA      900
CTTCAGCATT TTTTCTCAAT GCCGCCTCAC CGAAATAACC ATCTACAAAT AATTGTTGAA      960
TAAATGTTCT CGGATAATAC GTCCCTTCAT CAACTTCTAC TAAATGAGGA TCTTATTTGGT     1020
CTTTGATAAG CGTTCTTAAG TCATCATCAT CTCTCCNTAT TCA                               1063

```

(2) INFORMATION FOR SEQ ID NO:852:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:852:

AACCCCTATA	ACTATTGCAG	TTAAGCACCA	TAGCTGTAAC	GAAGGGATCC	ACAAACAATT	60
GTTTCCACCA	GTTATTAATG	GTTCTGATCC	TACTAGAGCC	ATACGTTCCC	ATACTCATAA	120
TAATGAGATT	ACCAGCATGA	GTATATATTG	AAATTCCGAT	TACAATACGA	ATTAAATTGA	180
TTGATAAAAT	CATATATGTT	CCTATAAACA	CTATAAATCC	TATAACTAGT	AATAATATTA	240
AATTCATGAT	CGACCTCCGC	TAAGCGACAA	CATCACTGTG	ACAATAACAC	CAACAACCTGA	300
GAATAAAATA	CCTAATTCAC	AAAGTGTTAT	TGTACTTACN	TGGAATTTCC	CCTAAANTTG	360
GANNAAACCCA	ANTTNTTCAA	TATTGAGCCC	CAAATGGTTT	TCCAAGAAAC	ATAGGTATTA	420
TCGCAGTAAT	AGATGATACC	AATGCTCCAA	TAATCACTAA	AATTCTAAAA	TCAATCGGTA	480
AACTTTCTAA	AACCTCTTCA	ACATTAAAAG	CCAGAAACAT	TAAAATAAAC	GCTGAACTAA	540
ATATTAAACC	ACCAATAAAG	CCACCACCAG	GATTATTATG	ACCTGCGAAG	AAGACATAGA	600
ATCCGAAAGT	CAATAAAATA	AATACAACAA	GTTTCGTGAC	CGNTCTTAAC	ACGACATCAT	660
TCTCTTTCAT	CTTGTCCTCT	CCGATCTTGA	TAATTTAATA	ATGTGTAAAT	ACCCTAGCCC	720
AGGTAATAAT	TAACACTAAA	TCCTNCAAAA	TTAATGTATC	TAATGCTCTA	AAGGTCACCA	780
ANGTATCGGN	ATTTACAATA	TTTTTACCAC	CT			812

(2) INFORMATION FOR SEQ ID NO:853:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 530 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:853:

TCTACAATAA	CGGAAGTTTT	TCTTTTAATA	TTGAAATTTT	TTAAGGATAG	GTCTATACTT	60
TATAAATCGT	AATTATTACG	ATTTATAGTC	AAAAACAATA	ACTTGAAATA	GATCATTGAG	120
GGAGTGTTAA	TATGCAACAT	CATAAAGTGG	CTATTATCGG	TGCCGGTGCT	GCAGGTATAG	180
GTATGGCCAT	TACCTTAAAA	GATTTCCGTA	TAACAGATGT	CATTATTTTA	GAAAAAGGAA	240
CAGTAGGACA	TTCATTTAAA	CATTGGCCGA	AATCGACCGT	ACGATCACGC	CATCATTTAC	300
GTCTAATGGA	TTTGGCATGC	CTGATATGAA	TGCAATTTCC	ATGGATACTT	CACCAGCATT	360
TACATTTAAT	GAAGAACATA	TTTCCGGAGA	AACATATTGC	TGAATATTTA	CAAGTGGGTG	420
CCAACCATTA	CGAGCTGAAT	ATCTTTGAAA	ATACAGTTGT	CACAAATATA	TCTGCAGATG	480
ATGCATATTA	TACGATTGCA	ACGACAACAG	AGACATATCA	CGCTCGTGCC		530

(2) INFORMATION FOR SEQ ID NO:854:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:854:

```

CCCATTTTCA TTTTSTAATT CATAAACGAA TCAATAACCA CCTAATAACA AATCATATTA    60
TACACCTTTG TTCGCTATTT TTCTAAGGTT TAAAAAATAT TTTTAGGTAA GCCTAAAAAT    120
AGATGTAATA AAAACGCCTC CTCAGATATT TATATATCTA TGAAGACGTT TAAATACATT    180
ATAGATGGTC TGGTCTGGG TGAACGTATA CTGAGGAAAT ACCTTTNTTG TGCAATGAT    240
GTTTCGACATT GTCACAAATT TGATGCGCTT CTTACTAAGGA AAGGTTAGCA TCTACAACAA    300
TTGTGACATC AATAAACACA CTTACTCCAT GNGTAACGCC CTTTAATACT TTTAACTTCT    360
TGTACTTCAT CAACTTCTTA AAATATCATT GCGATACGCT TCTAATTCAA GTTTCATTGA    420
AACCCATCAC TCAACATAAA AATTGATTCC TTTAAAAATA CCAAACCAG TATTAAACGA    480
TTAGTAAGCC TAGGTAATNG TTGCTAAAT AATATCGGAC AAATTGGG    528

```

(2) INFORMATION FOR SEQ ID NO:855:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 978 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:855:

```

CGAACATCAA TACCGCAAAA ACAATCAATG CAATAATTCT AAATAACCAT CGCACCTCTT    60
TAACATCGGT CAAATGACTA AAGGAAAATA GCGTTTCACT TGCAATAATA AGTATTAAAC    120
ATGCAGCTAA TACGATTAGA AAACCTTNCC AACTNTGTTT TAAACGTTCT GTTACATACC    180
TTTTAGTATG CGGTAAGTTT TTAAAATATA AAATAATATT ATCTAGCATC TTTACACCTA    240
CAATTCAATA TAAATCCATN TGTCTTCTCT CAAATTGGCA ATACANTATC CATTCCCAAC    300
TTTAGTAATC CAAATGTTAT TGTTAATATT AANCTTATCT NCNAATTCTT NNNNNATCTA    360
CAANTGGATA AACAANACCG NATATACTGG ATTATTNTCC ANCGANANGN NANTAATTGN    420
ATCGGNTGTT GTGTANACCG ATNCAACCGA ANCCGGTTAT CATCATCAGG AACTAAAGTT    480
TTATAACTGA ACCTATGCTT TTTATGTAAT TGACTGTTAA AGTATGCATA GTAATTACTA    540
TAATTTGATT TCATATATGG CGCTAATTTT TAAAACTAT GCGTTTGATA TAAACCTGCC    600
GGGTAAAAAT ATTCTAATTT ATCTTTACTA ACATAGTAAG TCTTATTATC GGCGGTAACA    660
CGATAATTTT TACTATTTTC GCCAGTAATT GTAACCTACAC TATATTTTGG AATTGTGACT    720
TGTTTATCCC CTTGCATATC CACACTGCCA TAAAAAGCAA TTCCATAAGC TAACCTTTTCG    780
CCATATGGAT CTTTATTTTC ATTTTGCATC GTAGCACGAT TCGTAAAATC TGTATCGAA    840
ATAATTCCTA TATTATTGAA AATGAGCAAC ATCATCAATG CTAAGCCTAA AATAGTACCT    900

```


CGAGCCTAAA GTCCAAAAAC GCACTAAAAA CTTAGGCGGT TTTGCATGAT TATAGCGCTC 960
AACGCGGCAC GAGGTGCC 978

(2) INFORMATION FOR SEQ ID NO:856:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:856:

GAATTCCTAC CTAAACAGT TGTATAATT ACTGTAATA GTGCACTAAC CCCGAAAGAT 60
TGTATTGATT TATNCCATAA AACGATACCT GGTATGGTTG CAAATAATGC AAATATTACT 120
CCCAAACCAG GCACTAGATA TAAAGCTAAN GCGACAAATA CCAACGTAAT CACTGCAATT 180
ATTGTTGCTT TAGGTTGTAT TTGTGAAAAC ACATAAGCCA CTCCCATATT TTTAGCTATA 240
GCTATTATGT TANCCTCTTT AATGGAAATT AACACTTTAT AGATTGTATG CTTCTATTTT 300
ATTTAATTGA ATAATAACTT NCATGTTTTA TAAGTAATTA ACATACTCAT TTGAATCGCT 360
TGTG 364

(2) INFORMATION FOR SEQ ID NO:857:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 794 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:857:

CGGTCGCTTG TCTAAACCTT TCTTCTAATA TTTGGGTCAT ATTTCGCATCG GCACCGCTCA 60
TCGTAATCGC TTCATGTAAT GTTTGNTTGA AAGGTTTAC TATGCTCGCT GATGGTGGAA 120
TCCTTCCGAA TGTTTGNAGT AACATAAAAG CGATTAATGA AATTAAGCTC ATCGCTACTG 180
TTGTTACGTA TAACATTCTT TCTTTCGACG TTCTTCTTTT GAGCAATTGA CCAATAATTA 240
AACTTGCAAT TAAGACTAAT ATGATGGCAC TTA AACGAA AGTATTACCT AAAACAGTTG 300
TTATAATTAC TGTAATAAGT GCACTAACCC CGAAAGATTG TATTGATTTA TTCCATAAAA 360
CGATACCTGG TATGGTTGCA AATAATGCAA ATATTAGTCC CAAACCAGGC ACTAGATATA 420
AAGCTAAAGC GACAAATACC AACGTAATCG GTGCAATTAT TGTGTTGTTA GGGTTGGGTT 480

TTTGGAACA	CATAAGNCAC	TCCCCATATT	TTTAACTTAT	TGGTTATTAN	TTTAACCCTC	540
TTTAAATGGG	AAAATTAACA	AATTTATTAG	GATTGGNTTG	CTTCCTNTTT	TCAAANTAAA	600
TTTGAATTAA	TTAACTTTCC	AATGTTTTTA	TTTAGGTAAA	TTAACAATAC	TCCATTGGAT	660
TCGCTTTTGG	GGTGCTTTCA	ATTTTCAACA	ATGAATTATT	TAATCCCCAC	TACATAGCAA	720
ATCAAGCTTG	GATTTAGATT	TACAATTCAA	TTCCCACTCT	CAATGTACTC	TGGATGTCTT	780
TGGGATATGA	TAAC					794

(2) INFORMATION FOR SEQ ID NO:858:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 611 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:858:

ANCGTATAAA	CGAGACACAC	TTCGCGAAAT	GAAGTGGTGT	AGACAGATGG	TTATCACCTG	60
AGTACCAGTG	TGACTAGTGC	ACGTGATGAG	TACGATGGAA	CAGAACATGG	CTTATAGAAA	120
TATCACTACT	AGTTTAGCTC	TCCTAGATGA	TGGAGAGCTT	TTTTCATGAA	AAGAACACTT	180
AAAATTAACG	CCTTGCTCTG	ATATAATGAC	ACTGCCTTGT	TTTAAAATAG	TAAGCGGATG	240
CGTTAATGTA	TCAGCGATT	AATGTGTTGG	AAATGTATAA	AAAACACAAG	CTAAGAATAA	300
AATACCTGTA	TAAAAGGAGA	ATCATATATG	TCTCAATTAC	TTGCAGTGTG	CCCGATGGGA	360
TTAGAAGCTG	GTGTTGCTAG	GGAAATTCAA	GAATTAGGCT	ATGAAACAAA	TTGTTGGAAA	420
ATGGGTCGTT	TNTTTTGTGG	AAGGAGGACG	CAANGTGCAA	TTGGTNAAGG	CAAATTTATG	480
GGTTGGGCAC	AGGAGGACCC	ATCAAAATTG	TGGGGTGGGC	CGGTTTTAAC	GCAACAAACG	540
GTGGACGGAT	TTATCCGGAC	AAACCCAAGG	GCCCCCTGG	GAATCTTTTA	TTGGTAAAGG	600
AGGTNCTCCC	C					611

(2) INFORMATION FOR SEQ ID NO:859:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 628 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:859:

CGTTCTGTTT	TTGAAAATCC	GAGTATACAT	ACGATAGGAG	TTAAAAAAT	GATTGAACGC	60
TATTCTTGAG	AAGAAATGTC	TTATATTTGG	ACTGATCAAA	ATCGNTATGA	AGGATGGTTA	120
GAAGTGGAAA	TTTTAGCATG	TGAAGGATGG	AGTGAAGTAG	GACATATACC	GAAAGCTGAC	180
GTACAAAAAA	TTTCGTCAAAA	CGCAAAGGTA	AATGTCGAAC	GTGCACAAGA	AATTGAACAA	240
GAAACGCGCC	ATGATGTTGT	AGCCTTTACT	AGACAAGTNT	CTGAAACGCT	AGGTGAAGAA	300
CGTAAGTGGG	TACATTATGG	TTTAACTTCT	ACTGATGTTG	TAGATACAGC	TTTAAGTTTC	360
GTTATTAAAC	AAGCAAATGA	CATTATTGAA	AAAGATTTAG	AAAGATTTAT	CGACGTTTTA	420
GCTGAAAAAG	CAAAAAATTA	TAAATATACA	TTGATGATGG	GACGTACACA	TGGAGTGCAT	480
GCAGAACCCA	ACTACATTTG	GGTGTCAAAA	ATGGCATTGT	GGTACACGGA	AATGCAACNG	540
TAACTTACAA	CCGTTTCCAA	CAAGTAAAGA	GAAGAAATTG	ANGTAGGAAA	ATGAGTGGGT	600
GCAAGTAGGG	TACTTTTGCT	AACAATCC				628

(2) INFORMATION FOR SEQ ID NO:860:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1036 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:860:

ATTTAAATTC	ATAAAACNG	GACCACCTTA	TTTGTCATTA	ACCCAAATAA	TAACCAAAGA	60
CGTTATTATT	TCCAATCTTT	TTAATANAA	TAAATAGGAA	TCATAGTATT	GTCAATTTAA	120
AAGATAAAGT	AAGGACNGTT	TTTATTTTTC	AAGATTTTTC	AAATTATTAT	GAATATCTAG	180
TTTTAGGAAG	GAAATTACCA	TGTAAAAAC	AAGTTATTAT	TTCCGGCCTC	ATGTTATTTT	240
CACTATTTT	TGGAGCCGGA	AATTTAATAT	TCCCGCCCAT	TCTTGCCCAT	ACAGCGGGTC	300
ACAATATGTG	GANTGGTATG	CTAGGCTTTG	CCCTTACAGG	CATATTACTC	CCCTTTATTA	360
CTGTTATTGT	TGTTGCATTT	TATGATGAAG	GTGTTGANAG	TGTAGGCAAT	CGTATACATC	420
CATGGTTCGG	GTTTATTTTT	GNTGTCGTGA	TTTACATGTC	TATCGGAGCA	TTTTACGGTA	480
TTCCACGTGC	TGCAAATGTC	GCTCGTACCG	AAATTCGGCA	CAAGACACAC	TTNACCTGTG	540
CANAACCAAT	GGACTTTAAT	TATANTCGCA	GCAATCTTTT	NNGGCCATCG	TTTACTGGAT	600
TAGTTTAAAT	CCATCGAAAA	TCGGTGATAA	TTTAGGTAAA	TTATTAAACAC	CATNATTACT	660
ATTAATGGNC	GCTCTATTAA	GTATTGNTGN	CATTNACACC	CCTGAATCTG	CACTAAGTGC	720
ACCTAAGGAT	AAATATATAA	CACATCCTNN	CATTNCAGGA	AGTGTGGAAG	GCTATTTNAC	780
AATGGATCTT	GNTGNTGCGT	TAGCTTTCNC	CGGAGNCATT	GACAATGGTT	ATAAGTTTAA	840
AGGCCTCACA	GGATCGNATG	AAAATTTNAA	AATATTGTCT	GCTTCACAGG	TCTTTATTGG	900
AGGCCATATT	ACTTGGGGAT	TGATTTACTT	TTGNNACTTG	CAATACGGTN	GGGGGCATCA	960
ACAGCTCCCA	GGGAACTTTT	AAAGGTGGNA	CAAGATATAT	TGACGTACAA	CTCAATAACG	1020
AGTTTTTGGG	CTCAAA					1036

(2) INFORMATION FOR SEQ ID NO:861:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 557 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:861:

```

ATCAGTCCAA TTTGACATAG CAGCCATTTT TATTAATTTT CTTCTTAATA TTCTTCAACT    60
TGATAAAATC TATTTTTCAG TATATATAAC ACTAATGGTA TAAATAACAC AGCACTGATC    120
GTAAGTGCAT AAAATCCACC TTTATTTTCA AGTAATATAC CGCCTAAAAA AAGGGCTATA    180
GGTCTGAATG CAAAAACCAT TGTTTTAAAA ACACTATTAA CACGTCCTAA CATATTTTCT    240
GAACATTTCT TTTGGCTCAG TGTGATTATC GCTATATTTA AAATGGATTG TGTCATATAT    300
GTCAACCCTA AAAGTGGGAT GAGTATNAAA ATATAAGTAC TAAATGGGTA ACATTAATCT    360
TAAAAATTGN NTCTTAAAAA TAATATTAAT TACAATTAGG NNTCCCGAAA TTAATAATTT    420
CAAAGAGAAA ACTTGGAGGA TGATGAACCG NTTAGCGCAC TAATGATGAG ATACCTAAAA    480
CTAACCCCAA TGCTTGAGAT GATTGGATCA AGGTCTCCCT TACAAACATA ACTATTTTAA    540
TTTTATAGGG GGAGATC

```

(2) INFORMATION FOR SEQ ID NO:862:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 457 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:862:

```

GGCACGAGAC CTTTAGATAA AGTTGAAGAT GAAACTGTCC AATGGTGTAAG AGAGATTATT    60
GAAACACTCA CCAACCACCT TTNCCGATCC CTNAAACGCA GCTATGNATG CTGACACAGA    120
TGGTTTAGCT GGTTTACAAC ACATGNCTGG GGATCCAACA TTGCTTTATT ACACAACCTGA    180
TGAAGCGAAA GAAGCCCGTG ATGCGTTTAA AGAAAAACGT GATCCTGACT TCGATCAATT    240
CCCTAAATTC CCATAAGTTA TTTTGAATAT GATATTAAGT CACTTGCCTC GTTTATTAGC    300
GACGATAGGT GGCTTTTTTA TTTTATAAGA ATTTAAAAGA GAATTTTAAT TAATTATCAT    360
AAAGATAAGA TGGNTTGAGT AAATTAATAG AGAAAAGAATA AATGTTAAAG ATTATTATTA    420
CAATGAAAAA ACGAGCTGGT GAGAAANTGA TTCTCGC

```

(2) INFORMATION FOR SEQ ID NO:863:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:863:

```

ATTATTTTCA ATATGCACTA GCATTTACAG TTTAATTCCA GTACGTTGCT CTAATTCTGT      60
TAAAGTCATT CCTAACCTTT CACGTCTACC TTTAGCGCT TCACCGACCG TTTTCAATTC      120
ATAGCCTCCT TACACTTACT CGAAGAAACC AAAACCACCA CCAAACGGAT CTCCAAAATC      180
TAAATTATTC TTACTTTGGA CTGTCTGTTT CTTCAATTTCT TCGTAATGTA TTTCTTGATT      240
TTCATTTTCT CTCAATTCGA TAATATAGTC AAAATCTTCC ATTGTACAAG TACTTGTTTC      300
AACAAATAAA TCTGGATGGT TCAACGACTT TNGGATTGAT GGGTAACGGT CAATAACTTC      360
CGNTTAACAA GCTCTTGATG TTTGGGATTT AAGATTCTCT TGGCAAGGTA ACTTGCACCA      420
TCAAATAATG T                                     431

```

(2) INFORMATION FOR SEQ ID NO:864:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 924 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:864:

```

CTTNATAAAN ANCNATCNTA TGCCAATTTG ACCATTGTTT GAATCCATAT ANAAACCGGC      60
NACGGTTCCTT TTCAAATATA ATAGTAAGTG TATAATGAAA ATGTAAATAT TATTAAANAT      120
GGGGGTTTAC TCAATGAAAA TGAAACGTTT TATAGCTATT GTAATGGCAT TATTTTGTAGT      180
ATTAGNTGGT TGCTCTAATT CTAACGATAA TAATGAAAGT AAAAAAGATG ACGCAGACAA      240
TGGTAAGAAA CAAGAGATTC AAGTTCAGC GGCAGCAAGT TTAACAGATG TAACCAAGAA      300
ACGAGCTTCA GAATTTAAAA AAGAGCATAA AAATGCTGAT ATTAAATTTA ACTATGGTGG      360
ATCAGGGGCA TNAAGAAAAC AAATTGANTC AGGCGCACCN CTTGTTGACG TATTNATGNC      420
TNCCNAANTN CTAAAGATGT AGATGCATTN NNAAGACAAG GAATNNAGCG CATTTGATAT      480
CATATNAATA TCGGNNNNAT AGTCTAGTAT TAATTGGTGA TAAAAGATTC AAATTACACT      540

```

TCAGTAAAAA	GACTTAAAAG	NCAATGATAA	ATTAGCATT	GGTGAAGTGA	AAACTGTACC	600
AGCAGGAAAA	TATGCGAAAC	AGTATTTAGA	TAACAATAAC	TTATTTAAAG	AAGTCGAAAG	660
TAAAATCGTT	TATGCTAAAG	ATGTAAAACA	AGTATTAAAT	TATGTTTGAA	AAGGGTTAAT	720
GCGAAACAAG	GTTTTGTGTA	TAAAACTGAC	TTATATAANC	AANNCNNAAA	AATTGATACT	780
GTAAAAGTAA	TTAAAGAAGT	AGAACTTAAG	AAACCAATCA	CATACGAAGC	TGGTGCTACA	840
TCAGATAGTA	AATTANCAAA	AGAGTGGATG	GATTCTTAAA	TCAGATAAGC	TAAGAATATT	900
AAAGATACAC	TTTGCAGCAT	AAGA				924

(2) INFORMATION FOR SEQ ID NO:865:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 662 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:865:

CTATTCTTCT	ATGTCTTTGA	CAAGCGCGAA	TATTTTTCGT	CGTTGCTTGC	CGGTAATTTG	60
AAACGGATCT	ATGACGCTTA	CATCGACTTC	CACATCAAAT	CCGTTATCAA	GTAAGTAATGT	120
TTCTTTATTG	CCTAATTCAA	CACCCGAGAT	GACAACTGTT	GNTGTACCGN	CATCTTGAGT	180
GATATAACTA	GTAATTAATTG	GCATCTAATC	ATTCCAATCA	GAACGGGAGG	TCTGAAAAAT	240
CTTCTTCACT	ATTGTCAAAC	GGATTATTGC	CAGTTTGAGC	TTGTCCTTGT	TGTTGATAAT	300
TGTTGTTTTC	NTGTTGGTTG	TTATTCTTCG	GTTCTAAGAA	TTGAACGCTG	TCCGCTACTA	360
CTTCTGTCAC	AAATACACGT	CGCCCTTCTT	TGTTATCGTA	ACTGCGTGAT	TGTAAACGTC	420
CATCAACGCC	AGCCAATGAC	CCTTTGGATA	AATAATTATT	TACATTTTCT	GCTTGTTTTTC	480
TAAAAGTTAC	ACAGTTAATA	AAGTCTGCCT	CACGTTCTCC	TTGAGCGTTA	GTAAATGTTT	540
TGTTAACTGC	GATAGTGAAA	GTGGTNACAC	TCACACCATN	TGGGCGCTGT	TCTATATTCT	600
GGATCTTTTT	GGGTAAGCGT	CCCACCTAAT	ACTGTTCTCG	TNNTAACATT	ATTTGNTTTC	660
CC						662

(2) INFORMATION FOR SEQ ID NO:866:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 794 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:866:

AAGAAGTGGT GAAATTTAGT CCCANAACA TTAAGCCATT TGTATAATAA GTTAGTTAAT	60
TGCTTTTGAA GAAGAAGACA ATTTGATGAT GNTGTTGGTT GATTTTAAGA CTTTTAAGCC	120
AAAGAGCTGT TAAATCCATT TGCATCCACT TGAAGAATAT AATCGATTTT CCACAAGGGT	180
TATTTGAATG GATAGGCTAT AATACTAAAG TGTTTACGTA TCACAATGTT GAGAGACACA	240
AAAGGGAATC TAAGTGGTCC TTTAAAAAGT TATTTAATTA TGGTATTGAT GGATTGATTT	300
CCTTTAATAG TAAACCTTTG AGAATGATGA TTTATCTTGG CTGTTTATC TTTCAATAA	360
GCGTGCAATA TATTATCTAT TTATTCATCA ATATTATGAT ATCTGGTGTT AATATTCCAG	420
GATATTTTTC AACGATTGCA GCTATTTTAT TATTAGGCGG CATACAGTTA ATTTCAATTG	480
GTGTTGTAGG TGAATATATT GGCAGGATAT ATTATGAAGT TAAGGCACGT CCTAAATATA	540
TTATTCAGC TACAAATCTT TCAAGTATTG AAAATGATGA GAAGGATACC CATAAAGTTT	600
ATTCTAAATA AACAAAAAAA GAAGCCCTCA TTAATGGGAG CTTCTTTTAA GTCTTTGCAT	660
TTTATTTTAT AAATAAATCG GATTNTGACG TAATGTCTAA TTTGTGTAAT GTTACAGTCA	720
TCGTAGTTCC TACATCTATA TCACTGCTTA CACTGATTTT TGCGTTATTT TGNTGCGCGG	780
CACGAGCTCG TGCC	794

(2) INFORMATION FOR SEQ ID NO:867:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:867:

AAGATATTGG AANCATTAAA AAATTTANTT ACCGGGTCCG AAAATGTCTG GTAAATCGAC	60
ATATACTGAG ACAAGTTGCC ATAATTAGTA TAATGGCCCA AATGGGAGCT TATGTCCCTT	120
GTAAAGAGGC AGTGTTACCT ATATTTGATC AAATATTCAC TAGAATAGGT GCGGCAGATG	180
ATTTGGTTTC AGGTAAGAGT ACGTTTATGG TAGAAATGCT AGAAGCACAA AAGGCATTAA	240
CTTATGCAAC AGAGGATAGT TTGATTATTT TCGATGAAAT TGGACGTGGT ACTTCAACGT	300
ATGACGGTTT AGCTTTAGCG CAGGCAATGA TAGAGTATTG TAGCTGGAAA CATCGCATGC	360
TAAAACGTTA TTTTCAACAC ATTATCATGA ATTGACAACA TTAGGATCAA GCATTACCAA	420
GTCTTAAAAA ATTGTTACAG GTCGCTGGTA ATGAATATAA GGTGGAACCT ATTTTCTTGC	480
ATAANGTCAA AGATGGTGCA AGGNGGACGA TAG	513

(2) INFORMATION FOR SEQ ID NO:868:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 762 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:868:

```

CTGNAAATTC GATTTTCATGT TTATGCTTCA GAAAACCTGT CACTAAGGCA GAAATCCCAA      60
ATATGACTGT CAATTCTAAA AGAAGATGAT CTTTAACCTC GTCAATATAC ATGTTAAACC      120
AATTATCAAA TGTTCCCCTA GGTGCTAAGT CATAAGTATT CTCACAAATG GCGTCAGATG      180
GAGATTTATT ATCAAATTCC GNAGTAGTAT AGATTTCACT TAACGATACA ATAGGACCAA      240
ACGGGGTTTC CAGTATACCT ACCCCTTCAT ATAAGTAGGA AATGGGTAAT TGATTGCGCA      300
TTTGTTGCAA CGCATAACCT AAATCTTNTG NGTNTTTTTT ATTAATACTA AATCCCATAC      360
TTCANTAAAG ATGGNAGGTT TTGGGGTTGG TTAATAATATT CACTAGGANT CAACAAATTA      420
CTTTNTGAGG CCCTCGNCTG TAATAATTAC TTTTTCAGTG TTAGTMTTAG GGTCAATAAA      480
TTTATTTTCG ATAACGATAG GACCTGCAAT TTCAACTTCA ATAGGCATTC CTCCTTTTTC      540
TTTGGGAGGC TTGTCTTTAT ACCAACCTTT TTTTGATTGG TATCGTGGTG AAGGATTAAA      600
TGAAGGGTTA GTTTGAGTCA TTAGCGAACA CCTCCTTTTCG AAGGGTTGCT GTTATTATAT      660
GGATTTGGCC CTGTTTAAAG ATAAACCAAG TGTCCATGAG TATTTTACC AATAATAACA      720
AATGGAACAC GTGGCGCATG TTTTACAAAG TACGCTCGTG CC                          762

```

(2) INFORMATION FOR SEQ ID NO:869:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 718 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:869:

```

AAAAAACGGT TCGGATGTGC TTTTGTTTTA CCCTTCTTTT GTCTAAATCA ATNNCCCNAC      60
ACAAGATAAN ACACTTCTAC CTTCAAGTTGG AACAACATGT CTTTGTGNCA ANCTAGTGAT      120
NANNCGCTCA ATTACCTCTG TTNATTTTAT TCCTAAAATG CCGTCATNNN AACCTGTCAT      180
ACCAACATCC GTAATATACC CTGTCCCCTT TGGTAAAATA CGTTCACTTC TGTTTGAATG      240
TGTGTATGCG TTCCAACAAC AGCGCTAGCT CTACCATCTA AATGCCATCC CATTCGATAC      300
TTTTCAGAAG TTGTTTCTGC ATGAAAATCA ACAAATATAA ACGGAGTTTG TTCTTGCTGT      360
TCCTTGACTA ATTGATGCTG CCTTTTAAAG AGGATCATCA ATATCTGGCA TAAACGCTCT      420
TCCTTGCAGA TTAATAACTG CAAGTTTAAAT ATCATTAATT TGTATAAATC TCATACCAAT      480
TCCCGGCGCT TCATCCGGAA AATTCGCTGG GCTTACTAGT CGTTTGCTT CATCTATAAA      540

```


ATCATAAATT TCACGTNGAC CAGATGTGTG ATTACCCATA GTCATGAAAT CTACACCAT	600
TCTTAGTAAT TGTTTATATA TTTTTCAGT CACACCTTTA CCATGTGCTG CATTTTCAGC	660
ATTTACAATT GTAAGTGTG GTTTATACCT TTGCTTCAGT TGAGGTATGT CTCGTGCC	718

(2) INFORMATION FOR SEQ ID NO:870:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 656 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:870:

CTGGTAAAC AACATTAACA GCAGCAATCG CTACTGTATT AGCAAAAAAT GGTGACTCAG	60
TTGCACAATC ATATGACATG ATTGACAACG CTCGAGAAGA AAAAGAACGT GGTATCACAA	120
TCAATACTTC TCACATTGAG TACCANACTG ACAAACGTCA CTANGCTCAC GTCGNGTCCC	180
CAGNATCCCG CTGACTACGT TAAAAACATG ATCACTGGTG CTGCTCAAAT GGACGGCGGT	240
ATCTTAGTAG TATCTGCTGC TGACGGTCCA ATGCCACAAA CTCGTGAACA CATTCTTTTA	300
TCACGTAACG TTGGTGTACC AGCATTAGTA GTATTCTTAA ACAAAGTTGA CATGGTTGAC	360
GATGAAGAAT TATTAGAATT AGTAGAAATG GAAGTTCGTG ACTTATTAAG CGAATATGAC	420
TTCCCAGGTG ACGATGTACC TGTAATCGCT GGTTCAGCAT TAAAAGCTTT AGAAGGCGAT	480
GCTCAATACG AAGAAAAAT CTTAGAATTA ATGGAAGCTG TAGATACTTA CATTCCACTC	540
CAGACGTGAT CCTGACAAAC CATCAAGATG CCAGTGAGAC GTATCTCAAC ACNGTCGGGG	600
TCTGTTGGTA CAGGCCCGTT GACGTGGGCA ATCAAGTGGT GAGGAGGTGG GATCAC	656

(2) INFORMATION FOR SEQ ID NO:871:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 768 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:871:

ACCTTAAGTT TGAGTTCCCN AATAAAATAA AAAATAATAA ATTTGNAGAA TAAATATGAC	60
ACAATTTACA AGCCTGATAA ATCTGTGTAA CGTCAATTAC CTGTAACATT TTATTTTCATC	120
AATTTTACC GTTTGGCGTA CTTGAAAATT TTGATAAAAG GGGTTCCATT ATGATTAATG	180

AGCAAAGATT	ACTTAATACG	TTTTTAGAAC	TTGTACAAAT	CGATTCTGAG	ACAGGGAATG	240
AATCAACAAT	CCAACCTATT	TTAAAAGAAA	AATTCATAGC	ATTAGGGTTA	AGATGTTAAA	300
GAAGATGAAG	CGCCTAAACA	TCCTAAATTA	GGTGCCAATA	ATCTAGTGTG	TACAATGAAT	360
AGTACTATCG	AAGAAGGCGA	AGTACCTAAA	TTATATTTGA	CGAGCCATAT	GGATACTGTT	420
GTACCCGAAT	TCGCAATTAA	TGTAAAGCCA	ATTGTAAAAG	ATGNCGGCTA	CATATACTCT	480
GATGGTACGA	CTATTCTAGG	TGCAGATGAT	AAAGCAGGAT	TAGCANCGAT	GCTTGAAGTT	540
TTGCAAGTGA	TAAAGGANCA	ACAAATCCCA	CATGGACAAA	TTCAATTTGT	GATTACTGTT	600
GGGGAAGAAT	CAGGTTTAAT	TGGTGCTAAA	GAATTAAATT	CAGAGTTGTT	GGACGCTCGT	660
GACTTTGGTT	ATGCTATTGA	TGCAAGTGCT	GATGTCGGTA	CTACGGTTGT	AGGTGCACCG	720
ACGCAATGT	TAATTTCAGC	TAAAATTATT	GGCAAAACAG	CTCGTGCC		768

(2) INFORMATION FOR SEQ ID NO:872:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:872:

CAAGGTATAA	ATGAATCAGT	TGTTGGTAAG	GCACTTCTTA	AATAGGCAAC	AACGCGATGA	60
TATTTTCATT	GGTACAAAAG	TAGGCAATCG	TTTACAAAA	GATGGCAGTA	CAACATGGGA	120
TCCGAGTAAA	TCCTATATTA	AAGAGGCAGT	TAAAGGTTCA	CTAAAGCGTT	TAGGTATCGA	180
TCATATCGAT	TTATATCAAC	TTCATGGCGG	AACCATTGAT	GACCCATTAG	ACGAAACAAT	240
AAGCGCATGT	GATGAATTGA	AACAAGAAGG	AATTATACGT	GCTTACGGTA	TTTCTTCTAT	300
TCGCCCCAAT	GTAATTGATT	ATTATTTAAA	ACATAGTCAA	ATCGAAACGA	TAATGTCTCA	360
ATTCAATTTG	ATTGATAATC	GTCCAGAATC	ATTATTAGAT	GCAATTCACA	ACAATGATGT	420
TAAAGTATTG	GCAAGAGGAC	CTGTGTCTAA	AGGATTATTA	ACTTCAAACA	GTGGTTAATG	480
TGCTCGACAA	TAAATTTAAA	GATGGGATTT	TTGG			514

(2) INFORMATION FOR SEQ ID NO:873:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 583 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:873:

GGCACGAGCT	CGTGCCGCGA	ATTATACGTA	AAGAGCAACC	TGACGCTTTA	CTTCCAACCT	60
TAGGGTGGTC	AAACAGGTTT	AAACATGGCG	ATTCAACTAC	ACGAAAGTGG	TGTGCTTCAA	120
GATAATAACG	TCCAATTATT	AGGAACTGAG	CTAACATCAA	TTCAACAAGC	AGAAGACCGT	180
GAAATGTTTA	GAACATTAAT	GAATGATTTA	AACGTTCCCTG	TACCAGAGAG	TGACATTGTA	240
AATACAGTAG	AGCAAGCCTT	TAAATTCAAA	GAGCAAGTGG	GATACCCGCT	AATTGTTAGA	300
CCGGCATTTA	CGATGGGTGG	GTACCGGAGG	CGGTATTTGG	TCATAATGAT	GAAGAATTAC	360
ATGAAATCCG	TCTCAAATGG	TCTTCCATTA	TAGNTCCAGN	AACGCAATGT	TTATTAGAAA	420
ATCTTATCGC	AGGGTTTMTA	AAGAAATCGG	AATTACGAAN	GTAATGCGGT	TGATAAAAAC	480
GATAATGCCA	CCGTTGTATG	TAACATGGAA	ATATGGATCC	AGTGGTATTC	ATACTGCGAT	540
CAATGTGGTG	GTCCTAGTCA	AACATTATCA	GATGTGATAT	CAA		583

(2) INFORMATION FOR SEQ ID NO:874:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:874:

CTGATAAGCA	TGAGGATATA	AGTGCACGAG	NACNAAATAT	GAAGATGAAT	TTTAAAGTCA	60
AGATGAATTA	AAATGGTTTA	CTAAATCTAA	TAGAACGCTA	AAATCAAAAG	AAGTTCAGAA	120
AATTGNGNCC	CATAGAGCAA	AAGGAATTAA	AATGTATATT	TGTGNACAGA	AAAAAGATGA	180
TGATGGTATA	TATTINTATT	ATTTAGGAAC	TGCTGGATAT	ATAGAAGGNT	CAGAGAAGCA	240
AGATAAAATG	CCGAATGGCT	CAAACGTAGT	AACGATGGAT	CTAGCACTCG	ATAAAGCTGT	300
AAGAGATGAT	ATATATCGCT	ATATAACAAA	TTAATGGNAA	CCCCGAAAAA	ATGAATTGTT	360
AGTAAAGATG	TATTTAAACA	TCAATTGTAA	TAAGTAAAGA	CATTGAAGTT	TCAGCCGTTA	420
TTATTTTAAA	TATAAGCGCA	ATTCTCTTAA	TTAATAGTTG	GCTAG		465

(2) INFORMATION FOR SEQ ID NO:875:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 544 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:875:

ATGGGTGGAA CCACTAAGAT TCATTTCTTG GCGAATTTGC GGAAGCAAGA AGGTTTCAAA	60
ATAATACTAT GACAAAGATA GTGGTAANAA GCNTTGATCC TAGGTGTTAC CTGTCCGTTG	120
TTGATGGAAA AAAGAACACA TCGTATTTTC ATGATTGGGC AAAGAGGTAT TTTAGAAATA	180
CCTCACTCAA GAGGCGTTCC TTTTATCATG AGTGACACAG CTGGTAGAGA TAAACCTTTA	240
CCAATGAGGC CTGATAAACT TAAGAATCTT GGGATGTTAA CAGAGCCAGG TCTTTACTAT	300
TTATACACTG ATCATACAGC TCAAATCGAT GATTTCCCAT TNCCAAGAGA ATGGCGTGAT	360
GCAGCTTGGT TCTTGGAAGT TAAGCCACCA CAAACTGGCG GTGATGTAAT TCAGATATTG	420
ACGCGTAATA GTTAGGCAAG GAATATGATG ACTTTTGAAA GGGTCCTCTC TGAAGAAGT	480
GGAGACATTT CGGACTGGAA TTATGTGCCT ATAAATAGTG GTAAATGGGA GAGAGTCTCG	540
TGCC	544

(2) INFORMATION FOR SEQ ID NO:876:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 805 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:876:

GGAAGCAAGG ANCCNAATCT TGATGCTGCC AAAATACCAA ACAAGTGATG TNNCCAACAA	60
GCTAAAAGAC AATGGTNTTT GCTGCAATTA ATCCAAGTGC AAGCTGCCAC CNACTAAGAA	120
ATCGGATGCT AAAGCGGAAA TCGCTCCAAA AANCAAGTGA ACGTAAACT GCAATTGAAG	180
CAATGAATGA TTCGACTACT GAAGAACAAC AAGCTGCAAA AGATAAAGTT GATCAAGCAG	240
TAGTTACTGC AAACGCTGAT ATAGATAATG CTACAGCAA TACAGATGTA GATAATGCAA	300
AAACTACTAA TGAAGCGACA AGAGCTGCAA TTACGCCAGA TGCAAATGTT AAACCAGCAG	360
CAAAACAAGC ANTTGCAGAT AAAGTACAAG CTCAAGAAAC AGCAATTGAT GCTAATAACG	420
GCTCAACAAC AGAAGAAAAA GAAGCTGCTA AACAACAAGT TCAATCTGAA AAAACGGCTG	480
CTGATGCAGC AATAGATGCA GCTCATTCAA ATGTGGAAGT TGAAGCGGCT AAAAAATGAG	540
AAATTGCTAA AATTGAAGCG ATTCAGCCAG CAACAACATC TAAAGATAAT GCGACACAAG	600
CAATTGCTAC GAAAGCGAAT GAACGTAAAA CAGCACTCGC TCAAACGCAA GATATTACTG	660
CTGAAGAAAT TGCAGCGGCT AATGCGGACG TAGATAATGC TGTGACACAA AGCAAATAGC	720
AACATTGAGG CTGCTAATAG TCAAAATGAT GTCGGACCAC GCGAAAACGA CAGGTGAAAC	780
TAGTATTGAT CAAGGTACAC CACAG	805

(2) INFORMATION FOR SEQ ID NO:877:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:877:

```

TTGGTGCACC ACCTCAAAAC TTTGGTACCA TTGATGCATT GTACATTAAT TGCGCCAAGT      60
TTTTGTAAAT GCCACCAATG ATTCAGGTAA TAATTGTCCC AAAAGCAGCA GTTACAATTA      120
AATCTACATC TAATTGAANC AATTGTTCTA ATTCTTCTGA TCCACTTAAT TTTTCAGGCT      180
GATATACAGG TAAATCATAT TTCATTNCAA CTTTTTAAAC TGGTGGTGGT GTCATAACAC      240
GTTTACGTCC AACAGGTCGA TCTGGTTGCG TTACGACTGC AATGACATCA TGTTCTGCAA      300
TAAGCATTTC TAAAACAGTT GTTGAAAAGG CACGAGTACC CATAAATATT ATTTTAGTCA      360
TTTATAAAAT ATGCCTCCAC TTCCTTATCT GTTAAATATC GGTCCGCACG TTCNGTAAAA      420
GGGAGACCGT TCATTTGATC TATAATATGC AAAATCATTC TTGCTACATC TTCATGTGCA      480
GTTAGTTCAA CTTTGTTCCTC ATTGACGTCA TAACTTTCTGA CAACTATCAT TTTACTTCTT      540
GTCACTTCGC CGTAAACATC TGGCAATGTA ATTGAACCTT CTAAGTCTGT TATTGTTTCA      600
TTTGATTGAC TAATAATTTT CGGATTAACA AGTTGGTAAT AATCCTTCCA TTTCCATATT      660
CAATAATTGG CACTTGGCAA TGACTTGATT AATTTGAGGG TGCACATAAG CCAGCAGCTT      720
CTTGGTGCAT ACATTGGTAT CTTCTTAAAT CTTGGTAATA ATCTTTTCTA CGAATCACAA      780
TTGTTTTAAC TTGCTTGCGC TTTTCCGGT TAAATAGGAT GCGATGCTGG GTACTAACTT      840
TTTTAATCGC CAATACTCTT ACTCCTCAAT AAATCAATCA ACTATATACC G      891

```

(2) INFORMATION FOR SEQ ID NO:878:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 611 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:878:

```

ACCAANTTGG GCTAGGTGTN CCTGNTAATC CCGATAAATC TATTAATGAG TGGTANTTTT      60
NTTTTCAATA GAGNTNANCC NTTGACTCTT AGGACTTTTA AATGTAGACA GTTCATCAAT      120
TACAACCATA TCAGNATGGC CATTCCTTTT TATATTGATC GCATAACCAT TTAGTANTTT      180
CTTTATIGGT TCCATAGATA TCAGCCTCTG TGTTTAATGC ATCATTTCTT TCTTTAGGTG      240
TTCCTAAGAC TAAAGACACT TTCAGATGAT TTAAATGGTT CCACTTATCA ACTTCATCAA      300

```

CCCATGTATC	TTTAGCAACT	TGTTTAGGTG	CTATGACTAA	CATTTTTTTTA	GTGTCTAAQA	360
ACTGCAATTC	ACTAAATGCT	GTAAGTGTG	ATACTGTTTT	CCCTAGCCCC	ATATCTAAAA	420
ACAAACCGNA	TTTCTCATT	TCAATAACTT	TATCTATTGC	ATACTTTTGA	TAGCTATGTG	480
GTTTGAAGTC	AATCGNCAA	TGTTCCACCC	TACCATTCTG	GATAAAAGTA	TTTACTTGTT	540
CTTTTATTCC	ATAACACATA	TTACTTNATG	GATCTCTTAT	TTNCAAATTG	GCTTATGCAC	600
ATATTTTTGG	G					611

(2) INFORMATION FOR SEQ ID NO:879:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:879:

GGCACGAGCG	ACACATAATT	TTAACACTTT	TCTAATTAAA	AAATCAATAC	TCTTTTTTAT	60
CTTGNGGTTA	GTTTAATAAC	TTTAATTGTT	AATTAAAGCT	TTTCTATGTG	ATCGAATACA	120
NCTTCTACTG	GTGTTTCTCG	GNCAAACATA	TCTACTAATA	CTGTTAGCTT	AAACTTATCT	180
GTNACAATTT	CTTGAAC TNC	ACCAACTTGA	TTCGCAAATG	GACCTGATTT	AATACGAACT	240
TGCTCGCCAA	CTTCGAGTAC	AACATCGATA	GTCTTTTCTT	TAAGANCCAT	NTGGTTTNAG	300
ATGAAGCGAA	CTTCNTCTGG	GAACAATGGA	TGTGGNTTAG	ACCCTGCANC	TGGAGAACCC	360
TACAAAACCA	GTAACGCTGG	TGTATTCTAC	ACATACCATG	ATTCATCTGT	CATGATACTC	420
CACTAAAACA	TTCAGGATGT	TT				442

(2) INFORMATION FOR SEQ ID NO:880:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:880:

GGCACGAGCT	TTCAAATTCT	TCCACATGTT	TGTTGATTCA	TATCCTGGTG	TAGGTTTACC	60
TTCACTTGTA	CTCACAATGT	AATCACCAGC	ATATTTTACA	ATTTCTTCTT	GTTTCACFTC	120
AGCCCAACCT	GCTTTTGGAG	TTAACTTTTG	GTGCTCTGGN	TGTATTTACA	AACCAAATGC	180

TTGATATAAT ACTTCTCCAC CACGACCCCA GTTATCGCCG TAAGTGTATA ATTTTATC	240
AAATTCATCA AACAAATGACA CTGGTGTATC TTGTCCAATT GCTTTTTTAA TTTCTTTACC	300
GTCTTTAGGA GTTGTTCCTT CCCAATCTNT CTTCCAAGCT TTTACTTTAT CTTCTTNACC	360
AACAATTTTC CCTAACATCT CTGGTTGCTC TAAATATTTA TGCTTATTAT AGACAACAAC	420
TACTGTTGGG TGGTACTTTG TGATATTTTT TATATCTTGG CAGGAGAGTA TACAATAATT	480
AATCTTGCTT CTCTTTAGCA ACTT	504

(2) INFORMATION FOR SEQ ID NO:881:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:881:

GGCAGGAGCT AGTTTGGTAT CGGCAATTTT TCAAGGATAC AGACCAGGTG ATTTTGAATC	60
AATAACTGTA ACCGTAGATG CAGATAAACC GTCATCACCT TGTGGTGCAT GTCGTCAAGT	120
TTTAAAGGAA TTATGTGATG ATGATATGCC TGTGTATATG ACAAATCATA AAGGAGATAT	180
GGTTATGATG ACAGNCGCAG AGTTACTACC ATTTGGATTT TCAGGAAAGG ATTTAGAATA	240
AATGACAGAA CATAAATCAG GATTTGTTTC AATTATAGGT AGACCAAATG TAGGGAAGTC	300
AACATTTGTT AATAGAGTGA TTGGCCATAA AATAGCAATC ATGTCCGATA AAGCTCAAAC	360
AACTAGAAAT AAAATTCAAG GTGTTATGAC AAGAGATGAC GCGCAAATTA TATTCAATGA	420
TACGCCAGGT ATTCATAAAC CTAAACACAA ATTAGGTGAT TATACTGATG AAAGTCGCTT	480
AAAATACATA TCTGAAATAG ATGCAATCAT GGTTTATGGC TAATTGCAAT GAGAAATTGG	540

(2) INFORMATION FOR SEQ ID NO:882:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:882:

GGCAGGAGCG TAAAATAAAT TGAGTGGATG CGTTTATATG GCGAAACAAA AAAAGTTTAT	60
GAAGATTTAT GAGGCGTTGA AAGAAGATAT ATTAAACGGG CAGATTCAAT ATGGTGAACA	120

```

AATTCCGTCT GAACATGATT TGGTGCAATT GTACCAGTCA TCTCGAGAGA CCGNGCGTAA 180
GGCATTAGAT TNGTNGGCAT TAGACGGCAT GATTCAAAAAG ATTCATGGTA AAGGGTCACT 240
TGTCATTTAT CAGGAGGTTA CAGAGTTTCC ATTTTCTGAA CTTGTTAGTT TTAANGAAAT 300
GCAAGAAGAA ATGGGCGTCG CATATTTAAC TGAAGTTGTT GTGAATGAGG TTGTTGAAGC 360
GCATGAAGTT CCAGAAGTTC AACATGCTTT AAACATCAAT TCTAGGTGAN TCGCTCATT 420
ATATTGGNTA GGAACTCGGG CGACTTAACC AACAT 455

```

(2) INFORMATION FOR SEQ ID NO:883:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:883:

```

GGCACGAGCT TCACTCATGG CAGGGCTCGC ACCAATACTT AATAAACCAT TCGCTGTAAA 60
ATTTTAACT ACATCGTTTG TATAACAAAT TGTTAATGGG TTTTCAATAC GTATTTTATT 120
TAGATAATTC ATCGTCTAAT CCCTCTTTCT TTAAATATGC AAAATGATTC ACTGGTCCTC 180
TACCACGGNC GATTTCAGGT GTATATTGTA TACTCATTGA AATAAACTTT TTAGCCTTGT 240
GTACAGCCTC AAATAATGGT CTACCTTTTG CAAGTTCCTGC CGTTATAACT GCTGAAAATG 300
TACACCTGT TCCATGCGTA TGTTTTGTTT TAAATCGTTC ATTTTCAAAT GTTTGAACAA 360
CTTCGNTAGT AAATAAATAA TCTTTTGCTA TATCTAGGAT CATTTGAATG ACCGCCTTTA 420
ATGATGATAC CTTTACTACC AATCTCATTA ATAAAGATGC GGGCAGGCTG CATAATTT 478

```

(2) INFORMATION FOR SEQ ID NO:884:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 572 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:884:

```

CCACTTCATC GCACAATAAT ACACGGCACG AGTCGCCTAC GAGCGTTGAC GAGATCTTTT 60
CAATATCAAT TTCGGATAAA AGTTTTCCAT CGTCCATTGT CCTTTACAAT CACAAACAAC 120
GGACGGACGA AGTTGTTTAA TAAATCATTA CCATATTCTG TATGACGGTA CTTCTGGATG 180

```


GAATTGCACA CCATAAATGC GACGTTTCTT ATCTTCAATT GCTGCATAGT CTGTGCTTGG	240
GCTATCAGCG ATAACCTTCAA ANCCTTCTGG AATTTCAATA ACTTTATCAG AATGACTCAT	300
CCAAACAGTT TGTTCTGCTG GTAAGCCAGC GAATAACTCA TCTGACTTCG CATTAAATGAT	360
TGCTTTACCG TATTCACGTT CATTGGCAGC NTCAACTTTA CCACCTAATA ATTTAGTAGT	420
TAATTGCATG CCGTAACAAA TACCAAGTAC TGGAAATTCCT AAATTATATA TTTCCGGATC	480
AATGTAAATG AACCTCTTCA TAAACTGATT TGCACACTGA TAAGATGATA CCTGTGGGTT	540
CATTTCTTAT CTCTCAATTG AATTCAGATC GG	572

(2) INFORMATION FOR SEQ ID NO:885:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:885:

GGCNCGAGCG ATAATTTTAA AAATCCATGT ATAACCCCCC TCTTATAACC ATTTTAAGGC	60
NGGTGATGAA ATGGAGATTA TAGTTNATGA AACTTAGTG CTTAAAGAAA AAGAAAGGCT	120
GCAAGTATTA TATAAAGACA TACCTAGCAA TAAATTAAAA GTAGTTGATG GTTTAATTAT	180
TCAAGCAGCA AGGCTACGTG TAATGCTTGA TTACATGTGG GAAGACATAA AAGAAAAGG	240
TGACTATGAT TTATTTACTC AATCTGAAAA GGC GCCACCA TATGAAAGGG AAAGACCAGT	300
AGGCAACTA TTTANTGCTA GAGATGCTGC ATATCAAAAA ATAATCAAAC AATTATCGGA	360
TTTATTGGCC GNNGAGAAAG AAGACACAGA AACGCCATCT GATGATTACC TATGATTAGT	420
AATAAATACG TGGTGAATAT ATTAATTGTG G	451

(2) INFORMATION FOR SEQ ID NO:886:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:886:

GGCAGGAGCG TAAACCGATG TGCATACCAC CAGCCGTGAA GCCTTGAGGT GTACTGATAT	60
CGCCATGTTT AATAATTGAA AAGTTATATT GTTGTGATGT CGTTTCTTGA TGTTCATTC	120

TAACACCCCT TATGGATAAA CTGGTGATTG ATTTAGGCCA GTCGTTACTT CAAAATCATA	180
TAATATATTT AAATTTTGAA TGGCTTGACC ACTTGCGCCT TTGACAAGGT TATCAATCAC	240
TGATACTAAA ATTGCTGTTT GTGTTGTTTC ATCTACATAG ATACCGATAT CGCAGTAGTT	300
ACTACCGAGT ACTTCTTTTG TGGTTGGAAA AGTCCCAATA TCTCTAATTC TGACAAATGG	360
CTGATTAGCA TAATAAGAGG TCATTAATTT ATGTAATGAT TCAGTCGTTT TTCAGATGAA	420
ATTTGACATA AATTGTTGAT AAATACCTCG TGTCATGGTA CGAGATGTGG GNGTAATATG	480
ACTGATACAT CTTGACCGCA ATGATAGATA ATATTGTTCG A	521

(2) INFORMATION FOR SEQ ID NO:887:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:887:

GGGACGAGCG GACGAACATT AGAAGATGCA TTTGTAATTC TTGATGAGGC GCAGAATACG	60
ACACATGCGC AAATGAAAAT GTTTTACAA GACTAGGTTT TGGCTCAAAA ATGGTAGTTA	120
CTGGTGACCA AACTCAAATC GATTTACCTA AAGGTGTTAA AAGTGGAATT AAGGAAGCGG	180
NCAGTAGGTT ACACAACGTT AAAGGTATAA GTATATTGAA ATTAGCTCAG AGCGATGTAG	240
NAAGACATCC ATTGGTAAGT AAGNTCATTG AACATTATGA AGGAGAGAAT TAAATGTCTA	300
CGATAGATTT TAGCGATCAC ACAGGCTTAG TTAAAGATGC GTGGTATAAA CAAATTGAAG	360
ATTTATTAGA ATTTGCTAAA AAAGAAGAGC ATATAGAAGA CGATGCTGAG CTCTCTGTTA	420
CATGTGTGGA TTCACAAGAA ATACAAGANC TTAATCGAAC ATATTAGAGA TAAAGATAAA	480
GTCACAGATC GTCTCTCATT TGCTTTAGAA GAAGATGAGC CAGAGATTGA T	531

(2) INFORMATION FOR SEQ ID NO:888:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1149 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:888:

ATCTACATTT CGGAAGTTGG TATGTGTC TT TTTATTAAA TTAAAGGATG CTACGGTTAG	60
---	----

TTCAAATGAT	TATGAATGAC	ATTTAATGGT	ATCATCCAGC	CTCAGTACTT	GGAGATAACA	120
TTTTGGCGGT	GAGACATAAA	TCATATTTTT	ACAAAACCTTA	TTTCGTCGTC	TCCCCAATAA	180
AGATAAAGTA	TTTCTTTATT	GTGGTGTAAAC	TTCTCCACGT	TGTATTTTAC	TATCCAAATT	240
TTGTTTCATA	TTTTCAAACA	ACTCTTGAAA	TCTAACCTCA	TCTTGATCAG	AATAACCTTT	300
AAAAATAACT	GAATCTATAT	TTTCTTCCGN	TAAAATAATA	AATTTTCATCT	TCCACAACAA	360
CAATCGGATA	TTTACATGCA	GAATAGGCAA	ACATATTCTT	TGGATTTTCA	ATTTCTACAA	420
TTGGGCCTCT	ATTAATAATC	AATAACTTTN	GCGAACCCCTC	TTTTAAATAA	ATAATGCTCC	480
CTATTGTTTC	CATTTATTTT	CCTCCTTTGT	CACCGTCTCA	ATTTCAACAT	TCCTTCGCAT	540
TTCCAAGTCA	ATCATCTCTT	CTTCCGCTTT	ACGAATGNCA	TGTTGAATGT	GCTGTTGCTG	600
CTCGTATAAC	GCTTCCGNTG	AACGTCGTTT	CGAAAATGA	AATNCATCGC	GGAACGTGTC	660
CATACGACTA	GCCATATTGC	TACTATGATA	ACGNCACCT	AAATGTTGAT	ATAATTGTTT	720
TATCGAATGA	TTAAGCTCAT	CACTTTCGTC	TATCAAAGCT	TTAACCTCTC	GCTTNACATC	780
ATATAAGTCA	TCCATNTGCT	TATGTTTCGC	TGTGATCATT	TTATTGATTC	CATCAAGTTT	840
ATTCGACATC	ATTTCANCA	GGTTTAATTT	TTACCAATTT	CATTACCAAT	CATTACGTCT	900
TGTGTGATTA	ATTCTTCGAC	AACTTNGTGT	ATACTATCGC	TCGCATTTCT	TATTGCTTCA	960
AGCAACAGAT	TGATCCTTAC	TAATCAAATC	GTCTTATCAC	ACTATGAGNA	TTATTATTTT	1020
CACTTACTGG	TGACTTNCA	ACTTTATCCN	GGTTCGACAC	ATTATAAAAT	GTTTCAACGG	1080
CAATTTTATA	GATGATGATG	ACTATAGTCT	TGAAATATCA	CTTTGACTGT	ACTCAATATT	1140
TACACCCTC						1149

(2) INFORMATION FOR SEQ ID NO:889:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2635 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:889:

AAATTTTAAA	TAAACTTTCC	TGCTGGAAT	TTTAGGGGAT	TTAATCATTG	GCNGGATTGC	60
AGGGAATTTA	AAAATTTTAA	GCCCCACTT	ATGGAATTTA	TTATTGCATA	TTTTATCAAG	120
TGGCAAGTTG	GAAGCATTA	GTACAATGCA	CCACCTACTT	CCACTTGTA	GTATTTTAA	180
AAGAGCCTGC	CAAAAATTTG	TATTTTTAAA	CCAATGCGAT	TAACCCATGG	TGTATTCACA	240
CCGCTTGGTG	CAAGATCCAA	GCTGCAAAAG	CTGGTCAATC	AATTTTATAC	ACAATTGAAT	300
CTAACCCCTGG	ACCAGGTTTA	GGTATCTTAC	TTGCTTATAT	GATTTTGGGA	AAAGGCACTG	360
CAAAAGCAAC	GTCATATGGT	GCTGGAATTA	TCCACTTCTT	AGGTGGTATT	CATGAAATTT	420
ATTTCCCAT	TGTATTAATG	CGTCCTTTAT	TATTTATCGC	TGTTATTTTA	GGTGAATGA	480
CTGGTGTTGC	AACTTATCAA	GCAACAGGAT	TTGGATTTAA	AAGTCCCGCG	TCACCAGGTT	540
CATTTATAGT	TTACTGTTTA	AATGCACCTA	GAGGTGAATT	CTTGACATG	TTGCTCGGTG	600
TCTTCCTTGC	TGCACTTGTA	TCATTCGTTG	TAGCTGCTTT	AATTATGAAG	TTCACTAGAG	660

AACCAAAGCA	GGATTTAGAA	GCTGCGACAG	CTCAAATGGA	AAATACTAAA	GGGAAAAAAT	720
CAAGCGTTGC	TTCTAAGTTA	GTATCTTCTG	ATAAAAATGT	TAATACAGAA	GAAAATGCTA	780
GTGGTAATGT	TAGTGAAACA	TCTTCATCAG	ATGATGATCC	TGAAGCGCTA	TTGGATAATT	840
ACAACACTGA	AGATGTTGAT	GCACACAATT	ACAATAATAT	AAATCATGTT	ATTTTGGCT	900
GCGATGCGGG	TATGGGTTCT	AGTGCAATGG	GTGCAAGCAT	GTTACGTAAT	AAATTTAAAA	960
AGGCGGGCAT	TAATGATATT	ACAGGTTACA	AATACTGCGA	TTAATCAATT	GGCAAAAGAT	1020
GCTCAATTAG	GTATCACTCA	AGAAAAAACT	AACTGATCCG	TGCTATTAAA	CAACACAAAA	1080
ATGCCATCCA	TATTTCAAGT	GGATTAATTT	CCTTAATTCA	CCAAGATATG	AAGGAACTTT	1140
TAAATAATCT	TAAAAAAGA	TGATCAAGCA	TAATAATTAA	ATAAATTAAA	AAATGGAGGA	1200
TACCGCCATG	TTATTGAGTA	CACGTGAAAA	AGAAATGATA	GCCCTATTGA	TTAAGTACCA	1260
CAGTCAATAT	ATCACTATAC	ACGACATTGC	TCAGCAACTT	GCGGTGTCCT	CTCGTACTAT	1320
TCACCGTGAA	TTAAAAGGTG	TTGAAGCATA	TTTAACTTCA	TTTTCATTAA	CTTTAGAACG	1380
CGCAAACAAA	AAAGGGCTAC	GCATTGCTGG	CGCAGATTCT	GATTTAAACG	ATTTGAAGCA	1440
ATCGATTGCA	CAACATCAAA	CCATTGACTT	ATCTGTTGAA	GAGCAGAAAG	TAATTATTAT	1500
ATACGCTTTG	ATACAAGCCA	AGGAGCCAGT	TAAACAATAT	AGTTTAGCGC	AAGAAATTGG	1560
CGTTTCTGTC	CAGACTTTAG	CAAAGATGTT	AGATGATTTA	GAGCTTGATT	TAAATAAGTA	1620
CCAACATCT	TTATCTCGAA	AGCGTGGCGA	AGGCATTTAC	TTGGTAGGTA	CTGAATCAAA	1680
GAAACGTGAA	TTTTTAAGTC	AATTAATGGT	GAATAACTTA	AATAGTACTA	GCGTTTATTC	1740
AAGTAATTGA	AAATCATTTN	GTCTTTCATT	CATTAAATCA	AATCCACAAA	GACTTTGT	1800
GACTTAGAGC	GCATTTTAA	TGTTGAAAGA	CTATTAATGG	ACTACCTAAG	TGCCTTACCC	1860
TACCAACTTA	CCGAATCAAG	TTATTTAACT	TTAACTGTCC	CATATCGTGC	TATCCCATT	1920
CACGTATAAA	AAATGGAGAG	TATGTCGCAT	TAAACGATGA	TATTTATGAT	TCTGTACAAA	1980
ACACATTTGA	ACACAAAGTA	GCAAGCGAAC	TTGCTGATAA	ACTTGGTCAA	ATATATGACG	2040
TCACGTTTAA	TCAGGCAGAA	ATTGCTTTCA	TTACTATCCC	ATTTACGTGG	AGCTAAACGA	2100
AAAAATCTTA	ATGATACATC	ATTAAATAAT	CGTTGTGAAG	AAAACAAAAT	TAAAGCGTTT	2160
GTTAACAAAG	TAGAAATGAT	TTCCGGTATG	ACATTTGCAG	ATTTGGATAC	TTTAGTAGAT	2220
GGACTGACGC	TACACCTTAA	TCCTGCAATC	AATCGTTTGC	AAGCTAATAT	CGAGACCTAT	2280
AATCCGTTAA	CAGACATGAT	TAAGTTCAAA	TATCCAAGAC	TATTTGAAAA	TGTAAGATTA	2340
GCTTTAAATG	ATTGTTGGCC	TGATTTGATT	TTTCCAGAGA	GTGAAATTGC	TTTTATAGTT	2400
TTACACTTTG	GTGGCTCGAT	TAAAAACCAA	GGTAATCGAT	TTTTAAACAT	ATTAGTCGNT	2460
TGNAGCAGTG	GTATGGGAAC	TAGTCGTCTA	TTATCAACTC	GTCTAGAGCA	AGTTTTTAGT	2520
GAGATTGAGC	GTATTACACA	AGCATCAGTC	AGCGATTTGA	AGTCACTAGA	TTTAAGTCAA	2580
TATGATGGCA	TTATTTCTAC	TGTGAATTTA	GACATCGACT	CCCCCTATTT	AACGG	2635

(2) INFORMATION FOR SEQ ID NO:890:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 722 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:890:

```

CTTAAGGAAC GTACAGACGG CTAAAAAGCC TTAAAAAAGG TTTTAAAGGG GTTTGTAGAC    60
AAGGTAAAGG ATAAAACAGC ACAGTATTCC GAAGTAAGGT GTGTTTAGTG CTAAGTGGTT    120
AAGCACGAGC TTGTGCCTCC TCTATCGTTG ATCTTTGTTG TGACTTTGTC ACCTTTAGAT    180
CTCGAAGTAA CTTTCATAAT AATTTGTGTG ACATAGCCAG TACAAATAAG TAATAGTATT    240
GTTGAGACGA TTATTAGTCC AATGATTAAA AATGGTGCTT GGCTAATGAC ACCTAAAGAG    300
TTAACAACCTG AGATACCGGC TGGTACGAAG AGTAAGCCAA TGTATTGTTG TAGTGTGCGT    360
CCTACTTTTT CGACTTCGCC TAACTTAACA GCACCAGTAC ATAATAATAC AAATAATAAT    420
ACTAAACCGA TTAGTGATGC AGGCATAGGA ATTGGCATAA ATGANTCAAT TATTTGCGAT    480
ACAAAGAGTA CTAAAGCAAT TACAATGACT TGGNTGAAAA AAGTGTGCTG GTTGTGGATG    540
CGTCTTTGTG GTGTTTCACG ACCATTGNCT CCTACGTGTG GATTTANCTA AAGTATAGAT    600
GGCTCACTTC GATGTGCGTG ATTTTGTAGC CGAAATACAA AATATCATAG GTAAAATGCA    660
TAAAAAAAAG GATTACTGTT AAAGTAATCC TATCGACGCT TTAAAATCTT TCATAAATGA    720
AC                                                                    722

```

(2) INFORMATION FOR SEQ ID NO:891:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2632 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:891:

```

CCTCCNACAA AANCAACTTA ACTGTTGTAT TGATGAAGGG AGATTTTTGC GTAAAATAAT    60
TTGTTAAATTT TCGAACCACC AACGACCAAT CAATTGCTAT GGTCAATGCC NAAACCCAAA    120
TCAATATTAA CCTTGTAAGA CTGGTTACN TAGTAAGGGA ATATTTCCCT ATGAAATAAC    180
TAGATGTCAC AATCTTGGAT AAATTTTAAT TCTTCAAGNT TGTGGTCTT TTCTTAAGTG    240
AATCTTCTAA TTCAAGAATG CCATACCTGC ACCTAGAGCT AATTCAGCAT ATGGTAAATC    300
GTCATTATG TGACATACCA GTATCTGGTA AAGTTTTAGC TTGTGTTTA GGCTTATTAA    360
CTTTTCCTTG TTGGTCTGAT TTGCAATTTG CTTTGTTTTC TTCAGGCTTA GTTACATTAA    420
GCATATCTTG ATGCATACTA TGACTACCAT TTGAAACTGT TGCTGGAGAT GCATTGGCAC    480
CGTCGTTTTG CGTAGCTTTA TTGTTTGCAG CTGAACCAAC TGATTTTTGC GTATCATTAG    540
TTTGCATATC TTTAGCTTTA TTGTTTNCAA CTGGGCCAAC TGATTTTTGC GTATCATTAG    600
TATCTGCTGT TGCCCGNATC ATCTNNTTGC CTAACATNAG NTGAAATCAT TTTATCTTTT    660
GCNTCAAGAA GATGCAGATG TTGATGGTTT ATCCGAAACT TCAGTATCAG CTTTGCTTGG    720
CGANTTANCT GCTTCGTTAG ATGCAACGTT AGTTTCAGAC TTAAGTTGTC CTGCATCAGN    780
TTGATTGTG GTACTTTCTT CTTTATCTTT TGATGTATTA GAAGGTACAN TTGGTTCTGT    840

```

TATGTCTGCT	GAAGGCAATG	TTTCAGTTGT	TGANTCAACC	ATACNTTGAA	TTGTTGAATC	900
TCTACCATCT	TTTTCTGCCT	TAGCTTTANT	TTCAGANTTT	GGTTGTGCAA	CCTTGCCATT	960
AGTTGATTGA	GANTCAGCAC	TATTANTTAC	TTCAGCATTT	TGTTTTGAAT	CATTTACAGA	1020
TGCATTATCT	TTACTATCAG	CAGATGATGC	TGCTTCTGTG	CTCGCAGTTG	TTGGAGCCGG	1080
TGCTGNNGAT	CCGGGTCGNG	CATTCTCGNT	TGTTGCTGTA	GGTGTAATAT	TGTTAATTGT	1140
TGTGCTTTCT	GCTGGCGNTG	CATTATCTGT	TTCTGTTACA	GGTTTATCAG	TTGTGCCGTT	1200
ATTAGTTGAT	TCTACTTCTG	GTTTACTAGT	TACAGCGTTA	TCCATTGTCTG	GACTGTGTGT	1260
TGATGCATCT	GCACTAGAAT	TGTTATTAGC	TTGCGGTTTA	TCCTNTGCAT	CATCAGTTGC	1320
TGATGTTACT	GTTGTNTCAC	CTGTTGNCGC	ATCACTATTA	TTTGNVTGTG	GCGGAGAAGC	1380
GTCTGCTTTG	CCATTATCTG	TCGTCTCAGA	TACGTTAGGN	TGGCCAGTGT	TCTCTGGTGT	1440
NGCAATTAGC	ANTNNGAATT	TGGCTNGNNG	CATCAATNAT	TATCTTGTAC	CATTATTAGT	1500
ATCATTAGCA	TCTGGGATCA	TTCTTGAGGC	ACAATCGCTT	CAATTGCAGG	TATCGTTACA	1560
TTTTGTAAAT	CAGCAACCTC	TGTATTTGTT	TGTGTTTTAT	CTAATTTATC	AGCAAATCTG	1620
TCAAAATATC	TACCTAAATC	TGTACGTGCA	ATTTCTTTTCG	CCGATGCATC	TGCATCTGCA	1680
TTTTTAATTA	TTTCTATTTG	CTTGTTANCC	ACTTCTCTAA	TTGCTTCCAA	AGCATTTTTTC	1740
TAACTACTG	GATTAATACG	TTGTGCTTTA	AGTTGTTCAA	GCGCACTATT	TTTGACAGTA	1800
GCGATTTCTG	CATTTGTAGT	TTGATCAGAA	ATATCTTCAG	TTGCTTTTGA	GAAAATGTCT	1860
TCTAAAGCAG	TCGTAAACGC	TTCTTTTTCT	TCAGTTGTAG	CATCACCGTC	GACATTTACA	1920
CCTGCTTCAA	TCTGGGCTAG	TGCAGTTTCT	AATTCCTCGA	TAGCCTTTTG	TTTTTCTGTT	1980
GAGTCAATTT	GAATGTTATC	AAATGCCTCA	AGTCCTTGAG	CTTTCGCTTT	NTCAACTTCA	2040
GCAGTTGTTG	TTGCATCAGT	AATACCTTGT	TTAGCTTGAT	CTGTAATTTG	TTTAATCATT	2100
GCTAATGCTT	CAGTTTTTTTC	TTCAGCAGTT	AAC TG GTCAC	TATGATCAAT	TGATTTCTTTC	2160
GTATCTTCTG	CTTTAGCTTC	AATAGCTTGG	TTGCTTTTAG	GTTTAACAGT	AGCATCTACT	2220
TGAATAGTAT	CAATTGCTGC	TTTACCTTGT	GTTAATGCAT	CANCAACGTC	ACCATTATCC	2280
ACACCATTAT	TAATGTTTTTC	TAATGCAGTT	TGAACATTTT	GGTCAACTTG	CTTAATTGCT	2340
TGTTGCTTTT	CATCTTGTGT	TGCATTAGTG	TCAGCTGAAA	TATTATTTTT	CTTCTGATCT	2400
GCATAAGCAN	ATAAATCTGN	TGTAGCTGAT	TCTTTTTTAC	CGGTTGGAAN	TGTGTAATCG	2460
TTAATANTAT	CTAAGTCATT	ATGNATNTGN	NCTTCNATGT	CATCTTTAGN	AGNAGCNTGA	2520
GTAACATTTT	GATCCGCAGG	TTGTTTTNAT	TCAGCAAGTT	TTTGTTTCGC	TTCAGCAATT	2580
TCACNTGAAG	TCGATGCGTT	AGAGTTATCC	GCTTCGTTTA	CTTTAGCATT	AG	2632

(2) INFORMATION FOR SEQ ID NO:892:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1933 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:892:

```

ACCCCTTTGN NCGTATTGNA NTCNCNAGCA ATTTTNAATT CCCNAGTTGC AAGAGATTCC 60
AAGCTACCNC CAGATGCNGT AGTTGAAGNN ANACAAGCAG CTGATGCAGA ACCAAATACT 120
GNAATGGTA AACCAAATCA AGCCATTTCA GCAGCAACTA CTAACGCACA AGTTGATGAA 180
GCGAAAGCTA ATGCAGAAGC AGCAATTAAT GCGGTAACAC CAAAAGTTGT TAAGAAACAA 240
GCGGCTAAAG ATGAGATTGA TCAATTACAA GCAACGCAAA CAAATGTTAT CAATAATGAT 300
CAGAACGCTA CAAATGAAGA AAAAGAAGCA GCTATTCAAC AATTAGCAAC AGCAGTTACA 360
GACGCGAAAA ATAATATTAC AGCTGCAACT GATGATAATG GTGTAGATAC AGCGAAAGAC 420
GCTGGAAAGA ATTCAATTCA AAGCACACAA CCAGCAACAG CAGTTAAATC GAATGCGAAA 480
AATGAAGTTG ATCAAGCTGT GACAACCTCA AATCAAGCAA TTGATAATAC AACTGGCGCT 540
ACAACTGAAG AGAAAAATGC AGCAAAAGAT TTAGTTTTAA AAGCTAAAGA AAAAGCGTAT 600
CAAGATATCT TAAATGCACA AACAATAAT GATGTTACGC AAATTAAAGA TCAAGCAGTT 660
GCTGATATTC AAGGTATTAC TGCAGATACA ACAATTAAAG ATGTTGCGAA AGATGAATTA 720
GCAACAAAAG CAAACGAACA AAAAGCGCTT ATTGCACAAA CTGCAGATGC GACTACTGAA 780
GAAAAAGAAC AAGCAAATCA ACAAGTNGAC GCACAATTAA CACAAGGTAA TCAAAATATT 840
GAAATGCAC AGTCAATCGA TGATGTAAAC ACTGCAAAAG GATAATGCAA TTCAAGCAAT 900
TGACCCAATT CAAGCATCAA CAGATGTTAA AACGAATGCA AGAGCAGAAT TGCTAACTGA 960
AATGCAAAAT AAAATAACTG AAATACTTAA TAATAATGAG ACTACTAATG AAGAAAAAGG 1020
TAACGATATT GGCCCAGTTA GAGCAGCATA TGAAGAAGGT TTNNNTANTA TTAATGCAGC 1080
ANCTACTACA GGTGATGTAA CTACTGCTAA AGATACAGCA GGTACAAAAA GTTCAACAAC 1140
TTCATGCAAA TCCTGTTAAG AAACCAGCAG GTAAAAAAGA TTAGNTCAAG CTGCAGCTGA 1200
TAAGAAAACA CAAATAGAAC AAACACCAAA TGCATCACA CAAGAAATTA ATGATGCAAA 1260
ACAAGAAGTT GATACTGAAT TAAATCAAGC GAAAACAAAT GTCGATCAAT CATCAACAAA 1320
TGAATATGTT GATAATGCAG TTAAAGAAGG AAAAGCTAAA ATTAATGCAG TTAAACATT 1380
TAGTGAGTAC AAAAAAGATG CTTTAGCTAA AATTAAAGAT GCATATAATG CTAAAGTAAA 1440
CGAAGCGGAT AACTCTAACG CATCGACTTC AAGTGAAATT GCTGAAGCGA AACAAAAACT 1500
TGCTGAATTA AAACAAACTG CGGATCAAAA TGTTAATCAA GCTACTTCTA AAGATGACAT 1560
TGAAGTTCAA ATTCATAATG ACTTAGATAA TATTAACGAT TACACAATTC CAACAGGTAA 1620
AAAAGAATCA GCTACAACAG ATTTATATGC TTATGCAGAT CAGAAGAAAA ATAATATTTT 1680
AGCTGACACT AATGCAACAC AAGATGAAAA GCAACAAGCA ATTAAGCAAG TTGACCAAAA 1740
TGTTCAAACG GCATTAGAAA ACATTAATAA TGGTGTGGGA TNAATGGTGA CGNGGGAGGG 1800
GATGCATTAA ACACAAAGGG TNAAAGCAGG AAATTGATAC TATTCAAAGT AGGATGCTAC 1860
TGGTTAAACC TAAAGCGGAA CCAAGCTATT GGAGGCTTTA GGGAGGCGGT TCCGGGAGGA 1920
TTCCNATTGG GCC 1933

```

(2) INFORMATION FOR SEQ ID NO:893:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1778 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:893:

AAATTCATAA	TAAAGNCTTT	TGNCATTAAA	GTTNNAAAGA	AGATAAAGAA	NCTGCTNNAA	60
ATTGACGTAT	CNNAAGAAG	TAAAAGAAGT	TTAAATANTC	AAATAATAAA	TCNACAACAC	120
AAGANATTTT	TGAAGAACAA	AAAGGTGAAT	ATCAAAGAAA	GTCAGAGGCA	TTAAAAGAAA	180
GATTTATAAA	CAGACAAAAA	TCTAAAAATG	AGTCTGTGGT	TTCACTAATC	GATGACGAAG	240
ACGACAACGN	AAACGACAGG	CAACTTGTGG	TTTCTGCGCC	ATCAAAGAAA	CCAACAACAC	300
CGACTACATA	TACTGAAACA	ACGACTCAGG	TANCAATGCC	TACAGTTGAG	CGTCAAACCTC	360
AGCAACAAAT	CGTTTACAAA	ACACCCAAAA	CCATTAGCTG	GATTAAATGG	TGAAAGTCAT	420
GATTTACAAA	CAACGCATCA	ATCACCAACA	ACTTCAAATC	ATACGCATAA	TAATGTTGTT	480
GAATTTGAAG	AAACGTCTGC	TTTACCTGGT	AGAAAATCAG	GATCACTGGT	TGGTATAAGT	540
CAAATTGATT	CTTCTCATCT	AACTGAACGT	GAGAAGCGTG	TAATCAAGCG	TGNACACGTT	600
AAGAGAAGCT	CCAAAAGTTA	GTTGATAATT	TATAAAGATA	CACATAGTTA	GAAAAGACCG	660
ATTAAATGCA	CAACAAAAAG	TAAATACCTT	AAGTGAAGGT	CATCAAAAAC	CGTTTAATAA	720
CCCAATCAAT	AAAGTANCCA	TGCCAATAAT	ATTAATGCAT	GGCTGCAAAG	CAAATAATGA	780
GTTTGTCGTA	AAAATACCAA	CATTTAAACT	AGCAATAAAT	AATATCCAAG	TCATCATTTTC	840
ATTGATGCAA	TCTAGTATAG	TCCACATTCT	AAACAGGTGT	GGACTATTAC	TTTTTTCACT	900
TTATATTACC	GAAAAAATTA	TTATGCTTAA	CTATCAATAT	CAATAATTAA	TTTTAAGCTG	960
AAAAACAATA	AAAATGTAA	GACAACGTTT	ACTTCAAGTT	AATTATTATA	CTGAAAATTC	1020
TGGTATATAA	TGCTGTTAGT	GAATATAACA	GGGAAATTAT	ATTGGTTATA	ATATTGAGTC	1080
TATATAAAGG	AGAAATAACA	GATGAAAAAG	AAATTATTAG	TTTTAACTAT	GAGCACGCTA	1140
TTTGCTACAC	AACTTATCAA	TTCAAATCAC	GCTAAAGCAT	CAGTGACAGA	GAGTGTGAC	1200
ACAAAATTTG	TAGTTCCAGA	ATCAGGAATT	AATAAAATTA	TTCCAGCTTA	CGATGAATTT	1260
AAGAATTCGC	CAAAAGTAAA	TGTTAGTAAT	TTAACTGACA	ATAAAAACTT	TGTAGTTTCT	1320
GAAGACAAAT	TGAATAAGAT	TGTAGATTCA	TCGGCAGCTA	GTAAAATTGT	AGATAAAAAC	1380
TTTGCCGTAC	CAGAATCAAA	GTTAGGAAAC	ATTGTACCAG	AGTACAAAGA	AATCAATAAT	1440
CGCGTGAATG	TAGCAACAAA	CAATCCAGCT	TCACAACAAG	TTGATAAGCA	TTTTGTTGCT	1500
AAAGGCCCCAG	AAGTAAATAG	ATTTATTACG	CAAAACAAAG	TAAACCACCA	CTTCATTACT	1560
ACGCAAACCC	ACTACAAGAA	AGTTATTACT	TCATNCAAAA	TCAACACATG	TNCATTAAACA	1620
TGTNNATCAT	GCAAAAAGGAT	TCTTTTAATA	NACACTTTAT	TGTTACACAT	CAGACTCGCC	1680
TAGATATACA	CATCCATCTC	AATCTTTATT	ATCAAGCATC	ATGTGCAGCT	CCTGGATATC	1740
ACGCGCATAA	TTTGGTACAC	AGGGCATGCT	AGCATTA			1778

(2) INFORMATION FOR SEQ ID NO:894:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:894:

TANAATNTCA	CAGNAAAGTN	TAANATATAA	NGATCATTTCA	CATNANCATA	CGAATAAGCC	60
AGGTACATAT	GTTTCTGCAA	TTAATGGTAT	GGAGAAGGAA	ACGCACAAGT	CAAAAANCNC	120
TCACATNATA	TGTATTCTAN	TAANACAAAT	CATCGCGCTA	AAGATNCACC	TCCAGATTNT	180
CACANAGANA	GTNTCACGGA	CTTCAGAGCG	TACCGGCAGN	TNTTNGGGGN	ACAATGAAAC	240
CTNAANNGTT	NGAAAATGGG	CGNTATCCCA	GTAAGTAANC	CTGCAGAANA	TGTTGANTCA	300
GATAAACAAA	ACTATGATAA	NTATGTAGCT	AAGACGCAAA	CGTCTCAAAA	TAAGCAATTA	360
GAACAAGAAA	AACAATTTGA	TAGTGTGGC	AAACAAGGAA	CTGCATCTAA	ATCATCTGAT	420
GAAANTGTAT	CATCAACAAC	AATNTCAATG	CCTAATTATT	CAAANGGTGG	NTAATACTTT	480
CAAAATTGGA	AAT					493

(2) INFORMATION FOR SEQ ID NO:895:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:895:

GAATTCTNAA	ATATCACAGC	AAAGTATAAA	ATATAAAGAT	CATTACACATT	ACCATACGAN	60
TANGCCTGGN	ACATCTGTCTN	CTGCANTCNC	TGGTATNGAG	TCGGCATCGC	ACNCGNCATA	120
CCCTCTTTNN	TATGTATTCT	AATANCACAN	NTCATCGCGC	TATCGTTTCA	NCTCCAGATN	180
ATCACAAAGA	AAGTTTCAAG	ACTTCAGAGG	TACCGCCAGC	TATCTNCGGC	ANAATGANAC	240
CTAANNAGTT	AGAAAATGGT	CGTATCCCTG	TAAGTAAACC	TTCAGAAAAA	GTTGAGTCAG	300
ATAAACAAAA	ATATGATANA	TATGTTGCTA	AGACGCAAAC	GTCTCAAANT	TAANCAATNN	360
GGACAAGGAN	AANCAANN TG	ATNGNGTNNG	CAAACAANGN	ACNGGATCTA	AATCATCTGA	420
TGAANATGTT	TCATCAACAA	CAAAATCAAT	GCCTANTNTT	CAANGGCNGG	TGATNCTATC	480
AAANTGGAAA	TTTNNGGCTC					500

(2) INFORMATION FOR SEQ ID NO:896:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 950 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:896:

```

TTTGAAGCTT GAAGTTAATA CACTTTATCA GTTGTANCGC ACTTTACAAA CGGAATATGA      60
GCCACAATNC GGCAGGCGTT GATGTTTCTG GGAGATGTTG CTTTGTCCGC TATAAGACCA      120
CCCACACATA TTAAAGCAGA TGGTGATGCC GATGTCACTT ATGGAGTAGC AATTGTCGGT      180
GATAAAGTTA CACGTAAAGA ACTTACTATT GAAGCAACTG TCACACCGCT ATGCCCTTGT      240
TCNCAAGANA TAAGTGAGTA TTCAGCGCAC ACCCAACGTG GTGTTGTCAC TGTAAAACA      300
TATATCAATA AAGATCANAA CATAGTTGAT GACTATAAAA ACAAATTTT AGATGCAATG      360
GAAGCTAATG CAAGTTCAAT TCTATACCCT ATTTTAAAAC GTCCTGATGA AAAACGTGTG      420
ACAGAGCGTG CATATGAAAA TCCACGTTTT GTCGAAGACT TAATTCGTTT AATTGCCGCG      480
GACTTAGTTG AATTGATTG GTTAGACGGN TTCGATATCG AATGTCGGAA TGAAGAGTCT      540
ATCCATCAAC ATGATGCTTT CGCTAAATTA AAGTATCGCA AATAATATCA TATTGATTAA      600
TTCAAACGCG TAACATTAGT TGCGCGTNTT TATTATACCT TCTAGAGTTG GATATCTCTT      660
TTNATTAAAT CTTCTCANTT GATGTGCCCG AGAGCATAAA TCAATATCCT AAGCTCTACA      720
AATGATATAT TGGTCGTAGT TGATTGAATA ACTACTATCA TTATAAATAT CAAAATTTGT      780
TGTTTTATAA ATAAACACAT CATCCAGTTA AAAGAAGTAA TTAAATATCA TGTGAAGTTA      840
ATTATAAAAA ATAGATATAA GTGGTGTGGT TAATGAATTA TTTTGTGGT TAATAGTTTA      900
GGTGTTTAAT TTACCTGGAA TGGAAAAAGC AATTATTATC CGTTTAAATT      950

```

(2) INFORMATION FOR SEQ ID NO:897:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:897:

```

GAATTCGGCT AAAAATNACT GAGNTGGTAC GCNNTNTTN GATCATGCGA NGNAANCAGC      60
GANACAGCAG TTAAGTAATA TGACGNATNT AACACCTGCA CAAAAGNCNG ATGNATCATA      120
NCANGTTAAT NGAGGGACTA CTGNTGCTGG NGTTCACACG GCACAATCAT ATGCCACCAC      180
ATTACATCAA GCGNNGAGTA CGTGNAAGAC ATCNNATNGC TANCAGTGAT NNGNNTAAAG      240
NANGNGANGA TNNCGTTGAN GCTANTNCTG CTAGNNAACG AGAATCTGGC ACCGTGGTAN      300
CTGCTNCTGN CACGATTTTT GGTGNGTANC AGAANTCCNG NCTTCGATTC ATCTGCCGCA      360
TACACANCTC CNAGNGCCGN CGNTTAGTCT TAGTGGGANT TAACCGNGNT GNATTNNCNN      420
TTCGCANCGC ATNGGCGAGA GNTCCCCCAG NNGATCGTGG GTGTTTNAGT TTCCAACCCN      480
NCAATTNGGT TGCCANTTNT NTGGNNNANA GNACCCCTCT NTTNTNCGGC C      531

```

(2) INFORMATION FOR SEQ ID NO:898:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1806 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:898:

```

ACCCACCTA TTGNCCCCC AATTATGTNA ATCCTTTGGA AANAACCACC CCTTAACNCC      60
TAAAGTTGAA ATACTGGTAA TCAAGNAGTT GATTATGGAA ATATTANACT TAGGGATTGG      120
TAGTACCATT ATTGCCCCAA TACAAGAATN GAAGTTATNN AGTTAACCCCT AATCACCAAT      180
TNCNTCNNAA GTAAAAAGAA TCCTATGATT TTAGTCAAAN CCGGAAGATG TNACCAAGTC      240
AATTTGATAA TANNNAATCA TTAAGTAATA ATGTACCNAC ATTGGATTTT GGGTGATATT      300
AATTCAGCCT ATATTATCNA AGTTGTTAGT AAATATACAC CTACATCAGA TGGCGAACTA      360
GATATTGCTC AAGGTACTAG TATGAGAACA ACTGATAAAT ATGGTTATTA TAATTATGCA      420
GGATATTCAA ACTTCATCGT AACTTCTAAT GACACTGGCG GTGGCGACGG TACTGTTAAA      480
CCTGAAGANA AGTTATACAA AATTGGTGAC TATGTATGGG AAGACGTTGA TAAAGACGGT      540
GTCCAAGGTA CAGATTCGAA AGAAAAGCCA ATGGCAAACG TTTTAGTTAC ATTAACCTTAC      600
CCGGACGGTA CTACAAAATC AGTAAGAACA GATGCTAACG GTCATTATGA ATTCGGTGGT      660
TTGAAAGACG GAGAACTTA TACAGTTAAA TTCGAAACGC CAGCTGGATA TCTTCCAACA      720
AAAGTAAATG GAACAACTGA TGGTGAAAAA GACTCAAATG GTAGTTCTGT AACTGTTAAA      780
ATTAATGGTA AAGATGATAT GTCTTTAGAC ACTGGTTTTT ATAAAGAACC TAAATATAAT      840
CTTGGTGA CTATGTATGGGA AGATACAAAT AAAGATGGTA TCCAAGATGC TAATGAACCT      900
GGTATCAAAG ATGTTAAGGT TACATTAAAA GATAGTACTG GAAAAGTTAT TGGTACAACCT      960
ACTACTGATG CCTCGGGTAA ATATTAAATT TACAGATTTA GATAATGGTA ACTATACAGT     1020
AGAATTTGAA CAACCAGCAG GTTACACGCC AACGGGTTAA AAATACTACA GCTGAAGATA     1080
AAGATTCTAA TGGTTTACAA CAACAGGTNG TCATTANAGA TGCAGATAAT ATGACATTAG     1140
ACAGTGGTTT CGATAAAACA CAAAATACA GTTTAGGTGA TTATGTTTGG TACGACAGTA     1200
ATAAAGACGG TAAACAAGAT TCAACTGAAA AAGGTATCAA AGATGTTAAA GTTACTTTAT     1260
TAAATGAAAA AGGCGAAGTA ATTGGAACAA CTAAAACAGA TGAATATGGT AAATATCGTT     1320
TCGATAATTT AGATAGCGGT AAATACAAAG TTATTTTGA AAAGCCTGCT GGCTTAACAC     1380
AAACAGTTAC AAATACAACT GAAGATGATA AAGATGCCGA TGGTGGCGAA GCTTAACAAT     1440
TACCGTCGAC CTCATGATGA TTTCACACTT GGATAACGGA TACCGCGATT CAGATTCCGA     1500
CAGTGATTCTN GACTCAGATA GNGATTCCGA CTCAGATAGT GACTCAGATT CAGACAGCGA     1560
TTCAGATTCA GACAGCGATT CTGACTCAGA CAGTGACTCA GATTCCGATA GTGATTTCAGA     1620
TTCAGACAGT GATTTCAGACT CAGATNGTGA TTCAGATTCC GACAGTGACT CAGACTCAGA     1680
NAGTGATTCA GATTCTGATT GCGATTCTNAG ATTCCCGACA GTGACTCAGA TTCCCGATAG     1740
NGTCTCGGGA TTCAAGCGAG TGATTCTNAGT TTTCAAGATT AGCGTATTCC AAGAATTCAA     1800
GATTGG                                           1806

```

(2) INFORMATION FOR SEQ ID NO:899:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:899:

```

AGAACTATGA TACGCAACGA AGACAAGTTG AAACTGATGT ACACCGAGAG TACACATATT      60
GATGTTGATG AANATTCCTG ATCNTGATAN ACATGTACNT CTTGATGTGC TTTGTGAATC     120
GCATAATGAT GTTGATGTTG AATCGGATTC ACTTGACTTT TCTGATGTTG AGCCGAGATTC     180
TGATGTACAT ACCGATGTTG ATAAACTTAC AATGGTCGAC ATGCGGTTTG AAGTTGATGT      240
ACNTAGCGAA TCACTTAATG ATGCTGATGT GCTTTGTGAA TCGGATTCAC TGCTTTGCAT      300
TGACGCAGAT GTTGAATCAC TTAAAGATGT TGACGACGAA TCGGATTCAC TTGCGCTTGC      360
TGAGTTACTG AGCGATGTTG ACGTACTTGC TGATCCTGAG TTACTTGTAC TTGTTGAGTC      420
ACTGAGTGAT GTTGACGCAC TTTCTGATGC TTGATTCACT TGCACTTGTT GAGATACTTT      480
GTGAATCAGA TTCACTCTCT GAACCACTTA AG                                     512

```

(2) INFORMATION FOR SEQ ID NO:900:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 919 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:900:

```

CTTACCCGAC CAAGATGTCT CGAAGAAGCA CNTTGTGATA TTGATTCACT TGATCCAGTT      60
GATGCTGATT GCTATCACTC GTTGAATCAC TAANACGACG TTGATATGCT CATTGANTCG     120
GATTGACTTG CACTCATTGA ACCAAGACGT ACTTTGCGAT TCCGAAGTAC GTACTGAAGC     180
ACTTGCCGAC GTTGATGTAC TTGTTGAACC TGATTGACTA GTACTTAGTG ATAATGACTT      240
ACTATCAGAA TCAGATGTAC TTTGTGATCA CNTAATGATT CTGATGTACT ACCTGACTGA      300
GACGTGCTCA TTGAACTACT TACAGACATT GATTTACTGT CTGATGCAGA TAATGACCCA      360
CTTGTAAGTA TAGAGTCACT TACTATCTCT GAAGTACTCA TCGAGTCTGA TGTACTTGTT      420
GAGACACTTT GTGATGCTGC TATGCTTAGT GATCCAGAAA CAGAACCACT TGTGCTCGTC      480

```

GAATCGCTCA	ATGATTCTGA	TGTACTCATC	GATTTTGGAA	TCACTTGTAC	TTAATGATAT	540
TGATGTA	CTT	TGTGAATCTG	ATTTGCTTGT	TGACGCAC	TT	600
TGAAATACTG	ATAGAGTCCG	AGGTGCTAGC	TGACTCGCTC	AATGATGTTG	ATGTACTAAT	660
TGCATTTCGAT	GTACTGTCCAC	TTAATGATGC	TGATGTACTA	GACGACCC	TG	720
TGATAAGCTT	TGTGACTTAG	ACAAGCTTCC	TGATGTACTC	ATACTTAATG	AGTCACTGAG	780
TGATGTTGAT	GTACGCAATG	AATCAGATGT	ACTTGTGAT	AGACTTTCGG	ATTTTTCAGT	840
ACTGTTAGAG	TTCGAAATCG	AATCGCTTAA	TGATGTTGAT	TTACTA	AACTGACAT	900
GCTTGATGAT	ACACTTTGT					919

(2) INFORMATION FOR SEQ ID NO:901:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2146 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:901:

CCCAAATGG	CGATAGCTAA	TATTTGATAA	TGATGCGCAT	TTCATACAAT	TTGTGACTTG	60	
GCAATTATTG	AATATTTATA	TAATTTTTTC	TCGTAATAAA	CACAACTTTG	ATAGCGCTAA	120	
AACAGCTGTG	TTAAGTTATG	AGTTAACGAA	TTTAACACAT	TTTACTAGGG	CGGCATTTAA	180	
GAATATTTAT	ACGTTTTTAN	CGAATATTTA	TTTATTGTAA	NACGCTACCA	AAAAGTTAGA	240	
CTTCCTTCCC	ACTAAAGTNC	CACTTTTTTC	TTTCAACTTT	TTTAANAAAC	GGATATGCAA	300	
CTTTTAGTAT	TGGTATCAAA	ATGATTGTTA	GGTCATATTC	TATCAATATA	TTTTTCTAAA	360	
GAATTGCTTT	TATTA	CAATTATGTA	CCTAACCTAA	AAAGAAGCCA	AGGCAACGAA	420	
TGTTACCTTG	ACTTCTAATA	CATATTCAAC	TA	ACTATATA	TTCAATCATA	CGCGCATGCG	480
AGAGTGATTG	TTGTACATCT	ATAATGCGTT	GATTTAAAGA	ACCTTTATAT	GGTAAATCAG	540	
GTTTGAATAA	GTGTTGTATA	AATAGACCAT	CGACTAAAAC	GTCAATGTAT	GATAATAACT	600	
CTCGACGTTT	TGTACAATCA	TTTGCTAAAT	ATTCATATAA	AAATCCAGTC	CATACCCAAA	660	
TTGTC	TTTGT	ATTTCCAAAA	CGTGCTCGAA	ATGCTTTGAC	AAGATTTAAT	GTAATATCCA	720
AATTACAAAA	TGGTTCGCCA	CCTAATAGAC	TTAGCCCAGA	TATATAATCA	TGATCGCAAT	780	
CATCTAATAT	TTCTGCTAAT	ATTTTCATCAG	TGTATTTCTC	GCCATATCTG	AAC	TTTGTG	840
AGGCTTTGTT	ATAACATCCA	ACACAATTAA	ATGGACATCC	TGATACATAA	ACACTGCATC	900	
TTACTCCTTC	ACCGTCAACA	AAGCTATTTG	AATCCTATTT	TAGCAATATA	ACCTTGTCCT	960	
TGTTTAATGT	CCTAAAAGTG	TCATCCTTTA	GGCGCCTTCA	TATGTTTTAC	TCGTGCGCAA	1020	
ATTTCTTTAT	GACGGCCTTT	AATTACTGGA	CGTTGAACTG	GATTGCCTAA	GTAACCCACA	1080	
TGTTTCGTTA	ACGACATCAA	CTGTTTTAGG	ATTATCATTG	NCACAAGTTC	GGGCATTTAA	1140	
ATCCTTTTTC	AGNTGC	TTCA	AAATCTCCAT	CCGNNATCAC	ATTCAATAAC	AATGGANCAA	1200
ATCGGNATAT	TTGGNNCCTA	AGGTTAACCA	ACTTNGGCAA	TAAGAGTNGG	GCCCAATACC	1260	
CGNTTCTAGG	GCTTTCAAA	TGTGTTGCAA	TTTCGGATAC	TCACAATAGT	GAATGAAACC	1320	

ACCACTCGCA	TAATAAGGAT	AATCTTTTTC	AAAATCTAAC	TTTTCAAAAG	GTGTAACATC	1380
TTTACGTACA	TCATAATGGA	AAGAGTTTTC	ATAATATCCT	TTATCTGTAA	TGTCTTTAAT	1440
ATCTCCAAAT	CTCTCTTGGT	CTAAACGACA	AAAACGATCC	GTTAGCGANN	CACTCGGCGT	1500
ACTCGTAAAT	ACTGANCCAA	ATGTCATATA	ATTCTGNCCA	TNGCGTGTGA	TAACGTNTCA	1560
TTTCTTTAAG	AATNACAAGC	GTAAATGCTT	GNGCTTCTNG	AGATGTCTCC	CAGTCTGGAC	1620
CATAGAAAAC	AGNAGCTGTN	TCATACAACC	CTATCTAGCC	CATTGAAATC	GTTGCACGTT	1680
TATTTTAAAA	TAATCAGCA	ACATCATCTG	TTTCTTTTAA	TTTATAGTTA	AAAGCGCCAC	1740
TTTTATATAA	AATTGGTGCG	TTATTCGGTA	CAGNATCTTT	CAAACGATTT	ATACGATAAA	1800
GTAATGCATC	ATGTAACACA	TCGATACGTT	CATAAAAGAT	TTCCCAGAAT	TCGTCATAT	1860
TACCGGCAGA	TTCTAATGCC	ATTCTAGGTA	AATTAAGTGT	NACAACACCA	AGATTACAAC	1920
GACCATTATT	TTCAAAATGA	CCTTCCGCAT	CTTTCCAAC	TGGGTAAAAA	TGAACGACAA	1980
CCCATTGGNG	CTTTGAAATC	ACCTAATATT	TCTACGAGTT	TGGTCAATAA	TTTAAAATAT	2040
CTGGATACAT	ACGTTTCGGN	GGAACAACCT	TAATGCTAGT	TGTTTAATGT	CATAGGTCGG	2100
ATCTTGGGGG	ACTAAAGTTC	GGGTCCCNCT	TCTATTGGAA	ATCAAA		2146

(2) INFORMATION FOR SEQ ID NO:902:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1015 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:902:

ATTGTCCCAC	ACCATTTACT	ACAAGANACG	AGCGTCCTCC	ACATTGTTAC	NTTGTGCNAT	60
CAATNCTTCT	NGTTTGTTTT	GAANNNAAGA	CCGAAGCATT	TGTANTCTGC	TGTGTTTCGCA	120
GCCTTGTTTC	GCACGTTCTA	AGGTATTGAA	TACCGTTTAA	TGCAGTATTG	GCTTGTGTAA	180
CAGCTTGCA	TGCTCTATCG	ACATCTGCNT	TAGGTGTATT	TCCTCCAGCT	GTTTTATNTA	240
AAATAGTTGC	TGCTGCATTT	ACTGCTTGAG	AATAAGCCGT	TCGTTTAGCA	TCATCAGCAT	300
CTTGATAATT	TTGACTTTGT	AACGTCGTGT	CTTTATCACG	AATTGATGTT	TCTAATTGAC	360
CCATAGCACC	ATCTAATTGT	TGCGCTTTGG	CTTTAACTGT	ATTAACACCT	CAACATTTGT	420
TGCTNGTGTA	ATTTCAATTAT	CTAACGCATT	ACGTTGTGCA	TTATTAATGT	GTGTTAATGT	480
ACCTAACGTT	TGTTTCGCAG	CAGCTTTAGC	TTCATTTAAT	TTCCGATCAC	CGCNCAACGC	540
CGTCTTCGTA	CTGTNCACAT	TGTGTAATGC	TTGNNCAACT	GCTGCTTTGT	CTACATTGTG	600
ACCACTAGCT	TTTGTTAAAA	TTGCTTTTGC	TGCATTTACT	GCTTGATCAT	AAGCTGATTT	660
CTTACTTGGC	TCAGCATCTA	GGTATTTCTG	AGTTTGTTTT	GGTTGTGTCT	CATCATTGAT	720
ACCATTTTGT	AAACTTGTGC	ATTGCGTTAT	TTAATTCTTG	TTGCTTTNGC	AGGTTCTTGG	780
ATTTACACCA	GCTACTGTAG	GTGGNACCAT	CAATGTTAAG	CGTTAACGCA	TCTTTTGTGT	840
CATTGTTAAT	TGATGTTAAG	TTATTCAAGT	TTGTTTTTCG	CTGTGTCTTT	AGCTTGAGCT	900
AAGTTTGGC	GCACCATTTA	ATGCATGTTT	TTTAGTNGGT	CATTGTGAT	GTTGCTTGGC	960

GTAATAGTAT TNGGGNTCCA TCCNNTGGNT TCCACGTTTG GATTAATGAT TGCTT 1015

(2) INFORMATION FOR SEQ ID NO:903:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 679 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:903:

ATAAATAATN CCGCTACAAT TTAATACATA TGCTTGANTG NCTGGNNAAT CGTGTTCCAA	60
GTANTNGCTT NTAAACTTAA TTGACCTAGT CCAGNCCATG CANAGATATA CTCGATAACA	120
ACTAGTCCAC CCATTATCAT TGGTATAGAC ATACACAAGN TTGATACCGC AACTTGATATA	180
GCATTACGCA ACACATGCAA CATTAATGTG ATAGATTTCA CACCGCTTGC TCTTAAATAA	240
AGTACATAAT CTTCATTTAA TTGTTCCACC ATCGAGCGTC TAACATTTNC TAAAGTAAAT	300
ACCAGCATAG GCAATCGTAA TAACGATCAC TGGCAATATG TAACTTTCTG GACCTGTAA	360
TCCAGAAGTC GGCAATATGT TTAAC TTCAC TGAAACGTAA ATAATAAGTA TTGAAGCTAG	420
TGCCGCTCGT GCCGAATTCG GCACGATGCT AATGCAGTTA GAAAGAAAGC CACTGAACGT	480
ATCGCACGAT CAGTGAAC TTCTCTTTTT AATGCACTAA CTACACCTAA AATAATTGAT	540
GTAATCATCA CCATAACACT TGAAATTATT GTTAATTTCA ATGTGTTTCA AAATGCTGGG	600
CCAATGCGTT CAGCAACAGG ATCCCCTGTA ATGTAAC TTG TACCAAAATT AAATGCATC	660
GCTTCAAGTA ACCAGTTTG	679

(2) INFORMATION FOR SEQ ID NO:904:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1550 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:904:

GGCACCAGCT AGAGCGAGTT TTTATATATA CAACACGAAA GAAGACATTG ATCAGTTAAT	60
AAATGCCTTG AAACAAACGA AGGAGTTTTT CTCTTATGAA TTTTAATAAT CTAGATCAAT	120
TATATAGATC TGTCATTATG GATCATTATA AAAATCCTAC AAATAAAGGT GTATTANATA	180
ACGGGTCTAT GACAGTAGAT ATGAATAACC CGACATGCGG TGACCGTATA CGACTAACAT	240

TTGATATAGA	AGACGGCATT	ATAAAAGATG	CTAAGTTTGA	AGGTGAAGGT	TGTTTCGATT	300
CAATGGCAAG	TGCATCGATG	ATGACACAAG	CTGTTAAAGG	GAATCCANTT	GGAGAAGCAA	360
TCCAAATNGA	CCCAAGGAAT	TTACCGNAAA	TGATGCTTGG	TTGGAAGCCT	ANTGTGATNC	420
AGGGAAGAAT	GGGGAGATAT	TGAAGCATTG	CNGGGTTGAT	CTCAATCCCA	GCTCGTATTA	480
AATTTGTCCA	CATACCTTGG	AAACATTGGA	AAAAGGGTCC	TTGTTCTTAA	AGGAGGGTAA	540
AACAGGAGGG	TCCGGCTTGA	AGAAGAAAAG	ATCCTGTATA	TCATAAGATG	ATTTTGATAT	600
TAAGACATAT	NNAAGTATNN	NAATTTTAA	TAAAGATGTC	ATGTCATTGT	AATAAATATG	660
GTTTACATCA	TTGAATTAAA	AACCTACGCA	CCGCCGTTGT	AAATATATTT	TTAAGGAGTG	720
ATTGAAATGG	CTAAAAAAGC	ACCTGATGTT	GGGGATTATA	AATATGGATT	CCCCGCCGAT	780
GATGTATCCA	TTTTCAGATC	AGAACGTGGT	TAACTGAGA	ATATCGTTAG	AGAAATTTCT	840
AACATGAAAA	ATGAGCCGGA	ATGGATGTTA	GATTTCCGTC	TTAAATCATT	AAAATTTGTT	900
TATAAAATGC	CAATGCCTCA	ATGGGGTGGC	GACTTATCAG	AATTGAATTT	CGATGACATT	960
ACTTACTATG	TAAAGCCTTC	AGAACAAGCT	GAACGTTTAT	GGGATGAAGT	GCCAGAAGAA	1020
ATTAAAAGAA	CTTTCGATAA	ATTAGGAATT	CCTGAAGCTG	AACAAAAATA	TTTAGCTGGT	1080
GTTTCTGCTC	AATATGAATC	TGAAGTTGTT	TACCATAATA	TGGAAAAAGA	ACTTGAAGAA	1140
AAAGGTATTA	TCTTTAAAGA	TACAGATAGT	GCTTTACAAG	AAAATGAAGA	ATTATTCAAA	1200
AAATACTTTG	CTTCTGTAGT	ACCTGCAGCA	GATAACAAAT	TTGCGGCGTT	AAACTCAGCA	1260
GTATGGTCAG	GTGGNTCGCT	CATTTATGTA	CCTAAAAATA	TCAAAC TAGA	TACGCCACTA	1320
CAAGCTTATT	TCCGTATTAA	CTCTGAGAAC	ATGGGTCAAT	TTGAACGTAC	ATTAATCATT	1380
GCTGATGAAG	GTGCTTCTGT	ACATTACGTA	GAAGGTTGGT	ACTGCACCAG	TTTATACAAC	1440
TAGNCTTTTA	CACTCTGCTG	TTGGTGGNAA	TCATTGGGCA	TAAAGATGCG	CACNGTCCGC	1500
NTTATTCTTA	CGAANCAAAA	CTGCGGGACA	ATGTTTTCAT	CTNNAGGTAC		1550

(2) INFORMATION FOR SEQ ID NO:905:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:905:

GAATTCCTAA	TGTAGCATT	ACTACAGATA	TTATTGNAGG	GTATCCAAAT	GAATCAGAGG	60
AACAATTTGA	NGAAACTTTA	ACTCTGTATG	ATGAAGTTGG	NTTNGNACAT	GATATACGTT	120
ACTTGTATTG	ACAACGTGAT	GGNACGCCCTG	CTGCTAAANT	GAAAGATANT	GTNCCCCCCA	180
NNTNNCANTT	AGGAACGATT	GCANCGTTTG	NNTAAAAAAG	TTGGTCATTA	TCCACAAATA	240
GCTATGAGTA	NGTNCGNCGG	ACANACTGTA	ACAGCCACNN	CGGNGAAGGT	AGNAGTAAAA	300
CCNGATGATC	AGGTTCTTGC	TGGCTACACT	GATNNCAATA	AGCTAGTTAA	TTTCAAAGCA	360
CCTAAAGAAA	TGATTGGGTA	ANTAGTGGNA	GTNCGATNGA	TGAAGCTAAC	AGCCTTCNAT	420
TAANTNNCAG	NTCGGNACGA	AGTTNGAGCC	GAATGGTGAT	CCACNAATNT	TTT	473

(2) INFORMATION FOR SEQ ID NO:906:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:906:

```

TGATAATACT GCTTAATACA ACATTTATTG CAATTAAAAG TGCAGTAATA GCCAGTTTTT    60
CNTTGANTTC AAAATGANTG TCCTCCNTTT TTGTTGTAA NTAATCACTA TGCTTGGCTT    120
TATTATGGTC ANNTAAACGT GTTTCATTT GTTGATACTA ACATTTTCAA TAATTGATTC    180
GCTTCATATT GTGAAGTTTG AAACGTGTCA NCTATGGGCA ATGTATTTAT TTCTGCTTCT    240
ATACTTTGAN TGGTATGTTT CGACTGTTCT AGCGCATTTT GTTCCCGTA ATTTTGAAAG    300
TTTACTGCTT GTTTTGTATG CTTTTTAAAC ATATCCATTT TAGTCTTTAT CGTTTGGTTC    360
TGATGAATCT GTGCTTCAAT TTGTTGATAT GTTTTGATAG AANCCCAAAT TTTAATTTTA    420
NTTGCAATAT AACCCGCTTG TTCCAAANCG TCATCTTTAT AAAACAATTT ATTTGAATCA    480
CCNATTTTCG GCTCCTACTT CCTTTACCAA ACTTGCCATT TAATGGAATA CTGTTTAGCT    540
TCATCTATTC GTACTTCCAC TAGTTTACCC AATCATTTCT TTAGGTGCTT TGAATTAAC    600
TAGCTTATTT TTATCAGTGT AGCCAGCAAG AACCTGATCA TCTTTTTCAC TACTACCTTC    660
ACAAAGTACT GTTACAGTTT GTCCTTCGTA CTTACTCATA GCTATTTGTG AATAATGACC    720
AACTTTTTTA TTCAAACGTT GCAATCGTTC CTTTTTGACA TTAAAGGTA CATTATCTTT    780
CATTTTAGCA GCAGGCGTAC CATCACGTTG TGAATACAAG TACGTATATG CATGTTCAAA    840
ACCAACTTCA TCATACAGAG TTAAAGTTTC TTCAAATTGT TCCTCTGATT CATTTGGATA    900
CCCTACAATA ATATCTGTAG TTAATGCTAC ATTAGGAAGT CTATCTTTGA TTCGTTTAC    960
TAAATCCAAA TAACTTTCTC GTGTATATTT TCTACCCATT ATTTTAAATA CTGCATTATT   1020
TCCAGATTGA ACTGGCAAGT GGATATGAGG AACGATATTA CCACCCTCTG AAATAACATC   1080
AATCATGTGA TCTGTAAAGT CCCAAGGATG ACTTGTGTGT AAACGAACTC TTGGAATCGC   1140
TATTTTAGAA ATTGCTTGTA AAAGATCTCC TAAGTCATAT TCTATATCCT GTAAATCTTT   1200
ACCATAAGAA TTTACATTGT GACCTAAAAG CGTTATTTCT TTGTAACCTT CACGAGCAAG   1260
TTCACGTA CTATCTATAA TGTCTTCAGG TCTACGGGTC CGGTCCTTAC TCCTTGTA   1320
TGGAACAATA CAATATGTAC AAAACTTATC ACAACCATAC ATAATATTGA CCCATGCTTT   1380
ATGTTGCTTC ACGGACTTGT GGNAGATTAC AATAACGTCT NCTTCTTTTA GACATACTCA   1440
CAACAATGT                                     1449

```

(2) INFORMATION FOR SEQ ID NO:907:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1589 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:907:

```

GTCGCTCAAT TTGTATCATC ATTTTCTTAG CGTTGTGATA GTGCCGGGTT CTCCTCCAGC      60
NCTGCCTGCA CCATCTTATA TTGCATTNCN TGGGTGGNTA ATCCGCCGGG TTAATATTCT      120
TTGTGANTCG ATATCCTNAA TTGNAAAATA TGGATAATGA TGNATTAAGT CGCTTGATTT      180
TAAATAGAAG TGTNAATGNA GTTGATGATA TGATTGAAGA ACCTGAAAAA GANNAACTA      240
AATAATAGAA GAGTCGCACA ATATACCTTC TTCATTCCGA GCGGTATCGT GCGATTTTTT      300
GTATTATANA TTGACATTTA AGACGAGGCA GCTGNACCTT ATATATAATT GCTAAGAGTT      360
TGGGCTGGAG CCATTTCTAA CAATATTTAT AATCGTTTAA AAGATTTTAC GAACCCAGAA      420
ACAATTAATT TGGAAATTTG GTCGGCGAAT AATAAACCTA ATGCGATGGG CGCCTGCAAT      480
AAGTGTTACT TCTAACATGG TATTGATTGC TGTGCTGAAA TTTAATAAGA CTAAATTTTT      540
TGTAGCATCG TATGCTAATC CCACCCTGGT ACCTAATGGA ATGATACCCG TTACCCATAA      600
AAATTGATGG CAGGTTCTTT TTTGTTTACG GACCAAAATA ATGACTTACC AAGCCTAATT      660
GCTAAACCTC CCAAAGAAAC TAGAGAATAT AGTGTGCACC ATTA AAAACCC GTTGGAAGAA      720
TAAGGTTGTA AACCAATCCA TCCAACATGT ACCCACCAGG CCACATGATA GATATAATTT      780
TCTAGGTGCA TCAAAAATGA CGCAGAAGAA CATTTGAAGCT AAAAAGCTAA AGATAAAGTT      840
TAAGATCCAA AACATAGTCT GATACTCCTA TACTAAAATT AATACGCTAC CAACGCCAGC      900
ACCGATGCCA AACGCAGTAA CCAATGCTTC TAATGATTTT GTTGTGAACA TCAACATGTG      960
TCCACCAAAT AAATCTTGTA TTGCGTTTGT TATTAATACA CCAGGAACAA TAGGCATGAC     1020
TGCCGCAATG ATAATAGTTG CCAAGTCACC TGTGGGATA AGTGTATGTC CAATAACGGC     1080
GATAATCCCA ATAACATG AACCATGAA TTCTGGGATA AACTGTGCAT GTAACCTGCG     1140
ATCTAAAATC TCAGTGACTA GGTATCCTAG ACTACCTGCT AATATCGCAG TTAAAACATC     1200
AATCAATCTA CCACCTTGTA AATATAAGAA ACTCATTGCA ATCATTGCTG CAGCAAAACC     1260
TTTAAAGGGA AGACTGCTGT CACGCTTAGC AACATATATT TTTTCAAGTT GTGTTTTTGC     1320
TTCGGCTAAA GAAATTTTAT TATTTGTAAT TTGACCGGAA ATTTTATTAG CTGCGAAAT     1380
TTTTATTAAG TTTGTATCTC GAGAGGTAAT TCTAAATATT CTAGGAAACG ATTCCCGAAT     1440
GTAACGTAAA CTGGATGACA GTGTTTGTA CAAAGCTTGT TACTTTCACT TGTAACCAAG     1500
TTTTTTTGCA ATACGTGTCA TGGTATCTTC TACAACGCTC GTGCCCTTCC TGCAACCAGA     1560
TCTTAATAG TATGGCGGAG CAGGAAGCA                                     1589
  
```

(2) INFORMATION FOR SEQ ID NO:908:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 948 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:908:

```

GCCCACCTTGC TTGTTCTAAT CCATAGGGTT TTTAAAAGAT CCCTCCTAAG AAANCCTAAT      60
TTCATTTCTG AATAAGAATT TAATTTGAAT ACCCGTTTGA AACAAATTAG GTTGTTCCTAA      120
ATTTGTCTTC ATCCAATATG AATAACATCA GTNGGGTGGT TTTTATAATG TTCAATATAA      180
TTCAATATGA TTTCTTTTAC TTCTTGCACC ATTTTGCCTA CTAGTGGTTC TGGCTTTAGC      240
ATTAAACATT TATTATATTT TGATAAATTA CGATATTCAT TCGGTGTTAT ATCCATATAA      300
CTTTTAAACA TTTTAGAGTA AGTGGAGCTA CTAATAAAC CTAAATGCTC ACTTATGCTG      360
CTAATAGTAC TATCAGTAGT AAGTAGAATT TCAATCGATT TACCAATTTT CAAAGTATCA      420
GATGTCTTTA CACTCCGCTA CTTCCGAAGC CTTTGTCTCC ACGTCTGAA ACACATGCCC      480
ATAAGTAAGT GGAATTGTGA TGACAAATTT GACTTTGAGA CAAATAATTT ATCAGCGACA      540
CTTTTTAATG TCAATCGNTG ATTTACATTG TGATAAATAT ATTCGAGCTC GTCACGTAAA      600
TCACCATAAT AGGCATATCG ATATTGATTG TGCGCAATCT TTTTATCCAT ACTTGCTTCT      660
TGTGNAATGA TTTTAATAAT ATCCTGTAAT TTTCTNATAT CAGCGTCATT GAGAGGTTGA      720
TTATCAAGAT ATCGATAAGT CAATTTTANT AGTAGACATT TCAAATTATA GGATGATTTA      780
ATCAACTTTG NTGTATAGTG GTAATTAAAG AAAGTAAAGC CTAATTCGCG AAACCAATCG      840
CTACTCAAT ACAACATGAT CGNTTNTTA TTATCTTAA TACTAAATAC ATCCAGATGA      900
TTAATAATAT ATATATCATC TTCAATTATT TTACTTTTAC GAAATTTT      948

```

(2) INFORMATION FOR SEQ ID NO:909:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1530 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:909:

```

GGGACGTTGN TGTTTTTTC NGAGGCTTGT GCTTTCATGT GATGACCCCA CCCAAACATT      60
TGTAGCCGCT AACNTTTGAC NCCCACGCCT ATTGAATACT TTCTAATACA ATACTTTCTT      120
TCTTCTTGTC CTCTTAACAT ATAATCACCC CANAAGTATT TTTTGGACCC CCTCTTGAGA      180
ATGNAACAACA ACTGCACCTT CAATATAACA TGACATATAT TATTTTGTGA TTAAGNCTAC      240
AAAATTAATA AAAATTTAAT AATNCGATAT TAAATCGATA CTAATCATTT ACAAAATATGT      300
GCATTTCCAA ATAATTTATA AACACTTTTA GTTGTGGCGT TGAATCCAAC ACAACCAACA      360
TTTAAGATAA ATATTTTATT AAGTAATATA GTTTCATCT ATATATAATT AGTTAATTTG      420
TATGGTATG AAAATAATTC AAACANACA ANTATAAGTA AGTTTCAAG ATTTTCTAA      480
ATTAAATAA TGATTCATCT CATTAAGGGG AAGATGCATC ATACAGTTT GTGTATTCAT      540

```

TTAAACANAG	GGGNTGCNTT	AATGAATCAA	TATCATTTCTA	ATGCACAACC	NNCCAAGTGC	600
ATGGCGTTTT	TTTGTCTATA	GTITAGTGGG	CATACTATGT	TTCTTTATTC	CTTTTACGAT	660
TAATGGTAAC	AACACTATTT	TCGTCGATCA	TGTTTCATCTA	GCCATTTCGT	CAATCATAGG	720
TCCACTTATG	CCCTATGTTG	CACTGATTAT	GATTTTAAAT	GGTACAGCGT	TACCAATAGT	780
GAGACGTAAT	TTTATGACTT	CAATCACAAA	CTTGGTCATT	ACATTATTTA	AAGTTCCAGG	840
TCCAAGTGGA	NTGGAATAAT	GTATGNATTN	AAAATCGGTC	CATCAATACN	ATTTAAAGCT	900
ANCTATGCTC	CGTTCTTGTT	TGAAAAATTA	ATGATGCCAT	TAAGTATCTT	AATTCCAGTA	960
GGTGCAATTG	CGCTTTCTTT	ATTAGTAGGC	TATGGCTTAT	TAGAATTTGT	CGGTGTTTAT	1020
ATGGAGCCTA	TTATGAGACC	TATTTTAAAA	ACACCAGGAA	AATCCGCTGT	CGATGCAGTA	1080
GCTTCGTTTG	TCGGCAGTTA	TTCTTTAGGA	TTATTGATTA	CTAATCGTGT	CTATAAGCAA	1140
GGGATGTACA	ACAAACGAGA	AGCCACGATT	ATTGCGACTG	GCTTTTCAAC	AGTTTCAGCA	1200
ACTTTTATGA	TTATCGTNGC	TAAGGANCCCT	TAGGGCTAAT	GCCGCATTGG	AATTTTATACT	1260
TTTGGATAAC	TTTAGTCATC	ACATTTGTCT	TGACTGCAAT	TACTGCATGG	CTACCGCCAA	1320
TCACCAATGA	ATCAACAGAA	TATTATAACG	GACAAGAAGG	AGAACAAGAA	GTGCTATTG	1380
AAGGAAGCAG	ACTGAAACT	GCATATGCAG	AGGCGATGAA	ACAAAATGCA	TTAACACCAT	1440
CTCTCGTGAA	GAACGTTTGG	GACAATTTCT	AAGATGTCCT	TACTCTCCGC	TACTTCCGAA	1500
GCCTTTTGCT	CCACGTTCTG	AAACACTTTC				1530

(2) INFORMATION FOR SEQ ID NO:910:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 595 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:910:

GGAAAGTTGC	CACCANTTGC	AAGAAATACC	TAGCTCAAGC	GTTATGGATT	GACCCAATAT	60
TCAATCGGAT	AGAAGAATAT	AAGAGGTGGA	TAAATTGGCG	AAGAAAGCAA	GGATTGTACC	120
AATAAATGAT	AAACCATATA	GTTTACCCAA	ATCTGAAATG	GAATTAATAG	AAAGTCNCGG	180
GTATAACCGC	TGGAATGGTT	TCTAAGAGAG	TAAAAGACGG	TTGGGAACCTA	CATGAAGCAG	240
TAGGGATTAT	GTCGGGGCAA	GTGGTCTATA	AATATGAGGA	GGAGCAGGAA	AATGAAAAAA	300
TTTAATGTTC	AAATCACATA	CACTGGCATG	ATTGAAGAGA	CTATCGAGGC	TGAAAGTTTA	360
GAAGAAGCAG	AAAATGAGGC	GCGTGATATT	GCGATGATGG	AAGTACCATT	TGATTGTGAT	420
GAATATGAAA	TTAATGTAGA	GGAGAAAGAA	TAATGACTAA	CACATTAACA	ATTGATCAGT	480
TACAAGAGTT	ATTACAAATA	CACAAGGAGT	TCGACGATAG	AATACCAACG	CTGAACCTTAC	540
GAGATAGCAA	AATAGCATAT	GTAGTTGACA	CTATAGAATA	CTCAAGCTTG	CATGC	595

(2) INFORMATION FOR SEQ ID NO:911:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2005 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:911:

```

GGCAGGAGCT CATAATCGC TAGTAAGAAT AATAATCTTA GTATTTGTTT AGTCATTCCC      60
CACACTCCCT TATATTTTCA AACAACTGAC TCACTTTAGC ATAATTCCAT CTCTCCTATC     120
TTAACCTTGT GCCTCGTANT TGCGCTCAGC TTCTTCTTTA CTCTCTGCCT CAACAACTGT     180
AAACGTCTGA TTATCTCTAG CAGTAGTAAA ATGTTTCATGT GGTTCCTCTT GTTGAATCTT     240
TGAATGTTGT GACTAAGTAT TGTGTCATTC CTCATAGCTC CCTTGAACCTT GTTTGAGCTT     300
ACTCATAAAA AACATTACTA AAAATGCTAT TAAGATATGC GTCTTTTGAT GTTTATAAGC     360
AAATGTAGAT ATCATAAAGA TAGTAGCAAG CATTAAACATT TCATATATGT TTGTGTGTAT     420
AGTCTTTTFA CTCTTAAGAA AAATAATTGC TATGCGATAA AAGAGATAAA CGCCAAACCC     480
TATTAAAAAT ATTTCTAACA TGTGCTCAC TTCCCCAAAA CCTCCTTGAC TCGATCTAAG     540
ATGTCTTTAT ACTCCGCTAC TTCCGAAGCC TTTTGCTCCA CGTTCTGAAA CACACTCGAA     600
TTCTCCACT TGCTTTAGTT CAGGTGTCCA TATAGGCACG ATAACCAATT GAGCTAGTTT     660
GTCGCCCTCG TTGATTTGAT AAGTTCCATA TTGTCTTATG GCGTCACTCA AATCGATTTT     720
TCCTTTAATA TCAAAAACAC CTGGTGTGAT ATAACCATTC GATGCAATAG CGTCATTCTT     780
GATATTAATC CCTAAATTGC CGTGATATCC CGCGTCTATC TTGCCTGTTT CAATCACTAA     840
ATGCGTTTFA CTACTTACAC CACTACGACT AGTTAATAGT CCGACATAGC CCTCTGGTAT     900
ACTCACAGCT ACATCTGTTT TGATCACTGC TTTTCTTGTG GTTTCGAGTA CGACAGTTTC     960
AGCTGAGAAT ATGTCATAAC CTGCATCCGT CTTATGATTT CGTTCGGGCA TTCTAGCATT    1020
TTTTGATAAT AGTTTTACTT GTAATGTGTT AGTCATTTTC CTATTCCTCC TCATATTTAT    1080
AGACAACCTG ACCTGCCATA ATCCCTACTG CTTTCATCAAG TTCAATACCT CNTTTAACTG    1140
AATGTTGAAT AGCATTGTC ATTCCCTCAA GTATTTTCATC AAACGCTTGC GCTTTCTTAT    1200
ACACGTCCCT AATCTCTTTT AGCAACCCCT CTGTGTCATT ACCGTATACG CACTAGCACT    1260
AATAACGGAC TGTTCGATTT TTTGCGGATT ATTCATTGGT GTCATCCTCC ATAAAAATTT    1320
TATTGTTTAA TTCCATTCCG AATTTAATC TTTTCATCCT GTTACCGAAT TCGTTTATTA    1380
AATCTTTTTC AACGCTCTTG CAATACCTAT CCCATGCGCT TGCTTTCTTC TCCAGTTCTT    1440
TGTTACAATC TCGTAACTTC GCTATATCCC CAATAAGCTC ATCTCGTTGC TTCTTGTAAT    1500
CTTCACGATC TTTTAATGCT TTGTGAAGTT TATCTAATAA CTTGTTAGAG TTAGTACAAA    1560
GATTTTATA TTGTTTCATCT GATAAGGTGA ACGTCATCTC ATAACCTCCA ATAGCATCTC    1620
ATTTTCAAAA ATATTTCCAA CAATTTCAAT AATATCGGCA TTTTCACTTA GTAATTCAGT    1680
TACATTGCTA AAAGTTATAT AAAAGGCTCC TTCTTTAAAC TCGATAAAAC TTACTTCTCT    1740
CGAATTAACA ATCTTGGAAC AATATCCCCT TCATAAATCT CCACAACCGG GCACATCTTT    1800
TAAATCCTGT GTATTGGTAA TAGGTTTTAC TTCAATTGAA ACTTTTATTA ACCTGGTGGA    1860
AATCAAAATG TACCACTTA TTAATAATCG GATTTGCGNC AATAATACTC AATAACTTNN    1920
NNTATCTTNA TCCCAAGCTT TTAATTTCAA CATCAATCTT ACCAACTCCC CATCTTTCCA    1980

```

AATCAATGTC AACCGGCAAN GTCAC

2005

(2) INFORMATION FOR SEQ ID NO:912:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1134 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:912:

```

CTACATGGTA ACCAAAGAAT TTTTAAAAAC TAAACTTGAG TGTTCAGATG TGTACGCTCA      60
GAAACTCATA GACGAGGCAC AGGGAGACGA AAACAAGTTA TATGACCTAT TTATCCAAAA      120
ACTTGCAGAA CGTCACACAC GCCCCGCTAT CGTCGAATAT TAAGGAGTGT TAAAAATGCC      180
GAAAGAAAAA TATTACTTAT ACCGAGAAGA TGGCACAGAA GATATTAAGG TCATCAAGTA      240
TAAAGAGAAT GAGAATGAAG TTTATTCGCT CACAGGAGCC CATTTCANCG ACGAANAGAA      300
AATTATGACT GATAGTGACC TAAANCGATT TAAAGGCGCT CACGGGCTTC TATATGAGCA      360
AGAACTAGGT TTACAAGTAA CGATATTTGA TATTTAGAGG TGGCGCATGG AAGTACATTA      420
CAGTAGTAAA ACNAACGAGT GGACNACNCC ACAACATTTA TTTGATGACC TAAGCGAAGA      480
ATTCAGTTTT ACATTAGATC CTTGTTCAAC AGACGAGAAC GCCAAATGCC GGAAGTATTA      540
TACAGTAAAA GATAATGGGT TAATTCAAGA CTGGTCTGAG GACATTGTTT TTATGAACCC      600
GCCATACGGT CGAAGTATTA AGCGTTGGGT CAAGAAGGCT TACGAAGAAA GTTTGAAAGG      660
CGCAACGGTA GTTTGTTTAA TACCCGCAAG AACAGACACG ACATATTGGC ATGATTACAT      720
TTTTAATAAG GCTGATGATA TAAGATTCCT ACGCGGTCGT CTGAAGTTTG GAGATAGTAA      780
AAACAGGGCT CCTTTTCCTA GCGCAATTAT CGTTTATAGA GGTGCACAAA TGAGTAAATA      840
CAACGCTAAG AAAGTTNGGA GTACAAAAGG AATTNGTTTT TGGATAGCAA AAGNAGAATG      900
TNGAATATTT ACCAAATATT TAGAAAAGTAA TATTGAATGG CACTAACTAT GATCGTATCG      960
AAATACAACC GAAATTTGGG AAACAAAGAC CGATTACGTA TATAGCCGAT TTCTCTTTGT      1020
GGAAGGAAGG GAAACTGGTT GGAAGTTATA GACGTTAAAG GTAAGGCGAC TGAAGTTGCC      1080
AACATCAAAG CGAAGATATC CAGATATCAG TATTGAGATG TGATTTTACC GTGG          1134

```

(2) INFORMATION FOR SEQ ID NO:913:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 867 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:913:

CNCCAAGTGA	GCTACCTTTA	ATATCGCCGT	CTATATGCAG	TTTAAATATT	GGAGACTGCG	60
TTGGGTGTAA	TTGGGTACTT	CTCTCTAAGT	TTNTNCACAT	CCCCANCACT	ATTATNCCTT	120
GTGNACTCTG	CTACATAATA	NGGAACATTG	ACANTGNTAG	ATATTCTTCC	ATTTNTATAA	180
TTTCACAAGT	CTNTAAAATC	GGCATATTGC	CCGAAAAATT	TAAAAATCTC	TATTTCTGTG	240
TTAAGATTCA	CATCTTCTAC	TGTGCCCAAT	AGAACTATCT	TATTGGTNTC	TANANACAAC	300
ACGATATTTG	GCNCGAGCGT	GNCAACTTAT	CCACTACATC	ATAAGTTGCT	CTTACAGTAT	360
AATATCCTGT	TGCTGCCCCC	GTATTTCTAT	TAAATGTAG	TACCATACCT	TCGCTATTCA	420
TTTCACCTTG	CTTGTTGCTT	TTAGCAAAAT	CTGTTGATAT	TGTCCAAGTC	CCTTTATCAC	480
CTTTTTTAA	TTGCCCATCA	CGATATCCTT	CTTTGTCATA	TAGATTCTCG	AGATTCTTAA	540
TTGGATACAT	ATCTAACGTT	TTGAAAAAG	CTCTTTTTAA	TTTGTGCTTT	CTTTGGAACC	600
TTCTTTTGGG	TTTTCATGCA	CTTTTGCCAC	AACCTGCTAT	CGCAAATATT	AAAATCATAA	660
CGCTTATGTA	CAATGCAAAC	CTTTTGAAT	ATCCCATCAT	TTCACGTCTC	TCTGCTTTAG	720
AATTATTTCT	ACATCTAATA	AACTTTAGCT	ATCTTCATCA	GACGGCCCAA	AATTTAAATA	780
ATCTCTTAAT	GTTGTCTCTT	GATCTTTAAC	TTTTGAAAAT	TTATATTCTA	TTTTTTTGTA	840
TCCAAGTGA	CTTCCTTTTC	TCGTGCC				867

(2) INFORMATION FOR SEQ ID NO:914:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 637 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:914:

GTTTTCTGT	TCTCTTTCAT	CAAGGCTTTT	TCTTTGAATC	AATTCTTCT	ATTGAAAAAT	60
AACCGNTGT	GGTCCTAGTA	TTTCTATTCA	TTGTATAATA	TCATTGCCTC	TTTGAAGTTA	120
AACTTTTACC	TTTTGGGTG	AATTATCATT	TCAGATCTAA	CAACCCACGT	CCCTTTGTCT	180
CCCTTTTTAA	ATTCTCCATC	TCGATATCCT	TCTTTATCGT	ATAAATCCTC	AAGATTTTTA	240
ATTGGATACA	TATCTAACGT	TTTCGCAAAG	CTCTTTTTGA	TTTGTGTTTC	TTTTGAATCT	300
TCAGGAGTGT	CAAATACGCC	ACTGCAACCT	GATGCTAATA	GAATTAAGAC	TGACGTCCTA	360
TACACAACGC	ACATTTTCTA	AAATTATTCA	TTGTTCCGTA	TCCCCTTTTT	TATCATAGCT	420
AATAGTTCTC	ACTTGAGGTA	AACTCCAAAC	TATCAGTAAA	AAATATATTC	TCTTCTAGAT	480
TCTCCACGAA	TGTAAACTCA	ATGTCCTTAT	GTCCGATTGA	TGAACCTTNN	AAATCTCCAG	540
TACCTTTCAA	CAACAATGTG	GGNAGNCNTC	NCTGGNGGAT	ATATCATATC	TAACACGTAA	600
TTGCNCNACA	TTATATTTCAT	TATTTCTCAG	TCGATAT			637

(2) INFORMATION FOR SEQ ID NO:915:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1122 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:915:

```

AACTTTGAGT NTTTTGTTTCN ATATGGAAC TTAAGATTT GGAAATTATN TAGATGGAGA      60
TATATCATAT AATCCAGAGG TGCCNAGTTA TTCAGCTAAA TATCAATTAN CTAATGATGA      120
TNACAATGTA AAGCAATTAC GTAAAAGATA TGACATNCCA GCAGAATAAA GCACCCAAAG      180
TTATTTGTTG AAAGGGTACA GGGTAATTTN AAAGCCTCAT CAGTTGGATA TAAAGACAGT      240
GAATTTACTT TCGTAGAGAN NAAAGGTGAA AATATATACT TTAGTGATAG TCTACATCTT      300
GANCCAAGTG AGGATAAATA AACGTGACCA ATAAAGAGTA TGAAATCGAA CCCGGAAAAA      360
GAGAGTGTGA AATGATGAAA CGATTAAATA AATTAGTGTT AGGCATTAGT TTTCTGTTTT      420
TAGTCATTAG TATCACTGCT GGTGTGGCA TAGGTAAAGA AGCGGAAGTT AAGAAAAGCT      480
TTGAAAAAAC ATTGAGTATG TACCTATTA AAAATCTAGA GGATTTATAC GATAAGGAAG      540
GCTATCGTGA TGATCAGTTT GATAAAAATG ATAAAGGTAC ATGGATTATA AATTCGAAA      600
TGGTTATTCA ACCTAATAAT GAAGATATGG TAGCTAAAGG CATGGTTCTA TATATCGAAT      660
AGAAATACCA AAACAACAAA TGGTTACTAC TATGTGCGATG TGAATAAGGA CGAGGATGAA      720
GGAAAACCGC ACGACAATGA AAAAAGATAT CCGGTTAAAA TGGTCCGATA ATAAAATCAT      780
TCCAACAAAA GAAATTANAG ATAANAACAT AAAAAAGAA NTCGAAAAC TTAAGTTCTT      840
TGTTCAATAT GGAAACTTTA AAGATTTGTC GAAGTACAAA GATGGAGATA TTTCATACAA      900
TCCAGAGGTG CCAAGTTATT CACCAAAATA TCAAGTAACT AATGATGACT ATAATGTAAN      960
ACAATTNCGN AAAAGATATA GATATACCGA CCGAATAAAG CACCANAGCT ATTGTTGANA     1020
GGTACAGGGA ATTTAAAAGG TTCATCAATT GGCTACACAA AAATTGAATT TACTTTTCGTA     1080
GAGAAAAAGG GAGAAAATAT ATACTTTAGT GATGGGCTAC AG                               1122

```

(2) INFORMATION FOR SEQ ID NO:916:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:916:

CAATTCAGAA	AGGGGGAGAA	GCCTTAAATA	TNAGAAGGTA	TGTTTTTGNA	GTTAAATAGA	60
AANACAAGGA	GTGCGNNAGG	ATTTTACTAT	GTTAATGCGA	TAAAGAAGGN	TGTAAATGGC	120
AGACCTCAGG	ATAACCAAAT	AGAATATCCC	GTTGAAATGA	TTGACAATAA	ANTCATTCCA	180
ACTAAAGATA	TCNAAGATGA	NNAAATAAAA	AAAGAAATCG	AAAACTTTAA	GTTTTTCGCG	240
CAGTATGGCA	ATTTTAAAGA	TTTGACGAAG	TATAAAGGTG	GAGATATTTC	ATATAATCCA	300
GAAGCCCCGA	TTTATTCAGC	AAAATATCAN	CTANCCAATG	ATGATTATAA	TGTAAAGCAA	360
TTACGTAAAA	GATATGATAT	ACCGACGAAT	AAAGCTCCAA	AGTTATTGTT	AANAGGCACA	420
GGAAATTTAG	ATGGCACATC	NATTGGATNC	NAAAAAATG	AATTNACTNG	CGGNNAGAAA	480
ANNGGAGAAA	ACNCTCACTT	TACANCTAAC	CTACATTTTA	AACCGAGTAA	TGATGAATAN	540
TCGTGACTAA	TAAAGAGTAT	GAACTCGACT	CAAGGAAACA	ATATAAANAG	AAGAGAGGTG	600
GTNAGGTGAT	GANACCGTCT	ANATAAATTA	GTG			633

(2) INFORMATION FOR SEQ ID NO:917:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1975 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:917:

CTCTTTAAAA	TCGGNATACT	GACTAAAAAA	TTTAAATTTT	TCAATTTTTT	GTTTAAGTTT	60
TTCTGCTTCT	ACATTATCCA	AAAGAATAAT	CTTATTATTT	TTAAGTTCAA	CACGGTATTT	120
TTTCTCATTC	TGATPTTTGN	TAATATCATC	ATAAATTTTA	TTTACAAAAT	AATAACCTGT	180
TGCCPTTGTG	GTATTTCTAT	TTAGATATAA	AACCATGCCT	TCGTCACTTA	TTTCACCCGG	240
TTTGTTACTT	TTTGAAAAAC	TTGTGAGTAA	AGTCCAAGTC	CCCTTATCGC	CCTTTTTTAA	300
TTCAACATCT	CTATATCCTT	CTTTGTCGGA	TAAATCCTCG	AGATTCTTAA	TTGGATACAT	360
ATCTAACGTT	TNCGCAAAGC	TCTTTGTGAT	NTGCTCTTCT	TGTGAATCTT	CTTGNGGCTT	420
TCTCCGAAGT	ATCGCTTGAN	CTATCACAAAC	CTATTATAAA	AATGCCCAN	ATAATAACAC	480
TTATGANAG	TGCAAGCTTT	TTTAAAGATA	TCCCAATTTT	TTCCACAATC	CTAANAATCC	540
TTATCCAGAT	ACCTAATTTT	TTTCTGCTT	TAATAACCTT	AAAAAATCCA	ATTGACTTGA	600
TAATTTGCTG	TTTTTCACCG	GTTTTGAAAA	AGTCAATTTT	TAACTTTCTA	ATAACCTTAC	660
AAGAACTGCC	TTTCAAATCA	CCCATCCAAT	ATGCATTTTT	AATATAGGTG	ATTTTTCAAG	720
TCGAAATATT	ATAACGACTT	CTTAATTCCT	TAACTATTTT	ATCTTTATTG	CTCATTTTGT	780
ATTCAACATC	ATAACTAGGA	ACATTTTCAT	TAATTGAAAC	ATCACCATTA	TTATATTTTC	840
TCAATTCCTT	AAGATTTGCA	TATTGACCGA	AAAATTTTAA	GTTTTCTATT	TTCTGCTTGA	900
GCTTATCATC	TTTTACTTCA	TCTAATAAAA	TAATCTTATT	ATTTTTCATT	TCAATTTTAT	960
AATTCPTTTC	ATCTGGTAGT	TTACCATTCC	GGTAAATGT	AGTAACCAA	ATAATGGCCT	1020
TTAGCGGTTT	TAGTATTCCT	ATCCAGATTT	AAAACCATAC	CTTCATCATC	CAATTCACCC	1080

GGTTTATCAC	TTT TAGCGAA	ATCTGTGATA	CTATAGCTGA	ATACAGAACC	CACGTCCCCCT	1140
TATCACCCCT	TTTAAATTCG	CCATCACGAT	ATCCTTCTTT	ATCGTATAAA	TCCTCGAGAT	1200
TCTTAATAGG	ATACATATCT	AACGTTTTTCG	CAAAGCTCTT	TTTAATTTGT	TCTTCTTTGG	1260
AACCTTCTTT	TGTTTCATCA	CCTTTACCAC	AACCAGCTAC	AACAACATTT	AAAATCAAGA	1320
TACTTATGTA	CCAATCCAAA	CCTTTNGGAA	TATCCCATCG	CTTCGACAAT	CCTCCCTATC	1380
AGTCATCATC	TTTATTTTTG	GCAGGGTTGA	AAATTTAATT	GAATCGACTA	TTGATAATTC	1440
GCTATTTTCT	TCTTTGGAAA	AAGTCTTATT	TCTTAACNTN	NNATATCCAA	CGGGAACTGC	1500
CTTTTAAGTC	CCCATCAATA	TGCATTTTTA	ATATTGGAGC	TTTATCAGTA	GGAATGTTAT	1560
AACGGCTTCT	TAATTGCTTA	ACATTTTCAT	CTTTATTACT	CATTTTAAAT	TTCCGCGCAT	1620
AACTTGGAAC	ATTACTATTA	ATTGAAACGT	CGCCATGGTT	GTAACCTTTC	AAACTCTTGA	1680
AATCGGCATA	TTGTCCGAAA	AATTTAAAGT	TTTCTATTCT	TTCTTTAAGT	TTTTGATCTT	1740
CCACCTTGTC	TAATAAAATA	ATTTTATTGT	TTTTCATCTC	AACTCTATAA	TTTTTACAAT	1800
AAGAGNTTTC	ATGATTGTCA	GATATAGTAT	CTACCAAATA	ATATCCCTTG	GCCGTTTCGTG	1860
TATTTCTATC	CAAATNTAAA	ACCATACCTT	CATTATCTAA	TACACCTGGT	CTATTACTTT	1920
TGGCGAAATC	TGTGTAAATC	GTCCACATCC	CTTTGTCACC	TTTTTTAAAT	TCGCG	1975

(2) INFORMATION FOR SEQ ID NO:918:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1048 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:918:

TTTGTCATGT	TCAGGTCGAT	TAACACCCGC	TAAATGCACG	ATAAAGTCTG	CTTCAACAA	60
TGCTGACTCT	AATCTTCCT	CTTTAGTGTG	TCGATGTAAT	TCGAAAATAT	GATGATCTGT	120
CGGTGATGTT	AAATCTGCTT	NCAAGTTTTT	TCCTACAAAA	CCTTGTGCTC	CTGTAATTAC	180
AATATNCAAC	GTCAATCTCT	CCTATCTCAT	TGAAGCTTTA	TAATCATNCA	ATTGCTTTCT	240
AACATATTCT	AGTGTTAAAA	GTTTCTCTTT	TATCTCTTCC	ACCGNTAAAA	TATGTGTATT	300
ATCGGAGTTA	TATTCAATAA	GATTGCGTAA	TCTTTTCGGN	TACCGGTTTC	AACATAATTA	360
CTATNATTTA	AATCTCTGGA	GGTCTGGCCG	GNACTCTAAA	ATAATCACCC	ATATCTTCAN	420
AATGGNGNGT	ATTCTTCNCT	CGGCAANAAN	GTNTCTGCTT	TTTCTCTCCA	TGGCAGGAGC	480
GNACCAATGA	TTTCAATTGC	ATTATCAGCT	TCAAACAATT	CTAATAATGC	GGTCGCAAGA	540
TCCCTACCG	TTGAGCTTGG	TGCTTTTTGA	ACCATAATAT	CTCCTGTCTC	TGCATGCTTA	600
AATGCATGAA	CAACTAGTTC	TACCGCATCT	TCTAAGCTCA	TTAAAAATCT	TGTCATATCA	660
GGATCTGTAA	TCGTTAAAGG	TTCTCCAGCT	TTGATTTTGT	CGATAAACAA	AGGTATTACT	720
GATCCTCTTG	AAGCCATCAC	ATTACCGTAT	CTTGTNCCAC	AAATAAGCGT	TTGTTCACTA	780
CGAATATTTT	TTGATTTGGC	TACGAATACT	TTCTCCATCA	TTGCTTTTGA	AATACCCATA	840
GCATTAATAG	GATACGCTGC	CTTATCTGTA	GATTAAACAT	ATGACTTTTTT	TAACAATTTG	900

AATGAATAGC	ACTTGGAAG	ACATTTTCTT	GTACCAATAA	TATTTGTCTT	CACTGCCTCA	960
ACTGGAAAAT	TCACATGACG	CACTTGTTTT	AAGCTGCTGA	TGGATACGTA	TCACATCTCG	1020
CATGTGGTTC	TCACTTGGAT	ATCAGACA				1048

(2) INFORMATION FOR SEQ ID NO:919:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:919:

GAATTCATCA	TGTTNCAAT	CCATTAGGTG	TAGGAGGTAT	CAATGATGCA	ACAACTATCT	60
CTGAAACATA	GATTAAACAA	TGGNGATTCA	GTTTATGGCA	TTTCCAATTC	TATACCGGAC	120
CCATTGATGA	TCGAGGTTAT	CGCAGCAAGC	GGGTATGACT	NTGTTGTGAT	NGATACAGAA	180
CACGTGGCGA	NTANTGATGA	GACACTAGCG	CATTCTAANT	CGCGCAGCTG	ANGCAGCGCA	240
TATTATACCA	ATTGNTCGTN	TCACTGTAGT	GATAGATAGA	GATATCATT	NTGTGTTAGA	300
TCTGGCTGCG	AGAGGCNTTA	TTGTGCCACA	CGTTANGATC	NNCGAGACAG	TTGGAGCAAT	360
NTTGTGATNT	TANCCCGGTC	TCTCCC				386

(2) INFORMATION FOR SEQ ID NO:920:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1677 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:920:

ATAAGAAATC	CACCGGTTGA	AGATAACCCA	CCTAATAACN	TCCAAGTTGA	GNNNTTGNTG	60
CCTTGGNCAA	TTGGTTTTTT	CATTTTAATC	CCTAATTATT	AATATTTTCT	TTTTNCCTAA	120
GAAACTTCAA	TTACCTGAA	GCCCAAACCT	AAAATATTAG	TGAATGCGAT	TGAGAATAAT	180
GATAACCCCN	NNAAGTAGCA	ACATTATTAA	GTNCTNAAGA	TAATAAAGTA	GATTCTGAAG	240
AAGCGAAAGT	ATACATTAA	TATATCAAAG	ATGAAGTTGG	GCTTAAGCAA	TTTGTACGG	300
ACCTTAAAAA	TACGGTACAT	AAATTGAATA	AGAGTAAGAC	CAGCGTAGCT	TCTTATATTC	360
AAACCAGATC	TGGTCAAAAT	ATATTACGTG	TAAGTAAAAA	TGGCACGCGT	TATATCTTTT	420

TCGATAATAT	GAGCTTTACT	GCACCTACCA	AGCAACCAAT	TGTTAAGCCG	AAAGAAAAA	480
CAAAATATGA	GTTTAAATCT	GGTGGTAAGA	AAAAGATGGT	TATAGCTGAA	GCAAATAAAG	540
TGACGCCAAT	AGGTAATTTT	ATACCGGGGA	CATATAGAAT	TCCAGCTATG	AAATCAACTG	600
AGAACGGTGA	TTTTGNAGGC	TATTTAAAT	TTGATTTTAG	ACAAAGTAAT	TCTGAAACGG	660
TAGATGTTAC	TGAAGATTTT	GAAGAAGCAA	ATATAACTGT	AACTTTAAAA	GGCGATACAA	720
AATTAAATGA	TAGTTCATAA	AAAGTAACTA	TAAATGACCG	TGAAATGGCA	TTTTCAAGTT	780
CCAAAACGTA	TGGTCCATAT	CCACAAAATA	AAGATATTAC	CATTTTCAGCT	TCAGGTAAAG	840
CGAAAGGTAA	AACATTTACA	ACACAGACGA	AGACGATTAA	AGCCAGCGAT	TTAANATACA	900
ATACAGAGGA	TAACTTTGAA	TTTTGGGACA	GNGAAGATAT	CGNNGGACTA	TGTTGAAAAG	960
AAAGAAAAAG	AAGAAAACAG	CTTGAAGAAC	AAATTGATAG	AATTCTTTGC	TGGATATTCT	1020
TTAGCGAATA	ATGCTGCGTT	TAATCAGTCA	GATTTTGATT	TTGTATCGTC	ATATATAAAA	1080
AAAGGATCAT	CTTTTTATGA	TGATGTAAAG	AAGCGTGTAT	CTAAAGGAAG	TTTAATGATG	1140
ATTAGTTCAC	CACAAATTAT	AGATGCTGAA	AAACATGGTG	ATAAGATTAC	CGCAACCGTA	1200
AGATTAATAA	ATGAAAACCG	TAAGCAAGTA	GATAAAGAAT	ATGAGCTTGA	ACAAGGCTCG	1260
CAAGACCGCT	TGCAATTAAT	CAAGACATCA	GAAAAATAGA	GTATTAAAC	TTAAATAAGA	1320
TGCATGTGTC	ATGGAATACA	AACAACATCC	TTTCAAAGTA	TTTACAATTA	GTGTGAATTA	1380
CTTTGAAGGG	ATTGGTTTTT	GGGTGAAAAA	ATTTATGGAG	TGCTGAGGTT	TATATCAATN	1440
TNATTACCCT	NNATAAGGTT	GGTAATGATN	GTNCAATGAA	ACTTGGTGAA	GTAATGCTTA	1500
ATATATAAAA	GAGCATATTT	AAATTTAGTT	TCTGTTTCGTG	ATAGTTATAA	ACTAATCATT	1560
ATATAAAGGA	GATAGTCATA	TGAATTGATT	TTAACGCATT	TTAACAAGCG	TTCACCGATA	1620
TTTATTATTA	ATTTAGGATC	TTTGGACGGG	CCATTGGGAG	CATTATCGAT	AGATATT	1677

(2) INFORMATION FOR SEQ ID NO:921:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 914 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:921:

GGAACTCGTT	TTTAAAAGTA	ACCAATCAAA	CAAACCTCTCA	GATTATTACT	GTATCAGTTA	60
CAACTGGGAA	TAAATCTGAA	TCTGACAAAA	TTGTTAATAG	AATATCTAAA	GTTTGTGCAC	120
ATGATATGCC	TAAAATTATG	AGTGTTGATA	ATGTTACGAT	ACTTTCCTCA	GCACATGATA	180
ATGCTGTAAA	AGTATCTCCA	ATAGTATCTG	TCAACTTAGT	GATCAGCATT	ATTGTTGGTA	240
TTGTTTTAGC	AATATTGATT	ATTTTCTTAA	AAGAATTATT	AGATAAGCGT	ATTAAGACAG	300
AAGAAGATGT	TGAATCGCAA	CTAGGATTAC	CTATTTTAGG	TTCAATACAA	AAATTTTAAT	360
TTACGAGGAA	TTACCATGAC	GAATACACGA	AGAAGTACAT	CAAGTTTAAT	TGGCCATGAA	420
CAACCAAAGT	CACCTATTAG	GGAGAAATTT	CGGAGGCATA	AGGATCAAAT	ATTATGTTTG	480
GAAATCCTGA	CAGGGCAGGT	CAAAGCATTG	TNATCACTTC	AGAGGCAACA	GGCGCAGGTA	540

AGTCTACAAA	TGCAGCAAAT	TTAGCAGGGG	CATATTGCGC	AAGCAGGGTA	TAAAAAATA	600
ATCCGNNGAC	GGGGATATGN	GTAAACCTAC	GCAGCATTAT	ATTTTTTAATT	TGCCAAACAA	660
TGAAGGCCTA	TCAAGTTTAT	TGCTAAATTG	GTCAACTTAT	CAAGACAGTA	TTATCTCAAC	720
TGAAATTCAA	GATTTAGACG	TCTTGACGTC	TGGGCCAATC	CCACCGAATC	CGTCAGAGTT	780
AATTACATCA	AGGGCATTTG	CAAATTTGTA	TGACACATTA	TTGATGAATT	ATTACTTGGT	840
CATTATCGAT	ACGCCACAGT	GAACACAGTT	ACAGGTGCGC	AATTATTTCA	AAGTTTACCG	900
GAATTTGGTC	TACG					914

(2) INFORMATION FOR SEQ ID NO:922:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 913 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:922:

GATCCATCAT	CTCTGTTTCA	TTTGCGGCCC	CGTCATCGAT	ATTAGNCAA	TATATGGTTA	60
TTGAATATCA	ATCAATACTT	AATCAATCTC	CATAAATAAG	TGATAATAAC	NAAGAAGATN	120
TATCCGACCC	TTTGCTCTTG	TTCCAAAATG	ACACCTAGAA	TGTTACCTGC	CTGCTTTTTTC	180
CATAAGTGCT	TTTGCTTTTT	TAACCTCATT	TTTATCATTT	TTTTCACTAT	CAATTACTAA	240
CAAGACTATC	TTTAATAGCA	CGAGCGCANA	NAGTTGTGCA	NCAGTCACAG	TAATAACTGG	300
CGGTGTANCG	ACAATAATAA	TGTCGTAACG	TTTATTAAAC	AGATCAACTA	ATTCTTTGAA	360
CCTTTCAGAC	CCAATTAACT	CAGATGGATT	TGGAGGTACA	GGGNCAGCTG	TTAGCAAATC	420
TAAATTTTCA	ATTTCTGTGC	ACGTAATTGN	TTCTGACATA	GTCGNTCGAC	CAATGATTAA	480
GCTTGATAGT	CCATTATTAT	TGTGCTCATT	AAAAATATAG	TTTTGTGTTG	GCTTACGCAT	540
ATCGCCATCA	ATAACTAATG	TCTTATAGCC	TGCTTGTGCA	TAAGTAATCG	CTACATTCTGA	600
TACAACGTGA	CTTTTACCTG	CACCAGGCTT	TTCAGAAGTA	NCCAATAAGC	GCTTTACTTC	660
ACCATTTGCT	TTTGAAAACA	TGATGTTTGN	ACGTATACCT	CGNNACTTTT	CACTAATTGT	720
TGAGTTTGGG	TTTTCATATA	CAAATAGTGT	TGTTGTCGTA	TTTTCTTTT	TTGACATAAG	780
TAGCAACCAT	CCTTAATTAA	ATTTTGNAT	TGAACCAAT	ACAGGCAATC	CTAATTCTTT	840
CTCTACATCT	TCTTCATCTT	TAATTCGCTT	ATCGAAAATT	ACTTTGAAGA	AGATATATAT	900
AAGCGCTCGT	GCC					913

(2) INFORMATION FOR SEQ ID NO:923:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 922 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:923:

```

CAATAAGCCA CCCANTTTT TGNTCCATT TTTTGAAGGA AGANGTTTTG ATTCATTNTG      60
GTTGTCCCAT CCACCNNGGA GCAGTCCCCA AGACCTCCCC CNTTGGCATT AAGCCCNNGG      120
AATNTTGATA ATATATAAGN ATTTNTGCCC NGGCCTAAGA CCAACCAATT NAAAGATNTT      180
GNATCCNTTA AGTNTGTGTG TAAACATTTN CCCAGGACCA AGTGCCNAAT ACGGGATTAG      240
CTTCATCACA TGNCCTAGAT TATAAAGAAA TATTANATGT TATCGAATAG ATAATAATTT      300
AAATGAAATT GAGTGAAATG AATATTTTAA ATATAGCATT ATAGTTTGGN CTAAAAATTT      360
ACACAACGGA AGGATGTAAT TATTATGACA NCCAACACAG TTACATTACA CACAGCACAT      420
ATTGTAAGTT TAGGAGATAT CGAAGAAGCT AAAGCAAGCA TTAAACCATT TATTCGTCGA      480
ACACCACTAA TTAAATCTAT GTATTTAAGT CANAATATCA CTAAAGGTAA CGTATATTTA      540
AAACTTGAAA ATATGCAGTT TACAGGTTCA TTAAATTTA GAGGTGCTAG CAATAAAATT      600
AATCATTTGT CAGATGANCN CAAAGCTAAA GGTATTATTG GCGCATCAGC CGGAAATCAT      660
GCACAAGGTG TAGCTTTGAC AGCAAAACTA TTAGGTATTG ATGCAACGAT TGTGATGCCA      720
GAAACAGCAC CAATTGCTAA ACAGAATGCT ACCAAAGGAT ATGGTGCAA AGTCATTTTA      780
AAAGGTNAAA ACTTTAATGA AACTAGACTT TAGATGGAAG AATTAGCGAA AGAAAATGGT      840
ATGACAATTG TTCATCCATA TGATGATAAG TTTGTCATGG CTGGTCAAGG AACAATAGGA      900
TTAGAAATTN TAGATGATAT AG                                          922

```

(2) INFORMATION FOR SEQ ID NO:924:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3165 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:924:

```

CAAGCCAGTT CAACTNACCG ACCCGGTATA TTTGGGGAAT ATACGAANCN CNNTCAGATG      60
ATCNAAATAT GANTGANACN CGGTNGCGTT CTCNAGNCAN AACAGNGTTA AATAANCGTA      120
AGTCGGCAGT TATGTCANAT GAGATTACTT CTNCTGATTG GGNAGTTACG NNTCCACACG      180
AGANNATATC ANNTGGTGAN NCAGNCAGAG TAAAACATAG AGATTTTGAC CCGCCATTGT      240
ATGTAGAGGC AGAAGTTATT GCCGAAGAAT ATAACATAAT TTCAGAAAAT AGCACATATA      300
CATTCGGTCA ACCTAAAGAG TTCAAAGAAT CAGAATTACG AGAAGAGTTT AACAAGCGAT      360
TGAACATAAT ACATCAAAAG TTAACGATA ATATTAGCAA TATCAACACT ATAGTAAAAG      420
ATGTTGTAGA TAGTGAATTA GAATACTTTG AACGCAAAAT ACACAAAAGT GATACACCGC      480

```

CAGAAAATCC	AGTCAATGAT	ATGCTTTGGT	ATGATACAAG	TAACCCTGAT	GTTGCTGTCT	540
TGCGTAGATA	TTGGAATGGT	CGATGGATTG	AAGAAACACC	AAATGATGTT	GNAAAATTAG	600
GTGGTATAAC	AAGAGAGGAA	AGCGCTATTC	AGTGAATTAA	ACAATATATT	TATTAATTTA	660
TCTATACAAC	ACGCTAGTCT	TTTGTCAAGA	AGCTACAGAA	TTACTGGAAT	AGCGAGTACT	720
TAGTAGATAA	TGATTTGAAA	GCGGACTTAC	AAGCAAGTTT	AGACGCTGTG	ATTGATGTTT	780
ATAATCAAAT	TAAAAATAAT	TTAGAATCTA	TGACACCCGA	AACTGCAACG	ATTGGTCGGT	840
TGGTAGATAC	AAAAACTTTA	TTTCTTGAGT	ATAGAAAGAA	ATTACAAGAT	GTTTATACAG	900
ATGTAGAAGA	TGTCAAAATC	GCCATTTTAC	ATAGATTTAA	ATTATTACAG	TCACAATACA	960
CTGATGAAAA	ATATAAGAA	GCGTTGGAAA	TAATAGCAAC	AAAATTTGGT	TTAACGGTGA	1020
ATGAAGATTT	GCAGTTAGTC	GGAGAACCTA	ATGTTGTAA	ATCAGCTATT	GAAGCAGCTA	1080
GAGAATCCAC	AAAAGAACAA	TTACGTGACT	ATGTNAAAAC	ATCGGACTAT	NAAACAGACA	1140
ANGACGGGAT	TGTTGAACGT	NTAGATACTG	CTGAAGCTGA	GAGAACGACT	TTNNAAGGGG	1200
AAATCAAAGA	TAAAGNTACG	GTTANACGAA	TATCGAAACG	GATTGGAAGA	ACAAAAACAA	1260
TATACTGATG	ACCAGTTAAG	TGATTTGTCC	AATAATCCTG	AGATTAAAGC	AAGTATTGAA	1320
CAAGCAAATC	AAGAAGCGCA	AGAAGCTTTA	AAATCATACA	TTGATGCTCA	AGATGATCTT	1380
AAAGAGAAGG	AATCCCAAGC	GTATGCTGAT	GGTAAAATTT	CGGAGAGAAG	AGCAACGCCG	1440
TATACAAGAT	GCTCAAGCTA	AACTTGNAGA	GGCAAAACAA	AACGCAGGAN	CTTAAAGGCT	1500
TAGANACGCT	GAAAAGANAG	CTAATGTTTA	TACAGACAAC	AAGGTCAAAG	AAAGCACAGA	1560
TGCACAGAGG	AAAACATTGA	CTCGCTATGG	TTCTCAAATT	ATACACAATG	GTAAGGAAAT	1620
CANATTAAGA	ACTACTAAAG	AAGAGTTTAA	TGCTTCTAAA	AGAACACTAT	CAAGAGTGTT	1680
AGCAGACATC	ACTGTAAATG	CTATGAAAGG	CATCTATTTA	AGGTATGACG	AAAATGGGGC	1740
GATTACTTCA	CATACTATTG	ATAAAGATGG	CGTGAAAATT	AGTGGCGATA	AAGTTGATAT	1800
AACAGCGAAT	AGAGAATTTA	ATGTATTCGC	AAATAATATT	AATAACAAAG	TTGGTAAAAA	1860
TGACATTGTT	AATAGCCTAA	ACTTATCAAA	TGAAGGTCTT	GACATCAATG	TGAATAGAAT	1920
TGGTATTAAA	GGCGGAAATG	CTAACCGTTA	TGTACAAGTT	CAAAATGATT	TTATTGAACT	1980
TGGCGGAATC	GTACAACGAA	CTTGGAAAGG	CAAACGATCA	ACCGATGATA	TATTCACACG	2040
TCTTAAAGAT	GGACATCTAA	GGTTTAGAAA	TAATACCGCA	GGCGGGTCAC	TTTATATGTC	2100
ACATTTTGGT	ATTTCAACAT	ATATTGATGG	AGAAGGCGAA	GACGGAGGTT	CATCCGGTAC	2160
TATTCAATGG	TGGGATAAAA	CTTACAGTGA	TAGCGGTATG	AATGGCATAA	CAATCAATTG	2220
TTATGGCGGT	GTAGTCGCTT	TAACATCTGA	CTACAATCGA	ATTATTATCG	ATTCATATGC	2280
TTTACGTAAT	ATTGAAAGTA	GAGAAGCGCC	GATATATTTA	TCTCCGAACA	CCCCAAAATT	2340
AAACCTGGNT	TTAANCCGAT	TCGCATTCAC	ATTATCAAAC	GCTGATAGGT	NCATTACGAA	2400
ACTGGCGGTT	ATATCATGTT	GGGTTCAAGA	TGNAANCTAT	AAGTNCGGTG	CTGGATTAAAG	2460
ATTTTCTAAA	CGTACCAATA	AAGGATTGGT	TCAAGTCGTT	AATGGTGACT	ATGCTACAGG	2520
CGGAGACACT	ACAATTGAAT	CAGGTATGGC	CAAATTC AAC	TTAGTTAANC	GGAAGAGATG	2580
GAAATAGTTA	CGTTAGCATT	CAAAGTTATG	ATTTATTGGC	GGTAGGTTCT	GATAATGCTG	2640
GCGATAGAGT	CGCTTCTAAT	TCTATTTATA	AGCGTACTTA	TTCAGCACCT	GCTAACTTAC	2700
ACATTACTTC	TGCTGGAACA	ATTGGGCGTG	CTACTTCTGC	CAAAAAGTAT	AAAATTTCAA	2760
TCGAAAACCA	ATACATCAAT	GAAGACGATC	AGTTCAGTCA	TTCAAAAGAG	ATTTTAAAGC	2820
TTCCAATTTCG	TACATGGTTT	GACAAATATG	AATCGGAAAT	AATGGCTAAA	GAATTGGAAG	2880
GTGGTAAAAA	GTTATCTGAT	GATACTTTTA	AACTTAGTCG	ACATACTGGC	TTAATAGCGG	2940
AAGAGGTTGA	AGAATTAGGA	TTTAATGAAT	TTGTTATTTA	TGATGACAAC	GGAGAAATCG	3000
AAGGTATCGC	ATACGATAGA	CTTTGGGTTT	ATCTANNACC	TATTATTACC	CNAAAACCAN	3060

CANTCAAANA NCGNAAAACN TANTGGNGGN NTTAACNTCT NATNGACNGC AACCAGGGTC	3120
CNCATNCCAC CTCCACATTA TACAANTCAC TTTCTCNCGT CACTA	3165

(2) INFORMATION FOR SEQ ID NO:925:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1714 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:925:

AATGGGNAAT TGTCGGATGA ATTGTATCAA CCAATTACAA GCGATTAATT AAGAATCTAA	60
TGTCGAAGAG AGTGAAGAAT ACTTGACAAT ATTAATAGCC AGATACAGTT ATACACTCAA	120
GTAAAAGTAA CAACACCNAT TTTAGTGAAA GCACCAATCG CTGTCGTCGT ATTTTACTTA	180
AAGAAGTAAG AGATTCAATT TTTAGAGAGA AAATGGTAGG TGAAGGCTTA GCAATCAAAG	240
CTCATGAAGA ATCCAAAGTA ATCGCACCGT TCAATGGTTT AATATCTATG ATTGTACCAA	300
CTAAGCATGC AGTTGGTATT CAATCAGAAG ACGGTGTGGA CATAGTCATT CATATTGGCG	360
TGAAGNCAGT TGACTTGGAA GGTAAAGGGT TCAAGTACTT TGTAAACCAA AATGATCATG	420
TTGAAGCAGG CCAAACGNTG TTGCAATTCG ACCAGCAATA TATACAACAA CNAGGCTACA	480
ATGCTGACGN TATTGTCTGT ATTAGCAACT CTGCCGATTT AGGAAAAGTA GAACTGACNA	540
TGAATGAAAT CATTACGACT GAAGATGTTA TTTTNNAAAT ATTTAAAAAC TAGGAGTGTG	600
TTGTAATAAT GACAAAANTA CCGCAAATTT TTAGTGGGG TGNCGCTCTT GCCGCAAATC	660
AATTTGAAGG GTGAATATGA AAAAGGTGGT AAGGGGTAA GTGTAATTTG ATGTATGACG	720
AGTGGTGCAC ATGCCAAAGC ACGTCAGATT ACAGAATCAA TAGACCTCAA TCACCTATAA	780
TCCAAATCAT TGGAGGTATT GATTTTTATC ATCGTAATAA GGGAAAGATAT TGCCTTGT	840
AAAAGAAATG GGATTGAAAT GTTTACGTAC GTCGATTGCG TGGACACGTA TCTTTCCGAA	900
TGGGGATGAA GATGTGCCAA ATGAAGAAGG ACTTGCCCTT TATGATCGTA TCTTTGATGA	960
ATTAATTGCA CAAGGTATTG AACCTGTTGT GACGTTATCA CATTTTGAGA TGCCACTTCA	1020
TTTAGCGAAA CATTATGGTG GATTTAGAAA TAGAGAAAGT GTCGATTATT TTGTGCATT	1080
TGCGCGTGTT GTATTTGAAA GATATAAAGA TAAAGTTACA TATTGGATGA CGTTTAATGA	1140
AATTAATAAT CAGATGGACA CATCAAATCC TATCTTTTTA TGGACGAATT CTGGGGTAGC	1200
ATTGACAGAA AATGATAATC CTGAAGAAGT CTTGTATCAA GTAGCACATC ATGAACCTTT	1260
AGCCAGTGCT TTAGCAGTTC GTCTTGGTAA AGAGATTAAT CCGAAGTTTA AGATTGGAAC	1320
AATGATTTCA CATGTACCCA TTTATCCATA TTCGTGTCAT CCGAAAGATA TGATGGAAGC	1380
ACAAATTGCG AATCGCTTAC GTTCTTTTTT CCCGGATGTC CAAGTGAGAG GTTATTATCC	1440
AAGCTATGCT AAAAAATGT TGGCACGAAA AGGATATGAT GTTGGATGGC AAGAAGGGGA	1500
CGACAGTATT TTACAGCAGG GCACGNTGA TTATATTGGC TTTAGTTATT ACATGCTTAC	1560
GGCTGTAAAA CATGATGTTG ATACTACAGN TGAACAAC ATCGTCAACG GTGGGTTTGG	1620
ATTCATCTGT GGAGAATCCG CATATCGCAA CGAGTGATGG GTTGGGCGAT GGATCCAGAT	1680

GGCTTAAGAT ATACAATTGG ACTGTGTTAT TTGA

1714

(2) INFORMATION FOR SEQ ID NO:926:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:926:

AAATACTTCT TCATAGAATA TGTTCGTAAAC GTTAGATTTA GTAGTTAAAG TAAGGTCATA	60
AATTTTCAAT ATGCCCTTGA TTAATTATG TTTAGACTGA GCAAACTCT CATTTTAAAC	120
ATCCGCTGTA CGCAAGGACA ATTACTTTAT CAAAATGACT TCCAATTTCT NAAAGATGTA	180
CTACAAAGTG TTGNTGNAAA AGTTATTGCG GAAGGTAATG TCATTACACC GGATATGTAT	240
NAACGCGTGA TGGACTTAGG CGTTCATTGT TCAGTCGGTG GTGGTGGAT AACACGACCA	300
AANGAAATTA CGAAACGTTT TGGNCANGTT ATGGAAGATT AAATGATAAC GATAAAAAAA	360
CGAGATGACC ANCATTAAAT AAAGGTACCN NATTATCTTA GGTGGNTGAA TGAATGTAAT	420
GGGTTCANCT CGNNTGTGT GTGTACGATA GTGATTTTAT TTTACNTTG AGTTATCCAC	480
AAATANGTAA AGCGACGGG ATGGTGATTA ATAGCGACAA NNGCCACGCC TTAAAAAACA	540
CATGATGATG AGTNTCCAGA CAGGGTATTT TAATTTTANA TGNTAGTATT ACAATAGCAC	600
TAC	603

(2) INFORMATION FOR SEQ ID NO:927:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:927:

GGCAGGAGCG GAAAGGTTTG AATTCATCTG ATGAATCATC ATAATCCTTG ATAGAACGTT	60
CATATTTATC TAAATCTGGC ATGCGTTCAT CGTCAACTG AGTTAATTGA TAGTGTTTAA	120
TAATACTGTT TAATTTCTTA GCATAGTTTG GATCTGTAGC ATATGTTTTA GATAAGTGTG	180
ATGTTGCATC TTTATAAGAA TCGGCTTCCG ATTTCCATGT TGGTTTATAA ATTGTTCCAT	240
TGCCATCAAT ACCATTTTAA ATAAGGTCAG AGTAATCTTT TAGTGATTCT TTCGTGCTTG	300

GATATTTTCG	GAATCCAGCA	TTAATACTAT	ACAATTTATT	ACCATCAGCT	TCCTAATGTG	360
TTAAAAGGAA	CAGAATPCCC	TTCAAAAGCA	CCTTTGATAC	CGAATAAAAT	ATGGTTTGGT	420
GACTTAGCTA	AAGCACTACG	ACCTGAGTCA	GATTCTAAGA	TIGCTTGGGC	AATCATGACA	480
GACGCATAAA	TATCGTTATC	TTGACCAATG	CGATGTGCAT	CTTTAGCAAT	TGATTTGACA	540
AATTGACGTG	TATCTTTTGA	GTCAACAACG	TTAAATTGTC	CGCTATCATC	ATTGTTAGAT	600
ATACTAGGAT	CTGTTTCGAA	TAATGATGTT	GCACGTGTAT	CCTTTTGATT	AACATCGNTA	660
TTGAATGATT	GAGCAGGTTT	AGATTTATGT	TTCAATTCAT	CTTGTGTTGG	NAACTGTGGA	720
TTCTTTGGTA	TTAGATTTNN	CATTTTGGG	CTTTTNNTAG	ATTGAGATGC	ATAATCTTTG	780
NGGGGTTTTC	TTTNGGATCT	TCACTGTATT	GGNCCCCAAA	ATAGAGTCTA	AAGCCCATCT	840
GACAATGATT	GATATCTTTC	C				861

(2) INFORMATION FOR SEQ ID NO:928:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 920 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:928:

GATTCTACCA	GCCGCATTAT	CCACACCGGC	ATTATTAAAC	AACACATCGA	TTCTTCCAAA	60
CTGTTCTTTT	ATGTCAGACA	CAAAGTCTAC	CACTTGTTGT	TCATCTGAAA	TATCCACATT	120
ATACGCCTTC	GCATTGTCAC	CGTTACTTTT	AATTTTATCG	ACAGTCTCCG	ATACCGCTTC	180
AGCTATGTCT	ACCGCCAATA	CATACGCACC	TTCTTGAGCT	AAAGCGATTG	CAGAAGCTTG	240
TCCGATACCT	GTACTTGCTC	CTGTTACGAC	TGCAACTTTA	TTTTCCAAAC	GTTTCATTCA	300
GTCACCTCTA	TACAACATAT	CTTAAACTTA	CAGGCCTTAT	TTTCCACTGN	TCAATGCTTC	360
ATAAACCTAA	TAGATAAGTT	TCCAGGCAGT	CTTAGCTACT	CTCTGCTATA	CAAATTCTTA	420
TTGAATTACT	CAAAATATTT	ACAATATTAG	TCTTTTTCAT	TTCTTTGAAA	ATTGGTACTT	480
GTGGAGAGTA	TTTGTGGGTA	CAACTTTAAA	TATTTTACAA	AGGGGGGAAT	CCAATTGATG	540
ACAATCAAAA	CATCAACAAA	AGGGGTCTTA	TCCGTCAATC	CGTTCCTTGA	ATAGTGTTGA	600
AAAAATTGGA	AATAAATTGC	CAGATCCTAG	CGTCTTATTC	TTTTTAATGT	GTGTGGGCTT	660
AGCCATTATG	ACGTGGGTTA	TCTCATTATT	NAATGTATCT	GTTAAGCATC	CAGGTACGCA	720
TCANACCATT	TATATTAAAA	ATATAATTAG	CCATGATGGA	TTNACGATGA	TAATGAATGA	780
TACGATTAAA	ANTTTCTCAG	AGNTCCCAGC	ATTAGGCTTA	GTA CTAGCAG	NGATGATTGG	840
TATTGGTGTT	GCAGAGNAAA	ACAGGATACT	TCGATAAGTN	AATGATTTC	GTTGNGAATC	900
GNGCACCACG	ATTTTAAATT					920

(2) INFORMATION FOR SEQ ID NO:929:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:929:

```

GGCACCAGCT AGCACAAACA GTTTGAACTA AAGAAGATTT AACTGAGTAC AATAAAATGT      60
CTAAGTCTGA ACAAGCCGAT ATAAAAGATG TTGGCGGATT TGTCGGTGGG TATTTAAAAG      120
AAGGCAAACG GCGTGCTGGT CAAGTCATGA ATCGTTCAAT GCTAACACTT GATATCGATT      180
ATGCAGCCCA AGATATGACT GACATATTAT CTATGTTTTA TGATTTTGCA TATTGTTTAT      240
ATTCAACACA TAAGCATAGA GAGATAAGTC CAAGACTGCG TTTAGTGATT CCTTTAAAC      300
GAAATGTAAG TGCAGATGAG TATGAAAGCT ATTGGGCGTT AAGTCCGCAG ATATCGTTGG      360
GCATGGATTA CTTGATGAT ACAACTTATC AACCACATAG GTTAAATGTT ATTGGCCTTC      420
CACCTAGTTA ACGATGCGGA ATTTTCCTTT ACCTATGAAG ATTTACCTTT GTTAGACCCC      480
GATAAAATAT TAAATGAATA TGTTGATTGG ACTGACC      517

```

(2) INFORMATION FOR SEQ ID NO:930:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:930:

```

CCTGTANANT CACCACCAGG TTCACGGAAA TGGAAGTTGN ACATCGACCA AATCCAGGTG      60
ACCCCCAAGT GACCTTTCGC ATCTATGATG CCCAACACCA TTGCTTGGGT CAATTGCAGG      120
TGCAATTTGT TTAATTACCT TACCATCAAT TAAAATATCT GCTTGTTGTA ATTCTCCATT      180
TTGTAATACT TTACCGTTTT TAATTAATTT CATCATTTTC GTCCCCTTAC CTATTTTAAT      240
AATTCATCAA TGACTGCCAT TCTTAAGTAA ACGCCATTTT CCATTTGCTT AAAAAATCTT      300
GATTTTGAAG CTTCTACTAA ATCGCTTTGT ATTTCTACTC CTCTATTAC AGGTGCCGGA      360
TGCATAACAA TAGCATGTTT TGTAATTTG TTATAGCGCA CTTCAATTAA GCCATGCTTT      420
TGATGATAAT CATCTGCTGC AAATCTAGTT TCTTCTGCAA GCCCATGTCT TTCATGTTGA      480
ATTCTTAATA ACATNACTAT ATCTACTGTT TCTATAACAT CATCTATATT TACATAAGGT      540
GCTTCTAAAG AATCATCAAT CCAAGCATTT GGGCTATTAA ACATTACGTT TGCACCTAAT      600
GCTTTTAAAC TATGGTAATT ACTACGTGCG ACACGTGAAT TTTTAATGTC TCCACAAATC      660
AATACATCCA AGCCTTCAAA ATATCCATAT TCTTCATATA TCGTCATTAA ATCAAGTAAA      720

```

CTTTGTGTTG	GATGTTGTCC	ACTACCATCA	CCAGCATTCG	CAATTGGGAT	GTTAATATTC	780
GCTAATTTTT	CATAGTAGTT	ATTAAACGGA	TGTCTAATGA	CTAATAAATC	ACAGCCAATA	840
CTTTCCTAAAG	TTTTACATGT	GTCATATAAA	GATTCAACCT	TTTGAAACAG	ATGATGTTGA	900
TGTTTCAAAG	CTAATCGTTT	TTAACCCTAG	CTCAAGTGCC	GCTCGTGCCA	TTTCAAAACT	960
ACATTTTGT	CGAGTAGAAT	TTTCAAAGAA	TAAATTTGCG	ACATATTTCC	CTTCAAAGTT	1020
TGGTAGTTGA	CGTTCACCAG	ATTTAAATTG	ACTTGCCTTT	TGGATAAGTT	TGTATATTTG	1080
ATCTGTAGAT	AAATGTTCCA	TTGATAATAA	ATGATTGATA	AAAGCGCCCT	CCTTAATTTG	1140
TAAATCTTAA	TTGTTTGT	TTTTCTCTTT	AGGTAAGATT	AAGTTCAAAA	TAATTCCTGA	1200
AAGTGCAGCT	CGTGCC					1216

(2) INFORMATION FOR SEQ ID NO:931:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 670 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:931:

TAGTGNCGGN	GNACCTGTAA	GATAGTAGTG	NTGGGGAATA	GCGNACCCTN	CTAANTACCG	60
NAAGGGGAAN	NATATTGCAG	TANCCACATG	ANTTGCCCAN	CACCNTCTTC	ACAGGGGNAT	120
TAATANAGAA	NCCAGAACGT	NCGCCGCNAG	CCCNCANNCA	GGNAAATACT	ACATCACTGG	180
TGACTTAGCT	CATGTAGATG	ATGATGAGTA	CTATCTGNGT	TGANGGNCGT	CGAGATGNCA	240
TTATTATTAG	ATCAGACTAT	ACGANTGGGC	CTGTTGAAGA	TGAAGATNCG	TTANCGNATC	300
ATCCANCCGT	TAAAGAATGT	GCTGTAGTAN	CANAACCTCA	TGATATACGA	GGAAATATTG	360
TTAAAGCATT	CGTTATTTTA	CAGGACCATA	CTGCGGGTGA	TGATACGTTA	GTTAAAGAAC	420
TACAACAATT	TGTTAAAAAT	GAAGTTGCAC	CATATAAATA	TCCGAGAGAG	ATTGAATTCC	480
CTTTCGTAAT	ATCAGGCATA	TTTGTAGTTG	CAAATAATTC	ACCTGAACGG	TTTGGATAAA	540
TGAAGAAACT	ATATTCTTCA	CCTACTTCTA	ATTCATCATC	ATCGTTCATT	TCTGATTGGT	600
TTAACTTTAC	GTTTTACCG	TTTGGTCCTT	TAAAAGGTA	AGTTGAGCCT	TGTAACCCTA	660
CTACTTCAAG						670

(2) INFORMATION FOR SEQ ID NO:932:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:932:

CTGAGAGGCA	TGACGATGAT	TCAGATTATC	GGTGAATTT	TAGTGACGAT	TGTNTTGCTN	60
AATCATTGGA	ACTTTTGGAT	TTTAGCGATA	GGATTTATCA	TTTAAATAGC	ACCAGNGACA	120
GGTGTGCGA	CACTTGGTTT	TNCAATAGCT	ATGGATGAAA	GTAGTAGTGG	TAGAGGGAGT	180
TCATCAAGTT	TATTAGGTTT	AGTGCAGTTT	TTATTTGGTG	GTGTNGCATC	GCCATTAGTG	240
GGGGTAAAAG	GTGAAGATAA	TCCTATACCT	TACATAATTA	TTATTATAGC	TACAGCAGNT	300
ATATTAATTA	TTTNACAGAT	TTATAATATG	AAGGTATTNT	AAAACAAATC	GATGATAAAC	360
ATAGNTTCTT	CTATTATATT	GAATTGANAA	ATTAANAAAC	AAAACCTGAG	CTATTCATAG	420
ACCTATGAAT	TTAGCATCAA	AAATAAAAAAT	GCCGAGATTA	TTATGTGGAA	ATCTCGGCAT	480
TTTTATNTTG	ATAGCACC GC	AACATATGTA	CTATNATCTA	TCCAGNTGGT	TTAACTTNAT	540
CTAGTTGTTT	TATAGCATTT	CTTTATTAGA	ATGANACCGN	ATTATTGGAN	TTGAAGTTTA	600
NTCGTATTAG	CCAATAAAAT	GTCAGCAACT	TCTTCAGGTG	ATTCATNACA	ACCNTTCGAA	660
AGCCAATTAA	TAAACACCCC	AGNTTGACCG	CCTATGATAT	ATGTAACATA	AAGCTGTTTA	720
TTGGCTACTG	TAGTACTATA	GTCATTCATA	ATTTGTTGGA	TAGTAATCTC	TCGCTAAATT	780
TATATAGTCT	ATGAATAATG	TTTTCATTTG	ATAGGTAAC	AAAATGTCTT	TGAAAACTG	840
CTCATTGTGC	TTGATATACT	TAGCAATAAT	AATGAAGAAT	TTATAAAGTT	TAAGCTTATC	900
CTGTTTAATA	TTTTTCGAAAT	TATGATGTAG	CGCGCTTAGA	AGAAATTGGA	ATTTTCTTTT	960
ATGCTTTGAG	TTGATGGTAT	CCAATAAATC	AAATTTATCT	TTGTAATAAT	CATAAAAAGT	1020
AGAACGATTA	ATATTACAAT	ACGCGCAAAT	CATTTTAGTG	GATATTTCTT	GAAAAGGATA	1080
TTCAGCCATC	AAATCAACAA	GTGCGTTTTG	AATTTCTATT	TTGGCTTGTC	GGTTCATATT	1140
GTTACACCTT	TGGGGAATTT	TTAANCCAAC	ACTCTTATTA	AAAATTTGGT	GGGGTCTTTT	1200
AGTTATCATG	TCTCTATAAT	AAATAAAGTG	AATTTTAAAA	GCAAATCGGA	GGAAATGTTT	1260
CATGAAAAAG	ATGATATTAA	TTAATGTCAT	TACGGTTGTT	GTACTGTTAG	CAATTGGGAT	1320
TGCTGGCTTT	TATTTCTGGA	ATAAAACAAC	AAGCTATGTA	ACAACTGATA	ATGCAAAAGT	1380
AAATGGCGAT	CAAATTAAAA	TAGCAAGTCC	TGCATCTGGA	CAAATTAAAT	CACTTAATGT	1440
TAAACAAGGT	GACAAACTCG	ATAAAGGTGA	CAAAGTAGCA	ACTGTTACTG	TACAAGGTCA	1500
AGATGGCGAA	ACGAAAGATA	TGGATCTTAA	AATGCCTCAA	AAAGGTACAA	TTGGCAAATT	1560
AGATGGTATG	GAAGGTTCAA	TGCGTGCAAG	CTGGTAACCC	AATCGCTTAT	GCATACAATT	1620
TAGATTGATT	TATATGTNAC	AAGCAAATAT	TGACGAAAAA	GATATTAAAG	ATGTTGAAGT	1680
AGGTAAAGAT	GTTGATGTGA	CTATTGACGG	TCAAAAAGCT	TCTATTAAAG	GTAAAGTTGA	1740
TAGTATTGGA	AAAGCAACTG	CTGCAAGCTT	TTCATTAATG	CCATCATCAA	ATAGTGATGG	1800
TAACACACT	AAAGTTTCTC	AAGTAATACC	TGTTAAAAATC	ACTCTAGAAT	CAGAACCGTC	1860
TAAACAAGTT	GTTCTTGGAA	TGAACGCTGA	AGTAAAAATC	CATAAAAATT	ANGGGGGGTC	1920
ATTAAATGAC	TACGACCTNC	ATTATTAGCT	ACATTATTTT	AGCGCTCATT	ATTGTTGGGG	1980
TTATCAATTT	ATTTTAAATA	AGATCCNAGA	AAAAAAGGCA	AACGCCANCA	AAAGGAACAA	2040
CAATTTACGA	CACGTCAATC	AAATCAATCT	AAATTTAAAG	CTAGTGATTT	AGACAAAAACA	2100
ACTGATCAAT	CGACACAACG	TATGACGCAT	GAAGAGTTGC	GTGTTGACAA	TCAAGATGAT	2160
CATAGCCAAG	TTAGTCTAAA	TGGTTACACA	AAGGGGTCTG	AGAAAGATCA	AGAAGCATTC	2220
ACTAATAATA	ATGGTGAGGA	AGCAGTTGCT	GCTAAAAATC	CTGAATCAGA	AGAATATAAA	2280
GTGAATGAAA	AAATAAAAAA	AGAACAG				2307

(2) INFORMATION FOR SEQ ID NO:933:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2044 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:933:

```

CCCCAATCAA NNACCCAATT TGTATTGATT TGTGTGTNAA CCATCAATNN ATTGATACAA      60
TTTAATTTCCA AGTNNNATTG CCCGTAATTT NCACNNNAAG AGANNAAAGA GAGGATGTAT      120
CGTTGTGATA AGAAACATTT AAAGCGTTTG TAATTTGATA AAGATGAGAG CGGTAAAGTG      180
ACACCCAACCT TTCAAACAAT TATCGCCTAC TTGATTTACC TAAAGGAGAT GTGCTGATTA      240
AAGTACATTA CTCTGGGTAT AAATTATAAA GATGCTTTAG CGACTCAAGA TCATAATGCA      300
GTCGTAAAT CGTATCCTAT GATTCCAGGA ATAGATTTAG CTGGAACAAT TGTTGAATCC      360
GAAGCACCAG GCTTTGAAAA AGGAGAACAA GTAATTGTAA CGAGTTATGA CCTAGGTGTT      420
AGCCATTATG GCGGTTTTAG TGAATATGCG CGTGTAAGAT CAGAATGGAT TATCAAGCTT      480
CCTGATACCT TAACATTAGA AGAATCAATG ATATATGGCA CAGCTGGTTA TACTGCCGGT      540
TTAGCAATTG AAAGACTTGA AAAAGTTGGA ATGAATATTG AAGATGGTCC TGTACTCGTT      600
CGCGGTGCTT CAGGTGGTGT CGGTACTTTA GCAGTACTCA TGCTTAATGA ACTTGGTTAT      660
AAAGTTATCG CAAGTACAGG TAAACCAAGA TGTAAACCGA TCCAATTACC TTGAAGTTGG      720
TTGCCAAAGA AGTTATCGAT CCGACTTCCT GTTGAAGATG ATCATAAAAA ACCCACTCGC      780
ATCATCAACT TGCCAAGCTN GTGAAGACCC TGTGGTGGC GAAGGTATTA ATTATGTTAC      840
NAAACGTTTA AATCATAGTG GATCAATTGC AGTTATTGGT ATGACTGCCG GCAATACTTA      900
TACTAATTCT GTATTCCCTC ACATTTTAAG AGGCGTAAAC ATTTTAGGAA TTGACTCAGT      960
ATTTACTGCT ATGAAATTAA GACACGAGCG TTTGGCGTCG TCTCGCAAAA GATTTAAAGC     1020
CTGAAAATTT ACATGAGATC AAGCAAGTTA TTACATTTGA TGAAGTTCCA GAACAACTTA     1080
ACAAAGTAAT TAATCATGAA AATAAAGGCC GCATTTGTTAT CGATTTCCGGT GTAGATAAAT     1140
AGTAGTCATG AAAAAGACAT CCCGTTATGC GAGATGTCTT TTTTAATTTA GTATTTGATA     1200
TACATACCGC CTGAATCTGG TTCGGTAGGC ATAAATCCAA ATTTTGCATA TAATTTATCC     1260
GCCGGGTAAG TCCTGCGGAT AAAGACTAAC GTATGCACTT TCGACAAGAA TACATTTTTA     1320
ATAATNCTTC ATAATATGTT CCATAATTAG CCTGCCGTAA TCTTGACCTT GATAACTTTT     1380
CGAAACAGCA ATATCAACAA TTTGAAAAAC AGTTCCGCCA TCGCCAATCA CTCTACCCAT     1440
ACCAATTAAAC CGATCTTTAT CATACAAGGT TACTGTAAAT AAGGCATTAG GTAATCCTTT     1500
TTCAGCTGCT TCGCGCGTCT TTGGACTCAT ACCTGCGTTA ATCCTTAATG CGCAATAATC     1560
CTCGCAAGTC GGAATATCAT ATGTCACTTT AACCATTATT TACCCCACTT TTCATCACAC     1620
AATATATCAA CCTAGTATAA ATGTTTATTT ACAATAGTCT TATTCGCTTC TTTAAACACT     1680
TCATGATGAC TTGAAACATA ACCCTCTGCA TTCGCATCTG GTTGGATATA TGTTTGTAGCA     1740
AGGTTGCTG CATTTGCACC ATCACTAAAT GCACTTGCAA TTAGATGTGA TTTTGCATCA     1800

```

TGATAAACAA	TATCTCCACA	CGCATAGATA	CCAGGTATAC	TAGTTGTCGT	ATTACCAAAT	1860
CCTTTAACAC	GACAATCATC	ATGCATATCT	AGCTTTGAAG	ATGTTTCACT	CAATAATGTA	1920
TTACAACGAT	CAAACCCATG	ACTAATAATG	ACATCGTCAA	ATTTAACTGT	ATGCCTATCG	1980
CCACTTTCAA	CATGTTCCAA	ACACTCACTT	ATATGCGTTT	CATCATCATT	GCCGACCAAG	2040
TATT						2044

(2) INFORMATION FOR SEQ ID NO:934:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3222 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:934:

CCAAGTAAGT	ATAGAAGCAG	CATCCTTAGA	AAAGAAAAAT	GTAAGTTTGA	ACGAATTATT	60
ACAGCGTCTC	AATGACGTTG	AACAAACGGA	ATACACCAGG	TTGCTTTNAC	CCTAAATTTT	120
TAAATGTTTC	GTCACCTTAT	CAATATATTC	AAGCAGCATA	TCATGAACCT	CTTAGAGAAG	180
AATTTAAAAA	TTTAACACCT	TATGTGACGA	AATTATCGAA	AGTACATGGA	CCTAACCATC	240
CATATTTAGT	CGAGTTAAAA	GAAACATATG	ATACATTTAA	AAGTGGCATG	TTAGAGCATA	300
TCCAAAAAGA	AGATGATGTT	GATTTTCAAA	ACTAATTAAA	TATGAACAAG	GTGAAGTAGT	360
AAACGATATT	AATACAGTGA	TTGATGATTT	AGTATCTGAT	CACATTGCAA	CGGGACAATT	420
GTTAGTGAAA	ATGAGCGATT	TAACATCTAG	CTATGAACCA	CCGATAGAGG	CATGTGGTAC	480
GTGGCGACTC	GTATTATCAGA	GATTAAAAAGC	ACTTGAAGTG	TTAACACATG	AGCATGTTCA	540
TTTAGAGAAT	CATGTTTTAT	TTAAAAAGT	ATCATAAATA	ACGCGATTAG	AAACTGTTGG	600
CAAAGTAATG	TCAGCAGTTT	TTGCTATAC	TTAACAGAAA	TTTAGTGATA	TGAACAGCAT	660
TATTTGAAAA	GAAAAATGGT	CAACTTAGCA	TAAAAATTGA	TATGAAAATT	TAATGGTATA	720
GATAATTTAA	TAGTAGCGTG	TTTTTTTAAT	AATTTATTCA	TGAATTTTAC	ATGCACTATT	780
ATGATAAAAT	AAACATAATT	ATAATTCACT	GAGGTGCTAT	CGTGCTATCG	CTAACAATGT	840
TATTACTTGA	GCGTGTAGGT	TTAATTATTA	TTNTGGGCCT	ATGTGTTGAT	GAATTATTCC	900
ATATTTTTAA	AAACTTTAAT	GAATCCGTG	ACGCTACATG	GAAAGCACGT	TGGCAATTAT	960
GTATTATTTT	CAGTTTGT	GCCTTAATGT	TCTAATTTAA	CTGGTATCGT	CATCGATCAT	1020
CAACATAGTT	TGTCAGGAAG	TGTGTACTTC	CGTTTAGATG	ATGATGTATC	TTTAGCTAAC	1080
ACACGTGTAT	TAACGATAGG	TGTCGCAGGA	TTAGTTGGTG	GCCCTTTTGT	AGGTCTATTT	1140
GTTGGCGTTA	TTTCAGGTAT	TTTCAGAGTG	TATATGGGTG	GGGCGGATGC	ACAAGTTTAT	1200
CTTATCTCAT	CTATATTTAT	CGGNATTAAT	TGCTGGTTAT	TTNGGGCTTA	CAAAGCTCAA	1260
AGGACGCAAA	GCGGTTACCC	GAGGTATTTG	GCGAAAAAGT	GGCCAATGAA	TTGGGANTTG	1320
GTTATTGGGA	AATGAATCAA	ATGTNGGAGC	AATTTTAAAC	TTTTTCCCCA	CGACAAAGCA	1380
TATTGCGGTT	GACTCATATC	ATTAATTGCA	CTACCAATGA	TTATTGTTAA	TAGCGTTGGT	1440
ACGGCGATTT	TTATGTCTAT	TATCATTTCC	AACATTAAAA	GCAAGAAGAG	CAAATGAAGC	1500

```

CTGTTCCAAA CACATGACGT ACTGCAATTG ATGAACCAGA CATTGCCGTA TTTTAAAGAA 1560
GGATTGAATA GAGAATCGGC ACAGCAAATT GCGATGATTA TTAAAAATTT AATGAAAGTA 1620
TCTGCCGTAG CAATTACAAG CAAAAATGAA ATCTTATCGC ATGTAGGTGC AGGTAGTGAT 1680
CATCACATAC CAACAAATGA AATATTAACA AGTCTGTCTA AAGATGTATT GAAATCAGGA 1740
AAGTTGAAAG AAGTGCATAC TAAAGAAGAG ATTGGTTGTA GTCATCCGAA TTGCCCGCTT 1800
AGAGCAGCTA TCGTGACACC ACTTGAGATG CATGGTTCTA TCGTCGGTAC ATTGAAGATG 1860
TATTTTACAA ACCCTAATGA TTAACTTTT GTGGAACGTC AACTTGCAGA AGGATTGGCA 1920
AATATTTTTA GTAGCCAAAT TGAACCTGGT GAAGCCGAAA CGCAAAGTAA GTTATTGAAA 1980
GATGCTGAGA TTAAGTCATT ACAGGCACAA GTGAGTCCAC ATTTTCTCTT CAATTCGAAT 2040
AACACGATTT CAGCTTTAGT TAGAATAAAT AGCGAAAAGG CACGAGAGTT ACTATTAGAA 2100
TTGAGTTATT TTTTCAGAGC GAATTTACAA GGCTCAAAGC AACATACGGA TTACTTTAGA 2160
TAAAGAGTTA AGTCAAGTGC GTGCATACTT ATCACTCGAA CAAGCACNGT TATCCAGGAA 2220
GATTTAATAT CAATATTAAT GTTGAAGACA AATATCGCGA TGTGCTTGTA CCACCATTTT 2280
TAATTCGAAT TTTAGTTGAA AATGCCATCA AACATGCGTT TACGAATCGA AAGCAAGGTA 2340
ACGATATTGA CGTGTCAAGT ATTAAGAAA CTGCAACACA TGTACGTATT ATTGTACAAG 2400
ATAATGGTCA GGGTATTTCT AAAGATAAAA TGCATTTGTT GGGAGAAAACA TCTGTAGAAT 2460
CAGAATCTGG AACTGGTAGT GCTTTAGAAA ATTTAACTT ACGCCTAAAN GGATTATTTG 2520
GAAAATCCGC AGCATTACCA ATGTGAATCC GACATCGAGN GGTACCACTT TTTGGTGTGT 2580
ACCTTCCTTA TGAAAGACAA GAGGAGGAAT AAATATGAAA GCATTAATCA TAGATGATGA 2640
GCCATTAGCA CGCTAATGAA TTAACATATT TATTAAATGA AATTGGTGGT TTTGAAGAAA 2700
TTAATGAGGC AGAAAATGTA AAAGAAACAT TGGAAGCACC TACTTGATCA ATCAATATGA 2760
CATTATATTT TTAGATGTCA ATTTAATGGA TGAAAATGGG ATCGAATTAG GAGCTAAGAT 2820
TCAAAAGATG AAAGAGCCAC CTGCGATTAT TTTTGCAACT GCACATGACC AATACGCAGT 2880
ACAGGCATTT GAATTAAATG CGACAGACTA TATTTTGAAA CCGTTTGGTC AAAAACGTAT 2940
TGAACAAGCA GTCAATAAAG TGCGTGCGAC TAAAGCCAAA GATGATAATA ACGCAAGTGC 3000
AATTGCGAAT GATATGTCGG CGAATTTTGA TCAAAGCTTA CCTGTTGAAA TTGACGATAA 3060
AATTCACATG TTAAAGCAAC ANAATATTAT TGGGATTGGC ACACATAATG GTATTACAAC 3120
CATACATACA ACGAATCATA AATACGAAAC AACAGAGCCA TTGAATCGTT ATGAAAAACG 3180
ATTGAATCCC ACTTATTTTA TACGTATTCA TCGTTCATAT AG 3222

```

(2) INFORMATION FOR SEQ ID NO:935:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1660 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:935:

TATTGTGATT CCTTGTNNNT GAGTGGAAAA TCCCTTAAAT AATTGGTGCC AACTCATCCA 60

AGCTTTGAAT	CAACCCATAT	CATCANNCCG	CNTTTTGGNCC	CCAATTGTCA	TCGTATCCTT	120
GGAATTGAAG	GATACCCAAA	TGATGCATAA	TCAGCTTCTG	TANAAAGCTG	TAATGTAATG	180
TCATCAAGGT	CACCTTTTCT	AACAAGCACC	TTATTAATAG	AAGTATGATT	CGCTTGCCAA	240
GTACCTTGAT	TATTTTGTTC	TAAATGAATG	ACTTCGCCTA	ACGATTTCAA	CGTAATATCT	300
GCACGCTCGT	CTTCGCTAAT	AGTATATGTC	TTACCATCTC	GCAAATTGAG	CATCTTCAAT	360
TGTTTGTTAT	ATTTTATAAT	CAATTTATGC	ATTGTCCTTG	CCTCAGTCCT	ATACTATTTT	420
TTTCTTTCAG	CTTCTTGGCG	TTTTTCTTTA	TCTTTTGTG	CTTGTTCTTT	TGTTTTCTTT	480
TCGTCTCTT	CTTGTTGCTT	TAATTTCTCA	TCTTTTCGCT	TTGCTTTCTC	TTCTTCAGAT	540
TTTCGCTTTT	CATCTTTAAC	TTGTTTTTCT	TTGTCTAAAA	TATCTTGCAA	TTTAACGNNNA	600
GACTTTTTTCG	TTTCTTCAGA	ACGTTTATCA	TTTGATAAAT	CTCCGTTATT	TTTAATCTCA	660
NTTAATTTAT	TAANCAACGC	TAACTTTGTA	ATATCGTTAT	CATCTAAAAT	AAAGTGGCAA	720
TATTAATCGC	TTTATCAAGA	GGTCCTTGTC	CTAAATTTCCA	TCCAAGATAA	TAAAGTAGTC	780
TTGGTTTGAA	TTTGGTGTCA	CGTTATTAAG	TAAATTTTCG	GTCTTATCTN	TTTNCNAAAC	840
CTAGTNGAGT	GGGGTGGAAA	TAACCCCTGG	CATAAATGTN	AAGTNCCTCT	CTAGCTAATT	900
TTTTTCCATC	TAAATCATCA	CACGTATTTA	GTACTTGCGT	ATAATCATCC	CTCACANATG	960
CGTGGNATCC	TTTTTCAATG	CGCTCATTAT	GCTTCATTAC	TGANAAATAT	ANAAAGGCTA	1020
AAAATGCAAT	TAATAACACA	CTTAACGTTG	TCATGCCGAT	AGCAACCCAT	TTGAAAACGG	1080
TATGCCCTAC	TTTGCCTACA	TATGCATAAT	TTTGACTATA	ATCTTGTTCT	TGTTTCTGAT	1140
ACTGTTTCATC	TAAAAATGCC	GTTAGTAAAT	CTAACGTTGC	CGCTTCAATA	ACTTTAGTTT	1200
CAAATGGCGT	TCCTTTATGT	AGTTCTAAGT	TTCTTCAAC	TAAAGCATCA	AATGATTGTT	1260
TCTCATTGAA	TGCACAGATA	ACCAGTGCTT	TATATCTTGT	TAAAAATTCA	GCTTCTGACA	1320
CCGGNAATGG	ATCAACAACA	TTTTGTAAAC	CTCTTGTTTT	AGCAATTGGT	AATCCATCTC	1380
TTGTGAAAAA	TAACTCATCT	GGTGCCCAAA	CAAATGTGTA	ACGTGTACGA	TTTACTTCTT	1440
CTAAATTTTT	GATATTGAGT	AAGTATCGTA	ATTTTTTATT	TTTAGTAAAT	GATTTAAGAT	1500
TATCACAAGG	TGTATGATTG	TCATTAAGGT	CATAATGTAT	TTGGAAACTG	TCACGTAGTT	1560
CAGTTAATTC	AGCATCTATA	AAATATGGAG	AATGTTGTTC	TAATAAGTAC	ATTAAATGAA	1620
AATGTTCTGG	NTTAATTGAA	GACTTAGGAA	TCTCTCTCAG			1660

(2) INFORMATION FOR SEQ ID NO:936:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1008 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:936:

GGTCGTGGTT	CATTGGTAAA	AATCCTAAAA	GCCNCCAATG	TAAAGTAACA	NTTCAAAGCG	60
TCATGGAAGA	NTCATTAANN	CTTANCTCNT	TGGTCCATCA	AACNGATGTA	TTTTAACTGA	120
TTGATCTNAA	CCCACCGACG	GCGTTGATAA	TGTTGATCCA	ATTAAATCCA	ATCCAACCCCT	180

TCTGGAAGCG	TTGAACCCAA	CCAATTCTAA	GAAGCTGATA	TTATNACCAC	CAACCTGTTG	240
GTTGTTNAAN	AATACTACCC	TATTATTTGC	TAAATCTTTT	GCCCCTTTCT	GAAAAAGAAA	300
AAACCAAACC	ATGTTAATAT	TGTTGCTTGT	GAGAATGCTA	TTATGGCAAC	TGATACATTG	360
AANAAAGCAC	GAGTACTTGA	TATTACTGGC	CCTCTTGGTA	ACNATATTCA	TTTTGCTAAC	420
TCAGCAGTTG	ATAGAATTGT	ACCATTACAA	NAGNATGAAA	ATATATTAGA	CGTTATGGTT	480
GAGCCATTTT	ACGAATGGGT	TGTTGAAAAA	GATGCATGGT	ATGGTCCAGA	ACTAAACCAT	540
ATTAAATATG	TTGATGATTT	AACACCATAT	ATTGAGCGTA	AATTATTAAAC	TGTGAATACA	600
GGACATGCAT	ATTTAGCGTA	TGCTGGTAAA	TTTGCAGGTA	AAGCTACCGT	ATTAGACGCT	660
GTAAAAGATA	GTTCAATTGA	AGCTGGCTTA	CGCCGTGTTT	TAGCTGAAAC	AAGTCAATAT	720
ATTACTAATG	AATTTGATTT	TACTTGAAGC	GGAACAAGCT	GGTTATGTTG	AAAAATAAAT	780
AGACCGNNTC	AACAATTCTT	ATTTATCTGA	TGAAGTGACA	CGTGTCCGAC	GAGGTACGGT	840
TACGTNAAAT	TGGCCCTAAA	GATAGAATTA	TAAACAATT	AACATATCTT	TATAATAAAG	900
ATTTAGAACG	CACTGGTTTA	TTAAATACAG	CTGCATTGTT	ATTGANGTNT	GATGATACAG	960
CAGGACCAAG	AAACTGTTGG	AGAAAAATNN	TNACATTAAA	GGACCACG		1008

(2) INFORMATION FOR SEQ ID NO:937:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 981 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:937:

AAGTTATTAT	GGATTTTGA	CCCAGGAACN	CGATGATNCA	ATAACATTAA	TTTAAGNNGG	60
GGCCAATTGA	CAATCCCCT	AGAGATATTA	NCTGTACAAA	CAGTCGCAGG	TAATCCAATC	120
AAGTTGACNA	AGAANACGAC	ANACNCCTTG	GACGTATTGG	ATATTATGGG	ACCCCAAGAT	180
ATAGCAGTAG	CGAAAGGTGC	GGATAGCCCCG	TTAATTAAAC	CANCTGCCTT	TGCTTCTGAA	240
ATACATGGGG	AATCTGGATT	AGATGGTCCG	AACTACCGT	CGACACCATC	ACGTCAAGCA	300
GTTGCAATGC	CAGCATCAGA	TGTGATTATA	AACAAAGTGA	TGACGAGTGA	TACACCTGTA	360
ACAATTGTAG	CGACAGGTCC	TCTTACGAAT	GTAGCAACGG	CATTGATTCT	TGAGCCAAGA	420
ATCGCTGAGC	ATATTGAATC	TATTACTTTG	ATGGGTGGTG	GTACATTTGG	AAATTGGACC	480
CCTACAGCAG	GAATTTCAAT	ATTTGGGTAG	ATGCTGAAAG	CAGCGAAGCG	TGTTTTGGAA	540
AGTGGGATTA	CTATAAATGT	GTTTGGTTTA	GATGTAACAC	ATCAAGTTTT	AGCCGACAAT	600
CACGTGATTG	AACGCTTTGA	AAGTATCAAT	AATCCTGTTG	CACAGTTCGT	CGTAGAATTA	660
TTGCAATTCT	TTAAGAAGAC	ATACAAGACT	CACTTTAATA	TGGATGGTGG	TCCAATACAT	720
GATGCTTGTA	CAAATTTGTA	TTTGTTACAA	CCAGAATTGT	TTACAATGGT	ACCCGTTAAT	780
ATNGACATCT	GAACATCAAA	GTCCACTAAC	TTATGGCACT	ATGGCTGTCT	ATTTAAATCA	840
TGTTACAGGT	AAGCCNGCCA	ANGCTTATTT	TGCTACAGCA	GNTGNTGTTG	AAGAAGTGTG	900
GNACTTGGAT	AGGACCATNA	GNTANGTCTC	GTGCCGATAT	CAAGCTTATC	GTACCGTCTG	960

CCTCGAGGGG GNCCGGCCNA A

981

(2) INFORMATION FOR SEQ ID NO:938:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1473 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:938:

TTTAACAACC	CTTGTTTAAN	TAAGGAATCC	ACTTGAATTA	TCAAGTTGTG	AACCACCTNC	60
TTTTTACATA	ATCTAAACCG	TACTTTTGAA	NACCCNCNNT	TANCAAATAT	CTNTTAATTC	120
TTCCACCTNC	NTTNACGCT	TTGTTGTGTA	CATGTTGGTG	AGTTGNNAAG	TAAGCTATCT	180
GAGATAATTG	CTGATAACAT	TAAACCGCCA	ATTTTCAGGT	TAATTTTANA	GCCACGTTCT	240
CTAAACATTT	TGTATAAAAT	TGTAGCTGTA	CACCCAACGT	GTTCAGCAG	ATAACATAAA	300
GGGCCAGCAG	TTTCGAAATT	TGCAATCTG	TGAGGATCAA	TTACATGCTT	AATGGTAGCA	360
GAGACAATCG	TATCNGAACT	TGGTNGGAAT	TCGTTATGAT	CAACTAAGAT	AACATCTTGA	420
CCATCTAAAT	CATCCGTTAA	TAATTCGGGA	GCAGGTACAT	TAAATGTATC	TAACGCGAAT	480
TGAGTTTCTG	CACTCACATC	ACCTAAACGG	TATGCTTTGG	CTCCTGAATT	ACCTCTAAGT	540
TGTTCAAATT	CTGCCATAAT	AATCGCAGAT	GAAATTGCAT	CAGTGTCTGG	ATTCTTATGT	600
CCGAAAATAT	ATGTTTTAGC	CATTGTCAAA	TATCTCCCTT	GTAAATTGTA	TTCTTTATAA	660
TTATTTTAGC	ACGATTTAAA	CGTGTGTTC	TACCTCTGCA	CCTAATGAGT	TTGTGGAAAT	720
GTGCAAGTGC	CCATTCATGC	CCTTTGTGGA	TTAAATGAAG	CCACTCCCTC	AGCAGGTACT	780
GAAATTTTAT	AACCTAAGTT	GTATTGCAGG	AAATTGCTGT	ATTGGTAACA	ACGCAAATAT	840
CGGGTACAAT	ACAACCAACG	ATTTGCACTT	GGATTAATAC	TTCTTTCTCT	CAAATAAACT	900
ATCAAGCGGG	GTACCAAAGA	ACGAATCATA	GCGCGTTTTA	TCAATGAAAT	GTACATTAGG	960
TTGCGCTTTA	ATTGTGTCGN	ATAATTTACC	TACTTTACCG	TATAATTCTC	TACCACTTGT	1020
ATCTACGATA	TTGTGTGGTG	GGAATAATTT	ACTTTTCAGG	TGATGAATGT	CATGTAAATA	1080
ATGTAAATCC	ATTAAAAAGA	ATATATGGTC	TTGATAATAA	TTAAAGTCAT	TGATACGAGA	1140
AACAATAAAA	TCTTCAATAT	TTTGTCCAGG	TTTACCGCAT	GTTAGTAAGC	CGTCATCTGC	1200
GATAAAGTCA	TATGAATAGT	CAACAACTAA	TAGTGCGCGA	TGTGTCATTC	AACATCTCTC	1260
CTATATAATA	AAATAAACTC	CCATCTATTC	ATAAATGCTA	GAGTAATTTT	TAACCCTAAT	1320
GGTTAATATA	TAAATATAGA	TTAANGTATA	TAGATTAATC	AACTTNGNTG	GAAGAGCAAA	1380
TCACGCAATC	ACAAATAATA	TTAGAAGTTT	TTGGCGATNG	TTCAAAATAG	CTGCTATAGA	1440
TACTAATTGT	GAAAACCTAG	ACTATTCAAG	TGT			1473

(2) INFORMATION FOR SEQ ID NO:939:

(i) SEQUENCE CHARACTERISTICS:

818

- (A) LENGTH: 1372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:939:

AAGAGTTGTC	GGATCATNAC	CGCCAAGTAA	AAAGCGGATG	ATTGACCTCC	CACCTGGATT	60
GCATTGTATT	TGCCAAATCG	TATCCAAGTA	CAATGGTACC	CGTAGTTTAA	TAAGTCTCCC	120
AAGCACCTTG	AGAAGTCGCC	AGTAAAGCAA	CTTGAATTAA	AGCAGTGGAA	TAAACCCTAC	180
TATGATTTGG	ACTTGCCACG	GGATATCACT	TGTCCTATGG	CTTGGAATGC	AATTGTAATT	240
AACGTCCACA	AACCCTGTAT	GATATTCATA	ACGTTTGTGA	TGATACCTAT	TACCACAACA	300
CCTAAAACCT	GCATGAATAT	TTGCCCTAAA	ACTTGCAATA	TAGGCATTAT	CGGTTGTAAG	360
GTAGATTGGA	TTTGTCCCA	CAATTCAGTT	AACCAGCCAA	CTACACCTTG	AATCGCACCA	420
GAAACCGCCG	TTTTAACACC	GTTCCACGCT	TCAGTAATAG	TGTTTCTGAA	ATTCTCGTTT	480
GPTTTCATA	AATAAACTAG	GACACCGATA	AATGCGCCAA	TTACTGCAAT	TACCGCTAAA	540
ATAGGTGCTG	AAATCGTTCC	AAAAACACCT	GTTAATGCTT	CCTAAGCTCC	AGTAACTAAA	600
CTTGATGTTT	TAACGAATTC	TAAAATCTTT	TCGACGACAC	TGAATAAACT	CAAGCCAAAC	660
ACATTTGTAA	GCACACTACT	TATAGCAACA	ATCGGAGCCA	TTAAAGCCCA	AAATACACCA	720
CCTAAAATAC	CCATAACACC	AGCAACTTGT	GCTATAGCTG	GGTGTGTCTC	GAATAGCTTA	780
GCGATAAAAC	CAGCTAGATT	AGTGATAAAG	TCTAACAATT	TACTAGCTAT	AGGAGCCATT	840
GCACTGCCAA	ATGCTACTAA	TGCTTTTATG	ATGTTACCGA	TTAATTGCAT	AATAGTAGGA	900
CCATTCTCTT	GAACGTAACT	TATAAAGTCT	TTGAACCCCT	GTGATTGTCC	TACTTGTCTT	960
GACCACGCTC	TAAATTGAGA	AGTTAATTTA	ACTAACCAGT	CAAAAATATT	AGAAGTGTTT	1020
TGGGCAAAAG	CAATCATTAA	NTTACCAATA	CCAGCGAATA	CATTACCAAT	TTCTTGGCCA	1080
ATCTTAGGTA	AGTTAGTGGG	AGGGTAGGCC	AATAAACGNT	TTAATAGCAT	CTTCAGACCA	1140
GGCTACACTA	TTAGCCCAAT	TGGGGAAAGN	TATAGACAAN	NTCCTGTNAT	CCTTGAGACA	1200
CGAATTTGAA	CAATGGCATT	AATTGAGTGA	GAATGTTAAA	TAATCCGTCG	CCTAATCGTC	1260
CTGCAGCGTT	CAATAAATCT	CCGAAGATTG	CACCACCTAT	GCTATTCAAT	GCTTCAAACG	1320
CTTCTTAGC	CGTTTCAGAA	TGTTTAACCC	AATCNTCAAA	CTCGCTCGTG	CC	1372

(2) INFORMATION FOR SEQ ID NO:940:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:940:

```

GGCACGAGCG TAGATTTAGC ATTTTCAAGA GACCAAGAAC ACAAAGAAAT ATGTACAGCA      60
TCGTATAATG GAAGAAAGTG AACGTTTCAA TGAATGGATT GAGCAAGGCG CAGCAATCTA      120
TATTTGTGGC GATGAAAAAT GTATGGCGAA AGATGTCCAT CAAGCCATTA AAGATGTATT      180
GGTAAAAGAA CGTCATATTT CTCAAGAAGA AGCAGAGTTA TTATTGCGAC AAATGAAACA      240
ACAACAACGC TATCAACGTG ATGTTTATTA GCGATTGGTG TTAAATATTT TAAGGTGTAA      300
TGATGTAAAA AGATATAAAG GATGTTGCTC AACATGAATA TGCCATTAAT GATAGATTTA      360
ACAAATAAAA ATGTCGTCAT AGTTGGNTGG AGGCGTCGTT GCAAGTCGTC CGGGCACCAA      420
ACATTAAATC AATACGTTGA ACATATGGAC GGTCAATCAGT CCGACAATCA CTGAAAAACT      480
TCAAAATATG GTAGATAACG GTGTCGTCAA TATGGAAAGA AAAAGAATTT GAACCAAGCG      540
ATATTGTAGA CGCGTATCTA GTTATTGCAG CAACCAATGA GCCACGTGTC AATGAAGCGG      600
TAAACAAGC CTTACCTGAG CATGCCCTTT TTAATAATGT TGGAGATGCA TCAAAATGCCA      660
ATGTTGTATT TCCAAGTGCA CTACACCGCG ACAAGCTAAC TATCAGTGTA TCAACTGATG      720
GTGCGAGTCC TAAGTTGACA AAATCAATTA TGGCAGAGCT TGAGGCGTTA TATCCACCAT      780
CATACAGTTC GTATATCGAC TTTTATATA CTTGCCGACA GAAAATAAAA GTACTTGATA      840
TAACATATAT ACGAAAAGCA ACAGTTACTG TCACAAATTG TGTCACAAGA ATATTTAAAT      900
CATGACAAAC AAGCTCAATT TTTAGCGTGG TTGGATGTAA GATAATAATA GCGGACCGTC      960
TAACCGTCTA AGGTAAGTCT TCTTATTTTA ACTTTAACGC TTAATCATTG AAATTAAGAC     1020
ATGGGTGGCT TTGTGAATAG TCTAATAATG AAGGATTTAA GCGATAATGA TATGCGTTTTT     1080
AAATATGAAT ATTACAATAG AGAAAAAGAT ACGTAGAACA AACTTAATAA AATAGATGGA     1140
TAAATTGAAA TCTGGTTGAA GTCGTTACTA TCATAGCGAC CTTTAGCCAG ATTTTTTGTG     1200
CAATAGAAAG CAATAATAAA AATGATAGAT CAANATGAAA TACAGGACAG GATATACAAG     1260
GATTAGTCAT GCCATGTTAT CAAGTAGGAA AATCAAACCT CACTATTGAT AGTTACGCAN     1320
AAAGATTTTT TTGATAAAAT GAGATAACTT AAAGATAAAA AATTATATTA ATTATAATAT     1380
TTAAGTTAAA GAGGGGGATT ATGTAAATTG TATTAAAAGT GGAGGGAGAA AATAATATGA     1440
ATAGTGAG

```

(2) INFORMATION FOR SEQ ID NO:941:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1642 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:941:

```

TGCCCCAAGAN CCCCTGTANT GGTAATGTCC CGGGGNAAAA TGCCANTTGA TGTGTNNNGG      60
TGATATGANC CCGCCATTGT AATATTATTA TTCCAGATAA ANCCGAAATA TGANNCGATG      120
CTCAATATAG CAGACCCACA GGTTCATCT CGTATTTTAC CAAGGCGGAT ATCTATATAA      180

```

CTATCGTAGT	CGTAATAGAT	ATACTAAAGA	AATTGTAATA	TTAACTAACT	CGGATCAACT	240
TCGTAACATC	AAGGTATTGG	GTGAAACTTT	ACCAGATTTT	AATTTTCACA	TCGCTGGCTA	300
TTACAGAGAT	GTCTGATAAG	CTAATGCAAC	TTGATCAATA	TGCTAATGTG	CACTTATACC	360
CATCTATTAA	TATTGACAGG	GTAAATGAAC	TNTACCAGTT	ATGTGATATT	TATCTTGATA	420
TCNATGAGGG	TAATGAAATT	TTAAATTGCG	GGTGGAACAA	GCGTTTGA	ATGAGTTGTT	480
GATTTTAGGT	TATCGTCAAA	CCGCACACCC	ATGCTAAAGT	AACATTATCA	GAGCACTTAT	540
TTGAGCATAA	TGATGAGATA	ACAATGGAAA	GTAAAGACCA	ATTAATACAA	ATGTTAGAAA	600
GTTTGAAAAGA	TCAACAACAG	TTTCGAGATG	CTTTATTAGC	ACAAAAAGCA	CATGCACACG	660
GCACGAGCGT	GAACAATTTC	AGCAAGTTTT	TAAACAGGCG	CTCGAAAGCT	AAAAAGAAAA	720
AGCAGTCTAA	AATAAAGCAT	CATTTAATTT	AAAAGATTTG	ACGTAATATG	ATGTTAGCGA	780
CATGGACAAT	ATGATATTAC	GTCAATGCTTT	TTTGTTTACT	TAAATATAAG	CTAAGTAATA	840
AGTTGATAAT	TACTAACAAC	AATAACTAGA	TAGATAAGTG	TAAATTTCTT	GTAAACAGGT	900
ATATAATAGT	ATGTAATTCT	TTGAAGGAAG	TAAGTGAGAA	AGGAGTATGT	TGATGGCTAA	960
ATATCGAGGG	AAACCGTTTC	AATTATATGT	AAAGTTATCG	TGTTTCGACAA	TGATGGCGTC	1020
AAGTATCATT	TTAACGAATA	TCTTGCCGTA	CGATGCCCAA	GCTGCATCTG	AAAAGGATAC	1080
TGAAATTTCA	AAAGAGATAT	TATCTAAGCA	AGATTTATTA	GACAAAGTTG	ACAAAGCAAT	1140
TCGTCAAATT	GAGCAATTAA	AACAGTTATC	GGCTTCATCT	AAAGCACATT	ATAAAGCACA	1200
ACTAAATGAA	GCGAAAACAG	CATCGCAAAT	AGATGAAATC	ATAAAACGAG	CTAATGAGTT	1260
GGATAGCAAA	GAAAATAAAA	GTTCACACAC	TGAAATGAAC	GGTCAAAGTG	ATATAGACAG	1320
TAAATTAGAT	CAATTGCTTA	AAGATTTAAA	TGAGGTTTCT	TCAAATGTTG	ATAGGGGTCA	1380
ACAAAGTGGC	GAGGACGATC	TTAATGCAAT	GAAAAATGAT	ATGTCNCAAA	CGGCTACAAC	1440
AAAAATATGGA	GAANAAGATG	ATAAAAATGA	TGAAGCAATG	GTAAATAAGG	CGTTAGAAGA	1500
ACTAGAACAT	TTGAATCCAG	CAAATACACC	AATCCGAAAG	ATGCATTGAA	AGATGCATCC	1560
GAAAGATCCG	GCAATGTTCT	ACCACAGAAT	TATTATCTCC	TGAATGTACG	CTAAAACGCC	1620
ATATAATGAG	GTCCCTGAGA	CT				1642

(2) INFORMATION FOR SEQ ID NO:942:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:942:

CTAGAAATAT	AACTTATAAG	TTCAACATGA	ACTGGCACTT	CTTTTAAACG	TGCTCTATCT	60
GATTTACAGC	CAGTAAAAGT	TGCATCTATA	AAATCTTGTT	GATGGNTTAA	ACGATATGTA	120
GCAACAAAAG	TATCTGTATC	GGACTCAAAG	TNTGGTAAAT	GTGCAATTAC	ACGCTTAATT	180
TCGCCAGTAG	AATCAGCAAT	CGTATGTCCT	GTAATATTTT	CTAATTCTCT	ACCTAATTCT	240
GGCAAAGTAA	TATCTNGACC	CTCTAAAATT	CTAANATCTT	GTTTCATGCAT	GCCGTTTCTC	300

TCCTTTATTA	ATTACGTTGG	TCTTATTTCC	ACCGTTCTGG	TCCTCAATCA	TGGAACACAT	360
TTTTAATTAA	TACATACCCT	NAAAATAAGG	NTTNAAACGC	NGCACCCNCT	CATCTATAAA	420
CAAGTAAGCA	ANACGANCAT	GANTGGTGTC	TGNCCACCCA	GCTTTTTGAN	CCTTATCTGT	480
TGATGTAGGN	TTNTTGTGAT	NATCTTTATC	CGATGACTTA	GTTTGATCCT	NTTGATTGNT	540
TATCTTGTGA	TGNCTCNFTA	TCTTTATCTT	TGTCTTTATT	TTTGTCTTCG	TCTTTTTTAT	600
CATCCTTGTT	ATCTTCTTTT	GAAGGGNTTA	AATCTTTCAC	NTTCTTTTTC	AAGGTCTTTT	660
TGCTTATCTG	CTAATTTTTT	TTTTTCTTGT	TGAAGCTTTT	CTNTTTTGTC	TNTTAATTCT	720
TTATTTTCTT	TTTTGTAAAT	TATCGATATC	CTTTTCCAGA	GTGGCTTTCCT	CTTGACTTTT	780
ACCACCAACC	TGTTAAAAAT	AGCATGACCG	CCAGAATACT	GATGATTAAT	TTCTTCATAT	840
AAAACTCCTT	AAACGTCATT	AAATCTTTTT	TAATTTTAAC	ATGAATTAGC	AACATAATCC	900
TAATTCCTAAT	CAATATCTTT	ATACAATTTT	ACATGACTCA	CTTGATAACC	TAAAGCTTTA	960
TTCAAAGATA	TCATTGGCAA	ATTANGTTTA	TGAATTGTAC	TGCTATTTCG	TTTGCAATCA	1020
TAGTTTTTGC	CCATTTTTTCA	AGCGCAATCT	TCAGTTGCGT	AGCTATTCCC	AGTTTGCGAA	1080
ATTGTGGGTC	AACATATAGC	AGTCCATGTT	ACCATACTTT	TTCATTACTA	AAATGTCCCC	1140
AAATAAACGC	TATTAATTGA	CCTTCATTTT	CATATATATA	AATTTTATCA	TTTGTATGTT	1200
CTAATCTTGA	ACATATCATC	TCGTACCTAA	GAGCAATACT	CAGTTTAGTA	CATTTATAGT	1260
TGGATTCTGC	TTGCGACAAT	AATGTCTCGT	GTATATTAGC	TATTTGCTTG	ATATAATTAT	1320
GTTTCATCTT	ATTAAGTGTC	CTCATTTTCC	TCTCCAATAT	TAATCGTTAT	ATTTATGCGT	1380
TTAATATGAT	ATGATTGACT	TTATTAATAC	TATAAAATCA	TTTCCATTTT	AATTAGGAAT	1440
TAAACATTTT	TAAAGGAGCG	CTTAAGTAAC	AATGAAAAGT	ACTGCGCAAT	TAACAAAAGA	1500
AAATAATGTT	AAATCATTA	GATTAAGCAA	TACTGATAGA	GAAATCTTCG	AGAATTATAT	1560
GACTTATATG	CGCTCTGACT	TTGCGTCAA	CCCTCATGAT	ACAGAGTTAA	TTATTAACCG	1620
TATACTCAAA	CAATTATTAA	GCGCAGAACA	ACATGGTTTA	TTAGCCCTTAG	ATTTTTTCAA	1680
TCACGACCCA	AAAGCACATG	CAATAAAAGA	ACTAAAAGCG	ATGCCTAATG	AAACATTTAA	1740
AAATATTTTT	AAATATATCT	ATCAACACAT	CGTTCATTA	ATTGGGATTG	TTAGTTTTCT	1800
CAAAGGATTT	TTAGGATTTT	TTTATGGAAA	AAAATGGAAG	TAATTTATAT	TTTGTTCAT	1860
TCCCGTTTTT	AGTAGTCGTT	GGATTCTTTA	TTGTCTTTTT	ATTTATATGG	GTTAGTTTTA	1920
AAACAATACA	ACTGCAGTGT	TTTAGCAATT	CAAATTGGAT	ATGGATATTC	ACCTATTTAG	1980
CAATCCATTC	TACTAATTGT	ACGATTTTTT	TATGTATTCT	TTATTCACA	ATCATTACTT	2040
GCCTTTGGAC	CATATATTCA	GGTAAGCAAT	TGGGTATTTA	TTATATTTTC	ATTTATAGTT	2100
ATGCCATTATG	GATTACGCAT	TGANAGAAAT	ATTTGAAAAA	AACATTCTCA	TACATTTTTA	2160
TAAACAAAAA	GCTTATTACA	TCATATGCGA	ATTTGTCTCG	NGCC		2204

(2) INFORMATION FOR SEQ ID NO:943:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 876 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:943:

GAAGANATAN CGTGGTNTTG AAGATTGGG ANGTTAATAG ATNAAGGGGA ATATGCANTT	60
ATTACCGGGA GNNAGTATC CAAGNAAATC TAGAGTCAAT AGGTAAATAA TCTTATGCCT	120
TTTTAATTTT GAATAAAAGT GGGGTGGTGT AATGTTTGGA TTTACCCANC CGACCCGAAC	180
AAGATTGNCG TTTNACGCGA TTAGAAGNAA ATGATAAGCC TATGTTTGNN AAATTCGACA	240
GAATAGAAGA CAGTCTGAGA ACGCAAGAAA AAATTTATGA CAAGTTAGAT AGAAATTTTCG	300
AAGAACTAAG GCACGAGCGA CAAGGTAGAA GATGAAAAGA ATAAAGAAAA GAATGCCAAA	360
AATATTAGAG ACATAAAAAT GTGGATTCTA GGATTAATAG GGACGATCTT CTAAGTACGA	420
TTTGTCATAG CCTTACTAAG AACTATTTT GGTATTTAAA GGAGGTGATT ACCATGCTTA	480
AAGGGATTTT AGGATATAGC TTCTGGGCGT GCTTCTGGTT TGGTAAATGT AAATAACAGT	540
TAAGAGTCAG TGCTTCGGCA CTGGCTTTT ATTTTGATTG AAATGAGGTG CATACATGGG	600
ATTACCTAAT CCGAAAAATA GAAAGCCAC AGCTAGTGAA GTGGTTGAAT GGGCGTTATA	660
TATCGCTAAA AACAAAATAG CTATTGATGT ACCTGGTTC TGAATGGGAG CACAATGCTG	720
GGAATTTACC TAATTATTTA CTCCGATAAA TATTGGGGAT TTAGAACATG GGGAAATGCT	780
GATGCTATGG CTCAGAAATC CAATTAATAG AGGTAGAGAT TTCAAGATAA TTAGAATCAA	840
AAGACTTGGT ACACAACCAG GCGACTGGGT TTTTGG	876

(2) INFORMATION FOR SEQ ID NO:944:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 584 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:944:

AANATAAGTT AATATTGCCA GGGCCTTTAA CCCNTGCCNA TCAAGTCAGT TGTAACCACC	60
CTCTTTAAAA GCTTGAATTG TCGTCTTCAG TGATAGGATT TCCTGAAATA ACTTCATATT	120
TTTLAGAAAC ATGTTTGT TTGGACTCATT ATTCATGATT AAAATCACCA TCATTCTGTTA	180
TCAATAAAAG CCCTTCTGTA TCTTTATCAA GACGACCAAC CGGAAAAATA TTTAGATGTT	240
GGTATTCAGG TATTAAATCA ATAACGGTTT TTGAATGATG ATCTTCAGTT GCTGATATAT	300
AACCTTTTGG CTTATTTAAC ATAATATAGA CATTTTCAAT GTATTCTATT AATTCTCCAC	360
GAAGTGTAT CTTATCGTTT TCTGGTCTA TATGTGTTTT TGGTGATTTA ATTACTTGTT	420
CGTTGACATT TACAAGGCCT TTTTAAAGTA ACTGTTTGAC CTCATTGCGT GTACCGACGC	480
CCATATTTGC TAAAAATTTA TCTATTCTCA TCGTAAAAAC CTAAGTCTAC GTCTTAATTT	540
TTCAAGGAAT TCACCTAAGA ATTCGTCCGC AAGACGCTCG TGCC	584

(2) INFORMATION FOR SEQ ID NO:945:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1852 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:945:

AATATCATTA	NTTGTAGCC	GGATTTGTTG	TTACCCTTTA	ATTTC CCANA	AAACCTGGGT	60
ACAAGTAACC	TTGATTAAAA	AATCGTGGTT	CAATATTTTC	TTGTATTATG	ATNATCTCCA	120
CAAAATTGAT	ACGGTGATAT	AACATCGTCC	GGTAAAAANC	CATTGTCATT	GAGTNCAATT	180
GTTAAATCTT	CTNCCAACCT	ACTGGCTTTA	AAAGACTCAT	ATAACTTTTCG	TGANTGATCG	240
TTAAAGTAAT	CAAATAATTT	AATCATGTAG	CACCTCTTGA	NCTAATGTTT	CCCATTTTAA	300
AATAATATCT	TGAGTCATAA	ATTGCTGTGC	CACCTCATAA	GAGATGTCAT	GTGGTGCCCTG	360
GGGACCATTG	TTAAATACAA	TTACAATGGC	ATGAGCTAGT	TTTGCGATAA	CATCATCCAC	420
ACGATCTTCG	NCGGTATCAA	AAGGTACCAA	GTAGCCATTT	TCCCCATCTC	GAATAAAGGT	480
TGGGTTACCA	TAATTCACAT	TTAATCCAAT	CATACCTAGT	CCTGAGNCGA	CCGCTTCCAT	540
TAGTGTAANC	CCAAAACCTT	CGCTAGTTGA	TGCAGNAAGA	AATAACTCAT	NATCAATATA	600
AATNTCATCC	AAGGTTNACA	TGCCCTAGTA	NACGGAATAT	AATCTTGTGC	GCGGGGTGTA	660
TCAATNATTT	TACGCAGTCG	CGTCTTCTCG	CTTACCTTCT	CCATACATAC	CAAATGTTAA	720
TTCTGGCACT	TGTCGTTTAG	CCGCGATAAC	CGCAGTTTGA	CAAGCCAATC	AATATGTTTC	780
TCANTTGCTA	AACGAGATGC	NCTAATCATC	GCATATGGCT	TTCTTGATNA	TNTAGGACAT	840
GATNACGCAT	CAATGCTTCC	CACCGGAATA	GTATAGACAC	GTGGACGATA	ACCTTGATAT	900
TGCTCNAATT	GTGACCAAC	CANATGATTT	TGAATATCTG	TTGCTGTAAT	AAAGAAATCA	960
ATGTATTTAG	CTTTTGAAAA	TTGATATTCA	TAATAATTGT	TCCATAGTAT	ATGCTGCTCG	1020
CTCATCATAT	TATTACTATA	ATGATCAGCA	TGAATCACAA	CACCAACTTT	ACTATCACCT	1080
TTATGCTGCA	AAACAGCCTG	NCCAATATCA	GAAGCGCGGT	CTAATATGAC	AATATCGTCT	1140
CGGGNTAAAT	TCAATCGTTG	TAAAAAGTAT	GCAATAAATT	CCGTTTTGTT	ATACAACACC	1200
GCATCTTCAA	ACACATNTAT	AGAGCGGTCT	CCATCAATAT	ATTCGTTATA	AGCGATGGAA	1260
CCNTCTTCAT	TATAGAATTG	TCGCATATAT	AATTTGCTT	TATTATCAGC	TGGTGATAA	1320
TACTCAGAAA	ATATACGCGT	ATAACTATAA	AAATCTTTAC	GTAATAACAT	ACTATTAAAT	1380
ACAAATTCTG	CACGATCCAC	AACATCTTTG	TGNTCATTTN	GNAGATAACA	TGTTACAAAT	1440
GATGATTTCC	CATTAAAATA	TAGACGGACT	ATCTTACCAT	TTCTTTCTCT	AAAATAATT	1500
TCATGACCAA	GCTCACGTTT	AATGTCATCT	AACGTGTACG	TTGTTGGTGC	TATAGAAATA	1560
TCACTAAAAT	ACTGATACAA	CCAAATAACT	TCTTGATCTT	TTAAACCCAA	TGTTGNGCGT	1620
TAATGTCTGT	ATGTTCTCTG	ACTGTACAAA	ATCGAAAAAC	ACAAATTTAG	TGTCTGGATT	1680
NGTACGTCTC	AATAATTNAG	NACGGNAAGN	TTGTGCATAT	TCAACACCGC	TACTCGCCCA	1740
GCCTATACCN	AAGNGTATAT	TATATATTGT	CATGCGCTAC	CCCTNGGCAT	TTATGGAAAA	1800
TGTATAACTG	GCATACCCTC	TTTATCAAAT	GTAATCATGC	TTTGACAAAT	AG	1852

(2) INFORMATION FOR SEQ ID NO:946:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:946:

```

AANCACCAAT CCNATTGGGA GGNAATCCAA ATCAATNCCC GGANNCCCCA TCCAAGTTAA      60
TTAAGTCCAA GGTTTTGGAA CATTACCAA TATGATTCCG ATGAGGTCAA ATGNCAANCG      120
GTGTTAATAA ACTACGAAAT GNTGTGNAAA TGATAGTAGA NCAAGTTGCG CATAACAGTNT      180
CTCNATTATA TGATGCTTTA GAATCGAATG AGCAACAACA GCGCAGTTAC AATCAATAAT      240
TTGTAAGTAG AAGATAATAA AGAGAACGCT CTATAGAGAC GAATTGAAGG TTTGATTTTA      300
ATGTCTGTTA GTAAGAATCA TATCAATGAG ATGCCTATAG TACTCAGATT ATATTAAATT      360
AAAACCGTCA TTAATTGTTT TTTTAGAAAA CATATAGTAT CATTTTAAAT GTAGTTGACA      420
TACTACGTAC TCAAATAATC TATAACAATT TCATATATAA TTCTTTCGGG GCAGGGTGAA      480
ATTCCCAACC GGCAGTAAAT AAAGCCTGCG ACCTGCTAAT ATGTTTCATA TTAGTGGCTG      540
ATCTAGTGAG ATTCTAGAGC CGACAGTTAA AGTCTGGATG GGAGAAAGAA TGTTAATTAT      600
CGACAAAGAT AATGTAGCGT ATTTGTAAAA ATGTGTACAA ATAGGCTTAT TTAACGATAA      660
ATTTTCTCTC TTTGCATCTT AATTCATGAT GTGAGGATTT TTTGTTTATA GAGGTGATCA      720
TTTGAGTCAA TTTATGGATT ATGCGATTCA ACTTCCAAAT ATGGTACAAG GTCANACAGG      780
TGTTAATCCA CCCGTTGGCG CTGTTGTAGT TAATGAAGGT AGGATTGTTG GTATTGGTGC      840
ACACTTGAGA AAAGGTGACA AGCATGCGGA GGTTCAGCA CTTGATATGG CACAACANAA      900
TGCTGAAGGT GCGACGATTT ATATTACGTT AGAGCCATGT AGTCATTTTG GTTCAACACC      960
ACCCTGTGTT AACAAAATTA TTGATTGTAA GATAGCANAA GTAGTATTAC NCAACANAAG     1020
ACAATTCCGT TAGACACACA TGGGTGATGA GACGTTACGG GGCTCCACGG TATTTGAGGG     1080
TTGAATTGCG TTGGATGATG AACGGGCATC ACAATTATAC CAAAGACTTT TTTTAAAGCA     1140
AAAAGCAAAG CAACTTGCCA CAAAATTACA GTGAAAGTNT CTTGAAAGTT TAGATGGGTA     1200
AACAAAGCGA ATTGATAATG GACAAAGTCA ATGGATTACT AACAAAGAGG TTAACAAGA      1260
TGTCTATAG                                     1269

```

(2) INFORMATION FOR SEQ ID NO:947:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1958 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:947:

TTTATGGGTC	AAGATTGATC	CCAAAAGAAG	TGGGATTNAA	CATTAGGACT	TTAAAAGACG	60
TCCCAAGAAG	ACAAATATCA	AGGGCCCGAT	GGTATTCCAA	TTTGAAAAAA	GCTGGGCCAC	120
ATCGCGTTAA	TCGGGAAGTC	CAGGATATGG	GAAGACCAAC	GTTCTTACAC	AACATTATTT	180
TCGATGTTGC	AAGACACCAT	CGTCCTGATC	AAGCACACAT	GTACTTGTTT	GATTTCGGTA	240
CCAATGGTTT	GATGCCAGTC	ACAGATATAC	CACATGTTGC	TGATTATTTT	ACAGAAGATC	300
CAAGAAGACC	AAGATTGCTA	AGGCGATACG	TATATTTAAT	GATGAAATCN	GGATCGTCGT	360
AAGAAGATTT	TAAAGTCAGT	ATCGTGTTAC	TAGTATTTCT	GGAAATATCG	GAAAATTAAC	420
CTGGTGAAAC	CAATCCCGTA	TGTCTTTAAT	CCTTATTGAT	AACCTTGACG	CAGTAAAANG	480
ATTACCTTTT	CCAAGAAGTT	TTTGAAAATA	TGATGATTAA	AATGACACGT	GAAGGGCTAG	540
CATTAGACAT	GCAAGTAACC	TAACTGCTT	CAAGAGCTAA	CGCAATGAAA	ACGCCAATGT	600
ACATTAATAT	GAAAACGCGT	ATCGCCATGT	TTTTATATGA	TAAATCAGAG	GTGTCGAACG	660
TAGTAGGGCA	ACNANAATNT	GCGGTTAAAG	ATGTAGTGGG	TCGAGCATTG	TTAAGTAGTG	720
ATGACAATGT	ATCATTCCAT	ATTGGCCAAC	CATTTAAACA	TGATGAGACT	AAATCATATA	780
ATGATCACAA	TTAATTGATG	AAGTATCGGC	GATGACAGAA	TTTTATAAAG	GGTGAAACAC	840
CAAATGATAT	TCCTATGATG	CCAGATGAAA	TTAAAATATG	AAGATTACAA	GAGAATCATT	900
AAGCTTACCA	GATATAGTTC	CCAATGGTCC	TTTACCAATT	GGATTAGATT	ATNGAAGGTT	960
GTTACACTAC	AANAAATTAA	ATTAAGTGAA	CCAGCAATGA	TTTCATCAGA	AAATCCGAGA	1020
GAAATTGCGC	ATATTGCCGA	AATTATGATG	AAAGAAATTG	ACATATTAAA	TGAAAAATAT	1080
GCGATTTGTA	TCGCAGACTC	AAGTGGAGAG	TTTAAAGCTT	ATAGGCATCA	AGTGGCTAAC	1140
TTTGCCGAAG	AAAGAGAAGA	CATTAAAGCG	ATTTCATCAAC	TAATGATTGA	AGACTTAAAA	1200
CAAAGAGAAA	TGGACGGTCC	ATTTGAAAAA	GATTCACCTT	ACATTATCAA	TGATTTTAAA	1260
ACATATATTG	ATTGCACGTA	TATCCCGGAA	GATGATGTTA	AAAAGCTTAT	TACAAAAGGA	1320
CCAGAACTTG	GCTTGAACAT	TTTATTTGTC	GGCATTTCATA	AAGAATTAAT	AGATGCTTAT	1380
GATAAACAGA	TTGATGTTGC	ACGTAAAATG	ATTAACCAAT	TTAGTATAGG	TATTCCGTAT	1440
TTCAGACCAA	CAATTCTTTA	AATTTAGATT	TATTCAACGA	GAACCTGTTA	TTAAAGAAAA	1500
CGAAGCGTAT	ATGGTCGCGA	ATCAAGCTTA	TCAAAGATT	AGATGGTTTA	AATAGTAATG	1560
AATTAAATAG	GAGGGAGGTA	TGTTATGAAT	TTTAATGATA	TTGAAACAAT	GGGCAAGTCG	1620
AAATTTAAAG	ATATTAAAAA	GCATGCTGAA	GAGATTGCGC	ATGAAATTGA	AGTTCGTTCT	1680
GGATATTTAA	GAAAAGCTGA	ACAATATAAG	CGATTAGAAT	TTAATTTAAG	TATTGCACTA	1740
NATGATGTTG	AAAGCACAGC	AAAGGACGTA	CAAAGTCAA	AATCTAGTGC	TAATAAAGAC	1800
AGTGTATCTG	TTAAAGGAAA	AGCGCCCAAT	ACGTTATATA	TCGAAAAAAG	AAATTTGATG	1860
AAACAAAAGC	TTGAAATGTT	GGGTGAAGAT	ATCGATNAAA	ATAAAGAATC	CCTCCAAAAA	1920
GCTAAGGGAA	TTGCTGGCGA	AAAGGCAAGT	GAATATTT			1958

(2) INFORMATION FOR SEQ ID NO:948:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 989 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:948:

```

CCAAATGTGA ATGCCAACAA CAGTAGACCA AATTATCAGG GAATGATGGT GCCATTCCAC      60
CAACCAATAG CCATTATAGA TGCCGAAATC AAAATTGGTT TAGAAAGCGA AGATTTAGAA      120
ATACTGGCAA CTAGTAAAAG ACGTTGCTAA AAGTATCTAA GAAGGGATTT AAGCAGAAGT      180
TGTTGCGATG AAGTGTGTTG GTGCTACTAC TGTAGCGACG ACGATGATAT GTGCTCCAAT      240
GGCTGGTATT CAATTTTTTG TTACAGGAGG TATTGGGGGC GTCCATAAAG GTGCAGAACA      300
TACGATGGAC ATTTTCAGCAG ACTTAGAAGA ACTGTCCTAA ACAATGTCA CTGTTATCTG      360
TGCAGGTGCC AAATCAATTT TAGACTTACC TAAGACGATG GAGTATTTAG AAACAAAAGG      420
CGTTCCAGTT ATTGGATATC AAACGAATGA ATTGCCAGCA TTCTTCACTC GCGAAAGCGG      480
TGTTAAGTTA ACAAGTTCGG TTGAAACGCC AGAACGACTT GCTGACATTC ATTTAACAAA      540
ACAGCAGTTA AATCTTGAAG GTGGCATTGT TGTTGCTAAT CCAATTCCAT ATGAGCATGC      600
CTTATCAAAA GCATATATTG AGGCAATCAT AAATGAAGCT GTTGTGAAG CGGAAAATCA      660
AGGTATTAAA GGTAAGGACG CCACACCGTT CTTGTTAGGG AAAATTGTAG AAAAAACGAA      720
TGTTAAAAGT TTAGCAGCAA ATATAAACT TGTTGAAAAC AATGCGGCGT TGGGTGCTAA      780
AATTGCTGTC GCTGTTAATA AATTATTGTA GGTGATGATA CATGAATATT TTATTCGCTA      840
TCACAGGGAT AGCATTGCA CTATTTGTTG CGTTTTTATT CAAGTTTTGA TCCGTAAAAA      900
CATAGACTTC CAAAAAACG TTAATAATGA TATTTATTCC AGTTGATTGA ATGTTAGTTT      960
ATTTATGAAT GAAACACAAC GAATGGTTT      989

```

(2) INFORMATION FOR SEQ ID NO:949:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:949:

```

CNTTATTGGA TNATNNGCA GAATCCCGTT ATCAAGATTT GTTGGATAAA TATCCCCCAN      60
NCTTTTCNNA ATAATNAAGC CNCNAANCNA GAGTTAGAAG ATTTAGANTC AGCAGACCCA      120
AGCATTGCTG CAGCGTTTAG ATTTAATGAA ATTCCAATTA GAAGAATTGT CTGAAGCACA      180
TCTAAAAGAA GCGGAAATAG AGCAACTTGA AATAGATATT AAACGCATTC ACAACTCTGA      240
AAAATTAAGC TTAGCGCTTA ATAACGCACA TATGACATTA ACGGATGAAA ATGCTATCAC      300
TGATCGTTTG TATGAACTAA GCAACCATTT GTTAACAATA AACGATATAG TTCCAAATAA      360
ATATGACAAA TTTAAAGAAG ATATTGATCA ATTTTATTAC ATTTTAGAAG ATGCAAAACA      420

```

TGAGTTNTAT	GATGAAATGG	CTANTACAGA	ATTTCGACGAA	CAAGTGTTAA	ACGAGTATGA	480
ATCTCGTATG	AATTTGCTGA	ATAATTTAAA	ACGTAAATAT	GGAAAAGATA	TTTCAGAATT	540
AATCGCATAT	CAAGAAAAGC	TTAATAATGA	AATCAATAAA	ATTGAAAAC	ATGAACAAAG	600
TACATCGCAG	TTACGAGAAG	AAATAAATGC	ATTGTATAAT	CAAGTTATAG	AGGTTGGACA	660
AGCGTTATCA	AAGCAGCGTC	GTATAGTCGC	TAGGGAGTTA	AGAGACCACA	TTGTATCGGA	720
AATTCAAAAC	TTACAAATGA	AAGACGCAAA	TCTTGAGATT	TCATTTAAAA	AATTAGAAGA	780
ACCGAATATT	GATGGAATCG	AATTTGTAGA	ATTTTNTANC	ACGCCAAATA	AAGGGGGAAC	840
CATNAAAAAG	TTTANATAAA	ATNGCATCAG	GTGGAGAACT	NTCTAGAATT	ATGT	894

(2) INFORMATION FOR SEQ ID NO:950:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1138 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:950:

AAATAATCCG	ANAATTTTCAG	GCGTTAAATA	CAATATCGCG	CCATAATAAG	CTAGGTGTTG	60
ATGGTGCCGT	ACCTTGTGCT	GGCTTNTCCA	ACACACTTTT	TCACTTCATA	CTGACGTCCA	120
TTTTTAGTTN	ATGGAGTCAA	TAATTCATA	NCGATGAGTA	TCTGCTCCG	GAACCTCTTG	180
GACACCTATA	ACTGAGTGCC	CCGTTTNCCT	CATAAAACGT	CAATCCAAC	GTTTCACTGC	240
TGGCACTTCA	GANTCNACAA	TATCGTCANC	TAATAATACC	GCACATGGTT	CATTGCCGAT	300
AAATTGGCAC	GAGCGCAGAA	CTAATCGCAT	GCCCTAAACC	TTTTNGTTC	TTCTGTCTTA	360
CATAAAAAAT	ATTGCAAGT	TCTGTCGAGT	ATTGAACTTT	TTCTAGTAAT	TCAGATTTAC	420
CTTTTTCTTT	TAACACCATT	TCTAATCTTT	TTTGACTATC	AAAATGATCG	GCAATCGCGC	480
GTTTGTGGCG	ACCTGTCACT	ATAATAATAT	CTTCAATTC	AGCTCTTGCA	GCTTCTTCAA	540
CGATATATTG	TATTGTGGGT	TTATCTAAGA	TAGGAAGCAT	TTCTTTTGGC	ATCGCTTTAG	600
TTGCTGGTAA	AAATCTAGTC	CCTAAACCAG	CAGCGGGAAT	GATTGCCTTT	TTTATTTTTN	660
ACAAAGTTAA	TGTGCTCCTT	TTCCCAAGTA	TTAAATCTAT	GTATCAACGT	CATTTTAACA	720
CTAATTAGAA	CGCCTACATA	GTGTCATTGA	GTATGTAATT	ATCTCTTGGG	AAATGTGGAT	780
TTAATTTTAA	AAAAACAGGT	TTACTACATA	TTAATTTATG	AAATAACCCC	GTCAATTTGT	840
GTTTAATTAT	GCTGTGATAT	TCTTTTTATT	TCTGCGTAAT	AATACTAAAC	CTAGAATGCT	900
GAATAATCCG	CCGAACAACA	TACCTTTGTN	TGNNGATTCT	TCTCCACCTG	TTTCAGGTAG	960
NTCAGATTTT	TTAGATTGTT	TNTGNTTAGT	TGGTGCCACT	GCTTTAACCT	TTTCATTGAT	1020
TTCAATAACA	GGTGTTACTA	CCTTACCTTG	NNCCACTGGT	TAAGAAGGTT	TTATAGGTTT	1080
TTCTTNTAGC	AGGGTGGGTA	CTGGTTTACC	AGGNNCAGAT	GGGTACCTCT	NGTGTGTTGG	1138

(2) INFORMATION FOR SEQ ID NO:951:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1146 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:951:

```

TTATTGTTGT GTTTGTGCG ATATACCAAC TTTTAGCTAT TAAAGAATAT TCAGAAGTAA      60
ATAATAAAAT TATGAATAAA TTATGTCATT GTGNAATTA TGATTAATAA AATCAATTCT      120
AAAAAACC GC CCGCNATAAC CAATGATTTT ATGTAAACAT TTATTTTNA AATTTTGATA      180
TTTTGTCCA CATAATATTC GCAATTAAAC TTTTTTTGTA TAGAATTTTC TTTAATATCC      240
TGAGAGACAT GTNCTATAAT GTTTGTGANA TAATTCACAC AGTATAAAGG AGTGGNTGTA      300
TATGTTAACT ATACCTGNAA AAGAAAATCG TGGATCGAAA GAACAAGAAG TGGCAATTAT      360
GATTGATGCT CTAGCTGACA CAGGGANAAA AGCATTAGAA GCATTATCTA AAAAGTCACA      420
AGAAGAAATT GATCATATTG TTCATCAAAT GAGCTTAGCA GCTGTTGATC AACATATGGT      480
GCTAGCACAA TTAGCACATG AAGAACTGG AAGAGGTATA TACGAAGATA AAGCGATTAA      540
AAATTTATAC GCTTCTGAAT ATATATGGAA TNCAATAAAA GACAATAAGA CAGTAGGGAT      600
TATTGGTGAA GATAAAGAAA AAGGATTAAC GTATGTAGCG GAACCAATTG GTGTTATTTG      660
TGGTGTACG CCAACAACAA ATCCTACGTC GACAACATTT TTTAAAGCGA TGATTGCAAT      720
TAAGACAGGA AATCCAATCA TTTGTGCATT CCATCCAAGT GCACAAGAAT CGTCGAAGCG      780
TGCAGCAGAA GTTGTATTAG AAGCGGCAAT GAAGGCAGGT GCACCTAAAG ATATTATTCA      840
GTGGATTGAA GTGCCTTCTA TCGAAGCAAC AAAACAATTA ATGAATCACA AAGGTATTGC      900
ATTAGTTCTA GCAACAGGTG GTTCGGGCAT GGTAAAGTCT GCATATTCAA CTGGCAACCG      960
GCATTAGGGG TGGCGGGGAC CAGGGGTAAC GGGGCCCGTC TTTNCAATTG ANAAAACAGC     1020
ACACATTAA N CGTGCAGNAA NTGATATCAA TGGGTCAAAC ACATTTGATA TGGTATTGAT     1080
TGGTGCTTCC TGACAAAGTT GGTGGCCATT GATAAAGAAT TTATAAGGTT GTTACTTATG     1140
ATTTTA                                           1146

```

(2) INFORMATION FOR SEQ ID NO:952:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:952:

TTTGTGCTTC	GTCAATCTTG	TCACCANCTA	ACTCTAAACG	CTTTCCTTTT	GTCGTTTTCG	60
GGNTCCCACC	ACAATTAATC	TGTTTTGATT	TCTGACATAT	CAATCTTCCT	AGTTAACCCA	120
AGCCAAATCT	TTACCATACT	CAATTTCTTT	ACCTTGGAAC	AAGCTGTTTT	TCTTGTTGAG	180
TACCACATAT	CTACCTTTGA	CGGTATTAGA	ACTAAGCTCT	ATATAAAAAT	CCAATGCCAT	240
TTTATAGGTT	GTACATAATT	GCTTTAAAC	TTCATATCTA	GTNTGATAAG	AAGTCCATGA	300
CGTAGTACGT	AAGCCATCGT	ATTCGGTNTG	TTCAGAAACT	TCCCAACCTG	TATCGCTCAA	360
CACATCTTTC	AATGCTTCTG	AAGTTGTCTT	TTTCTCAAAT	TTGCCTGGTG	CATACGGTTT	420
AGCTGTTGTT	ATATCAGCAA	GATAAGACGC	TATACATTCT	ATCTCTGTGT	AGCCGTCCAT	480
CGTATCTTGA	ACCCAGTTAA	TAATAAATTC	ACGCCATTGT	TTGTTTGAAT	CCCTTATAAT	540
AACACGATGT	CGTTCACGGA	ACNTTTCAGC	TCTTCTGAT	GATATGAGCA	GTTCAAGCAT	600
TTCTGAATTG	TCATTAACAT	TACGTTTATG	AATCGCTCTA	ACTAAGGAAG	GATCATCAGT	660
AGAAAGGAAA	TCTATAATCT	TGTCGTTAAA	ATCTAAAACA	TGTATCACAC	TCTCATCTCC	720
TTTCTATAAA	TATCTATCTT	GCCATTTAAC	CGTCGTATCA	AAGACGTTTT	CAGGTTGTAT	780
GATTAATTCA	CTGTACCCAG	AATCAACATT	GAAATAATTA	CTTCCAAACG	ATTTCTCGCT	840
CCAACATTGG	TTCTTCATTT	GATGACAACA	CTTNNNGCTT	GNATATCTAT	TTTCACTAAA	900
TCACCTTTTT	GTATAATGAC	ATCCCTTGCG	CCTTTCGGNT	TCGGTAGAAT	CTCCGTATTG	960
AATGAACCTA	ATCCATTTCAT	CTCCATCCAC	TTATAACCGT	NATACTTCGC	ACTATAGATA	1020
GCTATGATAG	AAGCTGGACG	CTGATAAAAC	TTACCGCCAT	CTATCCACTC	TTTCTCATCC	1080
ATATCAATAG	GTTTACGTCT	ATCTGGGTCT	TTAATGTGAT	CAAATTTCCA	AGTTTTAATA	1140
GAAAATTTAT	TACCTACTCT	TCTGAGCCGC	ATATAAACAN	CGATTCTGTC	CAAGTTATAC	1200
ATTATCGGTT	TATTCTGATA	GTCGTATATC	TTTTTGGGGT	CTCCTTTTTG	GTTATACG	1258

(2) INFORMATION FOR SEQ ID NO:953:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:953:

TCGAATTTGG	TGTTGNCCGT	TCCTGTATNA	CATTCTGNCT	TATCTAATGG	GGGACGTTAT	60
GATGAGTGCC	CACMNATTAG	GGATGATCGT	NCGAGAGTAA	GTGTTGGTGC	AAGGTCAAGT	120
GTGTTTCGCAC	CTTTCACAA	ANTTAGGGTT	AATCATCATT	GATGAAGAAC	ATGAATCTAC	180
ATATAAACAA	GAAGATTATC	CGAGATATCA	CGCTAGAGAA	ATTGCCCAAT	GGCGAAGTGA	240
ATATCATCAC	TGTCCAGTCA	TTTTAGGAAG	TGCAACACCA	TGTCTTGAAA	GTTATGCACG	300
AGCTGAAAAA	GACGTTTATC	ATTTGCTATC	ATTACCAAAC	AGAGTGAACC	AACAAGCTTT	360
ACCTGAAATT	GATATAGTAG	ACATGCGTGA	AGAATTGAGT	GAAGGTAATC	GGTCAATGTT	420
TTCAAAAGAT	TTACGTGAAG	CCATACAATT	AAGATNAAGA	TCGACAGGAA	CAAGTTGTTT	480
TATTTTTTAAA	TCCGACGTGG	TTATGCATCG	TTTATGTTAT	GTCGGGATTG	TGGATATGTA	540

CCGCAATGTC	CAANCTGTGA	TATTTTCATTA	ACGTATCATA	AAACGACAGA	CTTATTAAAA	600
TGTCACATATT	GTGGTTACCA	AGAGACGCCA	CCGAATCAAT	GTCCAAATTG	TGAGAGTGAA	660
CACATTCGAC	AAGTAGGTAC	TGGTACTCAG	AAAGTTGAAG	AACTATTGCA	ACAAGAATTT	720
GAAGATGCGC	GCATAATTAG	GATGGATGTA	GATACAACCT	CAAAGAAAGG	TGCACATGAA	780
AAGTTATTGA	CTGAATTCGA	AAAAGGTAAC	GGTGACATTT	TACTAGGTAC	TCAGATGATT	840
GCGAAAGGAT	TAGATTATCC	AAATATTACT	TTAGTTGGTG	TGCTGAATGC	NGATACAATG	900
TTAAATTTAC	CTGATTTTCG	GGCGAGCGAA	CGTACTTATC	AACTATTAAAC	GCAAGTGGCT	960
GGTAGAGCTG	GTCGTCATGA	AAAGGCAGGT	CAAGTCATCA	TTCAAACGTA	TAATCCAGAT	1020
CATTATTCAA	TATTGGATTG	TTCAAAAAAA	TGATTATTTA	ACATTTTATC	GTCAGGAAAT	1080
GGAATATCGT	CAAATTAGGA	AAGTATCCAC	CGTATTTATT	ATTTGGTTAN	TTTCACAATC	1140
TCACATAAAG	AAATGAAGAA	GGTTATGGAA	GCATCGCAGC	ATGTTCTATA	AATTTTATTA	1200
CAGCATTTAC	AAGAAAAAGC	GCTTGGTACT	AGGTCCATCC	TCCGGCAGCA	CTTGCGAGAA	1260
TCAACAATGA	ATTTAGATTG	CCAAATTTTA	GTGAAATATA	AAAGTGAACC	TGGATTATTA	1320
CAAGCCANTC	AGTTTTTAGA	TGACTATTAC	CATGAAAAAT	TTATAAAAGA	AAAATTAGCA	1380
TTGAAGATTG	ATATTGGANC	CACAGATGAT	GATGTAACAT	TACTAATTAT	TAGAAACAAG	1440
NNCAAGTATT	GTACGAGTAT	TTGAACCCAG	TGTGTGAATA	TTTACTTNAN	GNACAAGAAA	1500
AAGGGCAGAA	TATACAACCTG	TTAACTATTT	AAATTAGCAG	TTTATATTCT	GTCTTTTAT	1560
ATGGCTTTAT	AACTTACGTG	ATTTTGGTTT	GATAAGGAAT	TTATTAGTAT	TTTCATTTAC	1620

(2) INFORMATION FOR SEQ ID NO:954:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1126 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:954:

ATAAGTTTTT	AAAATGTATT	AAATTTGTGG	AGGCATGTAA	ACAATGAAAG	TATTAAACTT	60
AGGATCGAAA	AAACAAGCAT	CATTCTATGT	TGCATGTGAG	TTATATAAAG	AGATGGCATT	120
TAATCAGCAC	TGTAAACTAG	GTTTAGCAAC	TGGTGGTACA	ATGACAGATT	TGTATGAACA	180
ACTTGTTAAG	TTATTAAATA	AAAATCAGTT	AAACGTAGAC	AATGTATCCA	CGTTTAAATT	240
AGACGAATAT	GTAGGTTTAA	CCGCATCACA	TCCGCAAAGT	TATCACTATT	ATATGGATGA	300
CATGCTTCNC	AAACAATATC	CTTATTTTAN	TAGAAAGAAC	ATTCATATTC	CAAATGGAGA	360
TGCCGATGAT	ATGAATGCGG	AAGCGTCAAA	ATATAATGAC	GTTTTAGAAC	AACAAGGTCA	420
ACGTGATATT	CAAATTTTAG	GTATTGGTGA	AAATGGTCAT	ATTGGATTTA	ATGAACCTGG	480
TACGCCGTTT	GATAGCGTTA	CTCATATCGT	TGATTTGACT	GAAAGTACTA	TTAAGGCTAA	540
TAGTCGATAT	TTTAAAAACG	AAGATGATGT	TCCAAAGCAA	GCCATTTCTGA	TGGGACTTGC	600
TAATATTCTT	CAAGCCAAAC	GTATCATTTT	ACTCGCATTT	GGGTGAAAAG	AAACGTGCTG	660
CTATTACACA	TTTATTAAAT	CAGGAAATTT	CTTGTTGATG	TCCCAGCCAC	ATTACTTCAC	720

AAACACCCGA ATGTNGAGAT ATTTTTTAGA CGACGAAGCT TGCCCGAAAA ATGTTGCGAA	780
AATTCATGTC GATGAATGGA TTGATTGCAA TGTCTAATTA AGAAATGCCT CGGGAAAGGT	840
TCCAATAGAA AGATAAAAAG CATGTGGAAG GATGATCTTT AGTGCGAAT TACAATTAGC	900
AATTGATTTA TTAAACAAAG AAGACGCTGC GGCTGACTTA ACTCATGAGA GTTTAAGATT	960
ATGTAGATAT CGTAGAAATC GGTACGCCAA TCACTACCA CGTGGTGCTA CTAGTAGTTA	1020
AACATATGGC AGACAACCCT AGTAATGTCA AGTATTAGCA TACATGCAA TTATGGATGC	1080
AGCTGATTAT GTAGTTATCC TACCAATTAA ACTTGACGCT CGTGCC	1126

(2) INFORMATION FOR SEQ ID NO:955:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 875 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:955:

AATTGGGCAC GGGTANACAG TTGTAGCGTT ATTAAGNATT TTAACTTTTC CGAAGTTAGC	60
AACAATTINC CAATGATGTT ATTTTATCAA TGTTACCTCA AGCAGCAACT ACAANCGATT	120
GCGTTACCAG TATCAGCTGG TATCGGTGGT ATAAAAGAAT TAACATCATT AGCAGNTATT	180
TTAAATGGTG TCATTATTTA TGCCCTAGGT AATAAATTCN TGAAGCTTTT CCGAATTACT	240
AACCCATATG CCCGAGGATT AGCACTTGGA ACNAGTGGTC ACACATTAGG TGTAGCACCA	300
GCCAAAGAAT TAGGACCTGT AGAAGAATCA ATGGCAAGTA TAGCTTTAGT GTTAGTTGGT	360
GTAGTTGTTG TAGCAGTTGT GCCTGCTCTT GTAGCAATAT TCTTCTAAAA CGAAAAACCT	420
AAGCAAGATA ATAGCAATTT GAGCCATTGT TATTATCGTA AAAAAACGTC TATACTCCAG	480
TTTATAACTG GGATATAGAC GTTTTTATGT ATTTATTACT TTTTACTAGG AATATAAAC	540
TGTGCATGNC GATAATGAAA TACGATGTCA GACGAATCAA AGGGTTTGCC AGTCATTGTA	600
TAAAAAGTCT GGTGGTAACG TAAACATGGT TCACCTGTAG ACAATTGTAG TAATGAAGCT	660
TCACTTGAAG TGAGTTTATC TACATTAAAG AAAATATCTG AAAAACCAAT ACGAAGTTTC	720
ATGTTTGATT CTAAATAATC GAAGATAGAG CCCTTAGCAA TATCATCATT TAAATATTTT	780
ACGATTTCTT TATGATAATA AGAATATTCG ATACATAAAA CATCATCGTC CACGAATCTT	840
AATCGCTCTA AATAGTAGAC GGTATCACTC GTGCC	875

(2) INFORMATION FOR SEQ ID NO:956:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1187 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:956:

CAATTCCAAT	GGCACAATTA	CCAAATATTA	CATCTGAAAG	ACCTATCCCA	CCTGCACCAA	60
GAAGTTAAGT	CAAATGAATG	CAGGTACGCA	GTTATATCAT	ATAGTTGCTT	CAAATGCATA	120
TCATAAAGAC	ACTGAAGATT	TCTATATTAG	TTTAAAAATC	GTTGATGTGA	AACAACCTGA	180
AGGCGATCAA	CGTGTCTATC	GTACGTCAAC	ATATGATTTA	ACCACTGATG	AAATCTCAAA	240
AGTAAACAA	GCTTTTATTA	ATGCAAATAG	AGATGTAATT	ACGCTTGCCG	AAGGTGATAT	300
TTCAGTTACA	AATACACCTA	ATGGTGCTAA	TGTAAGTACT	ATTACAGTAA	ATATTAATAA	360
AGGTCGATTA	ACGAAATCAT	TCGCGTCTAA	CCTAGCTAAT	ATGAATTCT	TGCGTTGGGT	420
TAATTTCCCA	CAAGATTATA	CAGTGACATG	GACGAATGCA	AAAATTGCAA	ACAGACCAAC	480
AGATGGTGGT	TTATCATGGT	CCGATGACCA	TAAATCTTTA	ATTTATCGTT	ATGATGCTAC	540
ATTAGGCACA	CAAATTACAA	CTAATGATAT	TTTAACGATG	CTAAAAGCGA	CTACTACAGT	600
GCCTGGATTG	CGTAATAATA	TTACTGGTAA	TGAAAAAGCA	CAAGCAGAAG	CAGGTGGAAG	660
ACCAAACAT	AGAACAACCTG	GTTATTACAA	ATCAAATGCG	ACAACGATG	GTCAACGTCA	720
ATTTACGTTG	AATGGTCAAG	TGATTCAAAT	ATTAGACATC	ATCAACCCTT	CAAACGGTTA	780
TGGTGGGCAA	CCTGTTACAA	ATTCAAATAC	TCGTGCAAA	CATAGTAACT	CAACTGTTGT	840
TAACGTAAAC	GAACCGGCAG	CTAATGGTGC	TGGCGCATTT	ACAATTGACC	ACGTTGTAAA	900
AAGTAATTCT	ACACATAATG	CAAGTGATGC	AGTTTAGAAA	GCGCAGTTAG	ANTTNACGCC	960
ATATGGTCCC	NNACAATATG	TTGAACATNT	AAATCCAAAT	TACAGGAAAT	ACTNCTGACG	1020
CTATTAACAT	TTATTTTGTA	CCAAGTGACT	TAGTGAATCC	AACAATTTCT	GTAGGTAATT	1080
ACACTAATCA	TCAAGTGTTT	TCAGGTGAAA	CATTTACAAA	TACGATTACA	GCGAATGATA	1140
ACTTTGGTGT	GCAATCGGTA	ACTGTACCAA	ATACATCACA	AATTACA		1187

(2) INFORMATION FOR SEQ ID NO:957:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1159 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:957:

CGATACCGNC	AGTTGCCCCA	ATACCAATAC	TTTGATGTCC	GAATAAANCG	CTNNCCGAGC	60
GNNTGTCCGG	GATAATTTCT	GAGTAAAATA	CCNCATGCT	GGGGGGATAN	CGANANAAAN	120
CCCTTCAGGG	TGCCCCCATA	CCCAGAAGAA	GTTAGCCAC	AGCATTGGCA	TACCGCCATG	180
TGCACCTGTG	TAGAATGCTG	TGTCAAATAT	TCTATCAGTT	GTCAATTAATG	CTAACGCTNC	240
TGTTAAAGGA	GGGAAAGCAA	GAATAACAAT	TAATGTAGTA	ATAAATGTTG	TTACTGTAAA	300

CATTGNCATT	TGCATAAACT	TCATAGNTGG	TGTTTTACAT	CTTAAAATTG	TTACACAGAA	360
GTTGATACCT	GTAGCTAAGG	TACCAAGCCC	TGAAATTTGT	ATAGCTATTA	AGTAATAGTT	420
AACACCCGGA	CCAGGACTGA	ATTACCTGCG	TAGTGGCGCA	TAGTTTGTCC	AACCAGCTGC	480
TGGTGAACCA	CCAATAATAA	ATGACAGGTT	GAATAAAATC	ATACCTGCAA	AGAATAGCCA	540
GAAACTTACG	TTGTTTAATA	CTGGGAATGC	AACATCACGT	GCTCCAATTT	GTAATGGAAC	600
AACGATATTC	CATAAACCAA	AGATAAATGG	CATTGCCATG	AAGATAATCA	TGATTACACC	660
ATGTGTACTA	AAAATTTTCG	TATAGTGGTT	AGATTCTAAA	AATTTGTTAT	CAGGTACTGT	720
TAATTGCGCA	CGAATAAGTA	ACGCATCAAT	ACCACCACGG	ACGGAACATT	AATACGGCAC	780
AGGATTAAAT	ACATAATCAC	CGATTTTCT	TTATGGGTCT	TACAGATGGT	GAACCCCACT	840
CTTTGTAAAG	ATATTTCCAT	AATTTAAAGT	AAGTAATTAC	TGCGATTAAA	CCAATAACTA	900
AGAATGGGGC	ACCAATTTGT	GCCATTGTAA	TCATCCAGTT	ACCTTTAACT	AGTAATTGAT	960
CCCATGGAAA	ATTCATTAAT	GTCCACCTCC	ATGATCATCA	TTGTCTTGAT	CTTGCGCATC	1020
TTTTGAAATT	TTCTTCATTT	CTTTCGCATT	TTTCGATTCA	TCTTTCTTGA	ACTCATTTGT	1080
ATATGGTTTC	TCATTTCCAA	GAATCATCAA	CTTCATACCA	TGTCGTTTAT	AGTTTCGCAT	1140
TGTAATTTGA	GCTCGTGCC					1159

(2) INFORMATION FOR SEQ ID NO:958:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1090 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:958:

TGTCATTTTG	ATTAAAGTGG	CACGAGCGTA	GTCTCGTTGC	ACAACAGTCA	ACGATTTCAA	60
TGTTATCTTT	GCCTCCCAAA	CCAGCAACAA	TAGTTTGTGC	TCTTTCAGTA	GCCTCAACTT	120
GTTGTGCTGC	AGCTTTATCT	TCTCGACCAG	GTGTTTTGAA	ATTAAATTTT	GTAATTAAGA	180
ATCTGAAAC	GATGTAATAC	ACACAGAACC	ACACAATTCC	AATAGGTATG	ACGTATAGGT	240
AGTTTGT	ACTATTACCT	TGTAGCACAC	CAAAGAGTAA	GAAATCGATA	AAGCCTCCAC	300
TGAAGGTTTG	ACCAATTGTA	ATGTTGAAAA	TGTC TGCCAT	CATAAATGCT	AATCCATCAA	360
AGAAGGCATG	GATTACATAA	AGAATAGGTG	CGACAAACAA	GAAACTAAAC	TCTAAAGGGT	420
TCGGGTAATA	CCTGTTTAAA	AATGAAGTGA	GTGCAGCGGG	ATAACATTAA	ACCGCCGACA	480
ACTTNTATAT	GTTTCAGGTTT	AGCTGTGTGA	TAAATTGCAA	GTGCGGNACC	ACATAAGACC	540
GAACATCATC	CGATAATAAA	ACGGCCTGAC	ATAAAGCGTG	ACACACCTGA	ATAATACTTC	600
GTCACATCTG	GATCACCAAG	TTGAGCAAAG	AAGATGTTCT	GCGTACCTTG	AACTAAGTGC	660
CCTTTGACTG	NCTAACGAGT	ACCACCAAGT	GCCGTCTGCC	AAAACGGTAA	GTAAAAAATA	720
TGGTGTAAC	CGAGTGGACC	TAACAATCTT	AAGATGAAGC	CATAAACAAA	AGTACCGATG	780
GCACCTGTTT	TCGTTACAAA	TCCACCAACA	TGATAAATGC	CGGCTTGAT	GCTTGGCCAA	840
ATGAAAAACA	TCAATACACC	TAAAAAGATT	GCGGCAATG	CTGTGACAAT	AGGGACAAAT	900

CTANAGCCAC CAAAGAAACC TAAATACGGT GGTAATACCA CTTTGTGATA TTTGTTGTGA	960
AGTATTGCGG TCATAATACC TGTGATAATC CCGCCAAAAA CACCGGTTTC AACCGTTTGT	1020
ATACCGAGCA CCATGCCTTG TCCATTTTGT TGCAAGCTGA TCTTTTGCCA ATGTTGCCCCG	1080
TGATAGTTAA	1090

(2) INFORMATION FOR SEQ ID NO:959:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:959:

AATTTACACT AAACATTTCA TTCCTAACAC TTCANCGAAA AGTTTGAAAA TCCAANACGT	60
TNACCAATTG GTGCTAANAC AAATGGAATA AAGAACACAG GATTCAATAC TAGTGNTGCA	120
CCAAATAAAA TTGGTTCGNT TACACCAAAG GAATGTTGGT ACANCTGGAT GCACGTCCAA	180
TCGCTTTGTT TCGTTTAGAT TTCGTCATCC AACATAAACA TGAACGGGNC GACCAATGTT	240
GCACCCGTAC CTCCAAAAGT AACGATAAAC ATTTGTGTAC CTGATGTAAT AATTTTATCT	300
GCGTGTCTC CAGCTTGAAG CAACTTGAAG TTCGCTTCGA TATTCGCATA TGTAATGGCT	360
GCAATTGCTG GCTCTACTAT TGATGGACCA TGAATTCCTA CAAACCAGAA TAATGCAAAG	420
GCACCAAAGA TAATTGTGAC ACCAATCCAT CCATCTGCTG CTGTAAATAA TGGTTCGAAT	480
AATTTTAAAA TACCTCCGC TACATTTGAT TTAAAGCTGT TGCGAATGAC TAAATCTAAT	540
GCATAAGAA TGATGATTAC CGCTGAAAAT GGAATTAAAGT CCTTAAATAC TTGTGAAATA	600
TTCGCGCGTA CTTCTTTCGG CATTTTAATT GTAATATTGC GCTTCACACA GAAGTTATAA	660
ACAATAACAG TTACAAATGC TGATAAAAAT GCTGTTAATA AACCTTTAGT TCCCATAAAT	720
GCACTTAAGA ATCCACCATC TTTGGCTGGA TCAGAAGCTA AGAACAAGAA TCCACACATC	780
GNTGCTAGCA TTGTAGAAAT AAAGTTAATT TGATTGTGAC TTTCTAGCTT ACGGTAAAT	840
GAATCTTGTT AAAGATTTCG CTGTCGTTCC TGCTACTAAA AATGCTACAA GCCCCATCGG	900
ATAGTTATAT GGGTTCATTA AAATGGCTTC CATGCCTTTA TCCCATTTAA AACCAAATAT	960
ATTGGGCACG TATGCAATTA ATAGAAAGAT ACTTGAGAAT TAGATGACAG GCATTGCAGA	1020
AATAAATCCA TCACGGATNG CTCTTAAATA TTATGTTACG GTGATAATTT CTCGGAAAAA	1080
TGGCTTCCCT TTTTCAATTT GTGCGATCAA TTTTTCATC ATTGTCATCA CCCTCTTTTA	1140
TAAAATCTTA ATAAATGCTT CATTAAATCT TTCAGTAAAA TTGTTGTCCA TTAAATGGTC	1200
CTTGAACATG CATCATCCGT TACACTGTTA TGCAATATCA TCACCTTGCG CTTCTTTAGC	1260
TAACAGCTTC	1270

(2) INFORMATION FOR SEQ ID NO:960:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1455 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:960:

```

CAACCTGATT TTGATGGAAG AAATTACCTT GATAAATNAA AGCCTTCCCN NCNANGGAAG      60
AAACCAATGA TGAAAATAAT TGGTTCTGCT TCTAAGTCAT GCGAATGATA ATAAATATCG      120
ATGATTCTAC AAGACTCTAA TATTGAAAAT GAGGATTATA GATATAATCA AAGAAATTGN      180
CGACCCAAAA TGAATCGGAA TGGAAATTNCA AGTCGGCANC CGGACCAACC TCAATCAGCT      240
CCTAAAGAAC AAAATAGCGA CTCGAATGAT GAGGAAACAG TAACGANAAA AGAACGNAAA      300
AGTAAAGTAA CACAATTAAA GCCATTAAACA CTTGAAGANA AGCGGAAGTT AAGACGTAAG      360
CGACAAAAAC GAATCCAATA CAGTGTATT ACAATATTAG TATTGTTGAT TGCTGTTATA      420
TTAATTTACA TGTTTTACAC ACTTAGTAAA ATTGCCGCAT GTAAATATAA ATGGAATATA      480
TCACGTTAGT ACTTCAAAGA TAAACAAAGT TTTAGGTGTT ANAAATGATT CGAGGATGTA      540
TACGTTTAGT AAANAAAATG CTATTANTGA TCTCGAAGAG GATCCATTAC TCNCAAGTGT      600
TGAGATACAC AAGCAATTAC CANACACATT AAACGTAGAT ATCACAGAAA ATGAAATTAT      660
TGCTTTAAGT GAAAAAATAA NGGTAAATAT TTACCTTTAT TAAGAAATG GTAAATTGCT      720
TNANGGTTCA AATGATGTCN CAATTAATGA TGCACCTGTC ATGGATGGTT TCAAAGGTAC      780
ACAAGAAGAT GATATGATTA AGGCGTTATC TGAAATGACA CCTGAAGTTA GNCGATATAT      840
TGCCGAAGTG ACATACGCCC CAAGTAAAC CAAACATAGC AGAATTGAAT TGTTTNCGAC      900
AGATGGACTT CAAGTAATCG GTGATATTC GACGATATCT AAGAAAATGA AATATTATCC      960
GCAGATGTCA CAATCATTAT CAAGGGATAG GTCGGGTAAA CTAAAAACAA GAGGCTATAT      1020
TGATTTATCA GTCGGTGCTT CATTTATCCC ATNCCGTGGA AACACGTCTA GTCAATCAGA      1080
AAGCGATAAA AATGTGACTA AATCATCTCA AGAGGAAAAT CAANCAANAG AAGAATNACA      1140
AAGCGTTTTA ANCAAAANTA NCAACAATC AAGTAAGAAT AATTAAAAAA TTTTGATATT      1200
GTCTATGTTT ATAGTTCACA AGCCATTCAA CGTATTGTAA ACTAAGGATA GTGTATTTTT      1260
TTAATAGTAA TTTGTCAGGA GGTGCCGATC TATGGAAGAA CATTACTACG TAAGTATTGA      1320
TATTGGATCA TCAAGCGTAA AAACAATAGT AGGCGAGAAA TTTCACAATG GTATAAATGT      1380
GATAGGTACA GGACAAACCT ACACGAGCGG TATAAAAAAT GGTTTAATTG ATGATTTTGA      1440
TATTGCGCTC GTGCC'

```

(2) INFORMATION FOR SEQ ID NO:961:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:961:

```

TCGTCTAAAA GTAAANCTCN GATGTGTAGG TAGTGCGACG GCGTAGAGAA ACGTCATTGT      60
GTGCCCCCGG ATTCGTACTA ATGCGAGTAT TCCATTTGAC AAATCAATTA TTGACAGTGA      120
TAGCTCATTA AGAAGTGAGG ATAAAGCGAT GATATGAGTA CTTTAGTTGG TACAGTGTG      180
AGTGGTTTTG AATATCGAGC ACATAAGGAA GAGTTGGATA ATTTAACAGA AGTTTTAAAA      240
GAATATAAAA GTAAATATAA ATATACTGGT TATACTGAAA ATGCAATTAT GAAAACGCAG      300
AATAGTGGTT TTAGAAATGA GTATTATTAT TTGACTGCAA TTCCATATAC TTTAGATGAA      360
TATAAAAGGT ATTTTCAACC CTTAATCAAA GAGGATGATA AGTCTTTTAG GGACGGTATG      420
AGAAACTCAA AAAACAAC TAAAGATAAA TCACGTCCAT ATGTTGTTAC AACTTTATTT      480
AGTACTAAAG ATAATTTTAC TAAAGATAAT ACAATAGACG AGATGATTGA TTTTCTGAA      540
GTCTCGTGCC TAAAAAAGAA AAAGAATATT CCTCATGATG TGTAAATGTT CTCTTCAAAT      600
NTCTAATAAA TATATAAATA CAAAAGACC TAACTATAGT AAGAAGGAAG TAATAGAAGT      660
AGGTGTTTTT ANTCATGAAA AAGCTAACAC GANTTGATTA ANCTAATAAC AAATAAAAAG      720
GGGGGGTTCA AAAAAGGCA TCTCAACAAC AAGG                                     754

```

(2) INFORMATION FOR SEQ ID NO:962:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 624 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:962:

```

CCAATTTTTT ATGGATAACT TCGGTCTAAA AGTTAAAGCT ACGAATGTTG TAGGTAGTGG      60
CGACGGCGTA GAAGTATACG TGCAATTGTGA TGACCACGAT ATCGTATTTA ATGCGAGTAT      120
TCCATTTGAC AAATCAATTA TTGACAGTGC ACGAGCTCAT TAAGAAGTGA GGATAAAGGC      180
GATGATATGA GTACTTTAGT TGGTACAGTG TTGAGTGGCT TTGAATATCG AGCGCAAAAA      240
GAAAAGTATG ATAATTTATA TAAATTTTTA AAAGAAAATG AAAAGAAATN CCANTATACA      300
GGATTTACTA AAGAGGCAAT TAACAAAACA CAAAATAGTG GATATGAAAA TGAATATTTT      360
TATATAGNTG CTAATATNCC GACGCTCCAA GAATATAGGA AATATTACGA ACCCCTAATA      420
AAGAAAAATA NTCTGAATTT TAAAAAAGGT ATGAAACAAG CAAGGGAAAG GAGTTAGGCT      480
ATAAAGCTGC AATAGAAGNA CATACAAACA TTGTTTGCGA GAAGTTAGTA ACTTNNCAAA      540
GGACAAAAAA ATTAGATGAT GTTTAGATNT GTCTGAAAGT ACGAAAAAGT NACACCTTAA      600
TTGTGGAAAA TACGAAAATT TTTT                                     624

```

(2) INFORMATION FOR SEQ ID NO:963:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1096 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:963:

```

TTTTTACAAT TATTNACCCC ACGTTAACCA ATATATTTTT AAGTCGTTAT TGTAACNGTA      60
ATATCCAATA GCATCTTACC TGCATTTAAT TTTACCTATT GCGATGCTCA TTGCGTTAAC      120
CAGTATGTTT AATACCAACG ACAATCGGTG GTTTGTTATC GGCGATTGGT ATTGCAGGCA      180
TGGATCGTGT TACTCAATTC AATGTATTAG CGNAAAGTGG GCGTGCTGTA GAAGTATGTG      240
GAGATGTCGA TGTAATGATT TTAGACAAGA CAGGGACAAT CACTTATGGC AATCGAATCG      300
CTAGTGAATT TTTACCAGTG AATCAACAAA TGCTGGAAAA ATTGATAGTC GCTGCTTATA      360
TGTCATCAAT CTACGATGAT ACGCCAGAAG GAAAAAGTAT TGTACGATTA GCGAAGCAGA      420
TGTATATAAA TGAGCGGCCT AAAGACATTG ATGGCACATA TAAGCCCTTT TACAGCTGAA      480
ACTAGAATGA GCGGAATCAT TACAAATGAA ATATCGGTAT TCANAGGTGC ACCTAATAGT      540
ATGATAAATC TTGTCAAACA ACAACCCAAG GCAATATTCC TCTTAACATT GAGTCTCTCT      600
GTATGGATGT ATCGAGTAAA GGTGTCACAC CATTAATAAG TCATTGAAAA CAATGTCATG      660
CTTGCGGTGA TTTATTTAAA AGATGTGATT AAAGATGGTC TTGTAGAACG ATTTACTGAA      720
TTGAGAAAAA TGGGGATTGA AACAGTTATG TGTACAGGTG ATAATGCTTT AACAGCAGCT      780
ACAATTNCAA AAGAAGCCGG GGTGATAGA TTTGTTGCAG AGTGTAACC CGAAGATAAA      840
ATTAAAGTCA TCAAAGATGA ACAAGCGAAA GGCCATATTG TTGCGATGAC AGGAGATGGG      900
ACAAATGATG CACCTGCGCT AGCACAGCG AATATAGGAT TAGCTATGAA CTCAGGGACA      960
ATTAGTGCTA NAGAGGCAGC TAATCTAATT GATTTAGAGT CGAATCCTAC AAAGTTAATA     1020
GAGGTTGTAA AAATAGGCAA ACAATTATTA ATGACCAGAG GTGCATTAAAC GACATTTAGT     1080
TTGGCTAATG ACGTAG

```

(2) INFORMATION FOR SEQ ID NO:964:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 949 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:964:

CCACAATAAA	GTATAAGGCA	CGAGACTATA	TAAGCTATTT	GAAAATATAA	ACCTATCTTT	60
ATGAATGATT	TTTCTACATT	TTTTTCCATG	TCTATTCCCC	ATTTATTTAA	TATTTTACT	120
TTACCTTAAT	ATACCTTATT	TTATTTAATT	TTTATATGCA	AAATACAAAA	ATGGAGAACT	180
TCAATATTTA	TAAATATCA	AAAGTTCTCC	ACACTATATT	GTTTTATTAT	ATTTTCGCTA	240
TCAATACGCT	AAATCATCAT	ATTTCCCTCA	ACATCACAGT	AAAACATTG	CTCCACCAAG	300
TATACTTTTT	CAGTATAGCA	TCTCATATTG	GCAAACCTAT	CTGCTAAAAA	CTGCTTCCAA	360
TTACGCAGTT	GTTCAACATC	ATCATCTTGT	TTAAGTAATG	CCAGTGGTAC	TTGAAGATTA	420
AGACATCGTC	CTGAAATATT	AAAGCGTGTC	ACACCTGCTG	GCACAGTTTC	CCCTTTATGA	480
ACAACCGCTT	CAATTTCTCT	ATAACTCAAT	GGCTGATACT	TCATGAGTAC	ATCTTGTTGA	540
GAAAGACAAG	GATATGTACC	TTGTGCAATT	CTCTCTACAG	AACAACAACC	ACTATAACTT	600
GCGACAACCT	TTTCCCATAC	TTGAAAATGT	GCTTCGCCCTA	AATCTTTCGT	ATACAAATAT	660
TGTTCTGTAT	CACCATGACA	ACATCGTAAT	AAATGGCGCT	TCTTGCTCTG	TCTCAGTAGT	720
CCATGGCAAG	CGATGTTCTT	GTTGTAACGT	TTCCACCAC	ACACCAAATG	GAACCTTATG	780
TTGCCATGTA	CTAATTGAAT	ATTGTGTTTC	ATGGATTCTT	TGCAC'TGGAA	CTTTCTTACA	840
TCCTAACGCT	TTCAAACCTG	TATACCGATG	CACACCATCT	ATAACCATAT	ATCTACCATG	900
TTGCATCGCT	GTCAC'TAAAA	TAGGATGACG	TATAAAATCA	TCGGAANTC		949

(2) INFORMATION FOR SEQ ID NO:965:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:965:

ACGTCGTTAA	AACACTATAT	CCATCAGATG	GTTGTTCTAT	AAACTAATTT	CAACTATCGG	60
TGCATTAAAT	AATGGCATCG	GAGTCTATCC	TTGTTGTAGT	ATCGTATACA	GTCAC'TTCAA	120
ATCTCCACGT	GAAGCAACTG	GAGATAACTG	GGATGGCCTT	GGCCGTACTC	TAGAGTGGAC	180
TACTGCATCA	GCAAT'TCCAC	CTAAATACAA	CTTTGCCATT	ACACCAGATT	GGAATGACTC	240
CGACACATTT	GTTGATATGA	AAGAACATGG	TCGTCATTAC	TTAGACAACC	ATAATTACAA	300
AGACATTCAT	ATGCCAAACA	ATACTCCTGT	TGGATTCTGG	ATTGGTATCT	TTATGACTAT	360
CGGCGGTTTC	TTCTTAATTT	TCGAAACTGT	AATTCCAGCA	TTAATTTGTT	TATTCGGTAT	420
TTTTGGTACT	ATGATTTATC	GCAAGTTNCC	CAAATCCGAT	CNCGGGATAT	CATATCCCTC	480
CTGCTGAAGT	TGCTGAAACT	GAAGCTAAGA	TTAAGAGAAG	CGCGTATTAA	AGAAAGGGAG	540
CCTGTAANTC	ATGAGTCATG	ATACAAACAC	TATTGATTCA	CGCACACATG	AAGGCGAATT	600
AAATAAGCTT	GGCTTTTGGA	TTTTCAATTAC	AGCCGAATTT	GCGTTATTCTG	GTACCCTATT	660
TGCGACACTA	TTAACTTTGC	AACATGGTGG	CGATTATGCA	GGTAAAATGA	CTACTGAGTT	720
ATTTGAATTG	CCTCTTGTTT	TAATAATGAC	GTTTGCATTA	TTATTCAGTT	CTTACACATG	780
TGGTATTGCT	ATTTACTACA	TGCGCCAAGA	AAAACAAAAG	TTAATGATGT	TTTGGATGAT	840

CATTACGTTA	CTTTTAGGTT	TAGTCTTTGT	TGGATTGCGAA	ATTTATGAAT	TCGCACACCT	900
ATGCATCAGA	AGGCGTTAAC	CCAACAATTG	GTTCTTNCCTG	GTCTAGTTTC	TTTATCCTAT	960
TAGGAACGCA	TGGTTGGCAC	GTATCGCTAG	GTATCGTTTG	GCCCATTTGT	TTATTAATCC	1020
AAATCCAACG	ACGCCGATTA	GACAAATATA	ATGCGCCAAA	ATTATTTATA	GTAAGTTTAT	1080
ACTGGCACTT	CTTAGATGTT	GTGTGGGTTT	ACATCTTTAC	TGCCGTATAT	ATGATAGGGA	1140
TGGTGTATAG	CGGATGAGTA	CAATAATGAA	ACATACTGTA	GGATTTATCG	CATCTATCGT	1200
ATTAACGCTT	TTAGCAGTTT	ACGTAACACT	ATACACGTCA	TTAACATTCC	ACGCTCGTGC	1260
C						1261

(2) INFORMATION FOR SEQ ID NO:966:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 979 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:966:

GTGTTCAAGG	AGGTAAAAAA	TAATGGCTGA	AAATAAAAAC	AATTTGTCGA	TTAACGACGA	60
TCATTCTAAT	GCAGCTATGA	CGCATACCTC	TGACGCTATC	GCATCATCTG	ATTTTATTAT	120
TAGAGAATTA	GACTTGAATC	AGGAACCTGA	AATGCAACGA	GAAAGCAAAA	ACTTTGGGCA	180
AGATGCTTGG	GCTCAGTTAA	AACGAAATAA	GTTAGCTGTT	GTCGGTATGA	TAGGTTTAAT	240
TATCATTGTA	ATATTTGCTT	TTATCGGTCC	AGTTATAAAT	AAACATGATT	ATGCTGAACA	300
AAATGTAGAA	CATAGAAATC	TTCCGGCAAA	AATACCTGTA	TTTAGACAAA	GTTCCATTTT	360
TACCTTTTGG	ATGGTAAAGA	TGCAGGATGG	CAAGGATTGC	TTATTAAAGC	AGCAAATGCT	420
AAAGAAAATT	ATTGGGTTGG	GGTACTGATC	AGTTGGGTGC	AGATTTATGG	ACAAGAACAT	480
GGAAAGGTGC	TCAAATTTCA	TTGTTTATCG	GTGTTGTTGC	AGCGATGTTA	GATATTTTTA	540
TTGGCGTTGT	ATATGGTGCG	ATTTCTGGAT	TCTTCGGTGG	ACGTGTCGAT	ACGATTATGC	600
AACGTATACT	TGAAGTCATA	GCATCTATTC	CGAATTTAAT	TGTCGTAATT	TTATTTGTAT	660
TAATTTTGA	ACCATCCATT	TGGACAATTA	TATTGGCTAT	GTCTATCACA	GGCTGGTTAG	720
GCATGAGCAG	AGTTGTACGT	GGAGAATTTT	TAAAATTGAA	AAATCAAGAG	TTTGTCATGG	780
CTTCGAAAAC	ATTGGGGGCT	TCAAATTTCA	AATTGATATT	TAAGCATATT	TTACCTAATA	840
CGTTAGGTGC	TATCGTGGTT	ACATCAATGT	TTACAGTCTC	GTGCCATTTT	CTTCGAAGCA	900
TTTTTAAGTT	TCATTGGTAT	AGNGTACCT	GCACCTCAAA	CATCGTTAGG	GTCATTAGTA	960
AATGATGGGC	GCTCGTGCC					979

(2) INFORMATION FOR SEQ ID NO:967:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 791 base pairs

840

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:967:

```

GAAGACATGA ACGCATACGA AGATAGTTAT GAAAACCGAA CTAAAAAAAC AACTGCTGGC      60
AGTAGCGATT TAAGTATGTA ATTAACGAGG GCATTAGCCC TCTATTTTGT TGTACAAAAT      120
AACGATAAAC GAGGTATTTA ATATGACTGA AACAACTTTT AATCCAATTA CATCATTAAC      180
AATTAACAAT GAAGAAGTGA AAGCAAAAGC AACATTTATG TTCGATAAAA CCGCTAAAAA      240
ATTTGCAACT GAACAAGAAG ATAACAAAGG TAGAAAACAA ACGATTTTCAG GATTTACTAA      300
TGTTTATNAC GCTTTATTAG AACGTGACAC AGTGGCAATC GTAGACTTTT GGGGAATGTGC      360
AACAGCTTAT CTAGGTAAAA GCGCGCCTAA AAGAGAAGAT ATTGAAGCGG AAATCATGGA      420
AATCATCGAA AGAGAAAACG ACACGTTGAT CTTTTACAAG GTGCGTTGGA CGTAATGAAT      480
AATAGCGGTT TTTTCAAGCA GAAATCACGT CTATTCTGGA CACAGATGAA CCAACGCCCA      540
TCGTTAGCCA AAGAAGACGA GAAAGAGGGC GCGAAAGCTG GTATCGAGAT GATGAAGAAC      600
AACTACAAAG AAATCATGAC CGTAGCACCT TATTAGACTA TTCGGAAATA AGGCAGATGA      660
CAAGTCGTTA CATAGGTTAT ATGAGTAATG ACGAGCTAAT GAGCATGCTA CCTGCCGAAT      720
GGAATGACTG GATTATTGGC GCTAGACAAG CATTGATTGA CCAAAGGGAC NTCGCTCGTC      780
CCGCTCGTGC C

```

(2) INFORMATION FOR SEQ ID NO:968:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:968:

```

GGCAGGAGCT AAAATATATG AAGCTAAAGG CCGTCCATCT GACAATCCGC TTATTGTTCA      60
TATACACAGT AAAGTTCAAT TAAAAGATTT TACATATACT TTGGCACGAG CGTAGAAAAG      120
TTAATGCAGG CATTTCTGGC GGGCCCTATT TCGTTTATAT TGCCGCTAAA GCCAGGCTAT      180
CTATGTCGAA AAGTTTCTGG AGGTTTATCA TCAGTTGCTG TTAGAATGCC AAGCCATTCT      240
GTAGGTAGAC AATTATTACA AATCATAAAT GAACCTCTAG CTGCTCCAAG TGCTAATTTA      300
AGTGGTAGAC CTTACCAAC AACTTTCAAT CATGTATATC AAGATTGAA TGCCCGTATA      360
GATGGTATTG TTCAAGCTGA ACAAGTGAA GAAGGATTAG AAAGTACGGT TTTAGATTGC      420
ACATCTTTTC CTTATAAAAT TGCAAGACCT GGTCTATAA CAGCAGCAAT GATTACAGAA      480

```

ATACTTCCGA	ATAGTATCGC	CCATGCTGAT	TATAATGATA	CTGAACAGGC	AATTGCACCA	540
GGTATGAAGT	ATTAAGCATT	ACTCACCCAA	TACAACACTT	ACAATTATTA	CAGATATTGA	600
GAGCAAAATT	GGAAATGACG	GTAAAGATTG	GTCTTCTATA	GCTTTTATTG	TGCCGAGTAA	660
TAAGGTGGCG	TTTATACCAA	GTGAAGCGCA	ATTCATTCAA	TTATGTCAGG	ATGACAAATGA	720
TGTTAAACAA	GCAAGTCATA	ATCTTTATGA	TGGTGTTACA	TTCACCTGAT	GAAAATGAAA	780
ATATTTTCAGC	GGCGTATATA	TACGGCTTTG	AGTCGTGCC			820

(2) INFORMATION FOR SEQ ID NO:969:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 860 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:969:

CTGTGTTCTT	GGTCTCTTGA	AAATGCTAAA	GGCACGAGCG	TGTTAAGTTT	CCATTTTCAA	60
GCCATTCTTC	TATTTCTTCT	TCATATAAAA	AGTCAGAACT	ACGGTGTGTA	TCACCAAAGA	120
ACAACCATGT	TTTTCCAGTC	ATACCAAGTT	CTTCACGTTT	TTGTAAATAT	GCTCTAAAAG	180
GAGCAATTCC	AGTACCTGGT	CCAATCATAA	TAACCGGTAT	ATCTTGCTTC	ATCGGAAATT	240
TGAAGTTCGG	ATTTTCTTNC	AAATAAATTG	GTAATATATC	GCCTGGTTTA	ATTTCGCTCAG	300
CAAAATGAAC	CGAGCATACA	CCTTTCTCT	CACGTCCATG	TGCTTGATAA	CGAACCGTAC	360
CAACGGTAAT	ATGCACTTCA	TCTGGCGTTG	GCATAAAACT	ACTAGAAATC	GAATACTCTC	420
TTGGTGGTAA	TTTTCTAAGG	AATTTGATAC	ATATTCTCAG	GTTGTAATTC	TATAGTTGGG	480
AAAATCTGTT	ATTAAATCTA	TAAAGTCCCG	ATTTATAACA	TATTCACGCG	CCCATGACTC	540
ATCTTGAATA	CGTTCAGATA	ATCTTTCATT	GGCAAAATAG	ATATCTGCAT	TTTACAATAA	600
TGGCAATGTT	AATTTAGTAA	ATTCAANATG	TGATGTTAGT	GCNTCNACAA	TAGGAACGTG	660
ATCNACACGA	ACANTAATTG	GCACCGGAGA	TTGGCGGATC	CCAACCCNAA	NATGGATATT	720
AGTTTTTCAA	CCAATTCAGG	GTCGTTTTCG	GGTAATGCTA	CTATACAATC	TCCTGGTTCA	780
TATGATTCAC	TAAAATCATC	NAGTAAAAAT	TCTATATGTC	GTGTTTCTTT	ATTTGAATCG	840
GTACCATTTA	AATTGATATG					860

(2) INFORMATION FOR SEQ ID NO:970:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 542 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:970:

```

GGCACGAGCG CAAGGAGAAC ATTATGAACN AATTAAGGAG GCAATTATCC ATGAATTCGC      60
TGCTCATTGA TACATCGAAT CAACCATTAT CAGTAGCATT GATGCAAAAC GATGAAGTTT      120
TAGCTGAAAT AACTACGGAT TCTAAACAAA ATCATTCAGT GCAATTAATG CCTGCGATTA      180
GTCAGCTATT TGAGCAGAGC AAAATAGCTA AACAGCAATT AGATGCGATT ATTGTTGCTG      240
AAGGTCCTGG TTCATATACT GGCTTACGTA TCGGTGTTAC TGTTGCTAAA ACATTAGCGT      300
ATGCGTTAGA TGTTAAATTA TATGGTGTTC CATCATTAAG GGCATTGGCA GCAACAATCG      360
ATCATACTGA TAAATTATTG GGTTCCTGTG TTTGGATGCA AAGACGACAA GCAGGNTTAT      420
TCAGGCATAT TCCAGGTGGC AAAATGGGCA ATTAGTGACT TATTTTAGAA GGATCAATAT      480
ATTGTCGATA GAGGAATTGC GAGCTTTTTT TAGAAGATTT AAACCAACAT TTATTATATT      540
GG                                                                                   542

```

(2) INFORMATION FOR SEQ ID NO:971:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1040 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:971:

```

ATGATGTACG TGTTAGCAAG ATAATAGACA TATCTCATTA ATACTTGACG TATTCAAGGC      60
GTTCCCAAAG CTTAAGATAA CCGGACACTA CAATCAAGAT TTTGCANCGA ATTGAGCCAA      120
ACATATGAAT TGAGTCNAAG AAGAGTTAGA TAAGAGTGTC AACTAGTAA CTCAACAAAC      180
GAAGTTATCT AAAGTTATTG TAGATACNCA AATTAATCCA GATTTAATTG GTGGATTAG      240
AGTTAAAGTC GGCACAAC TG TAGATAGTGG TAGTGTTAGA AATGATCTTG TCCAATNACA      300
AAGAAAATTT AGAAGAGTTA ATTAATTATA AAGAGGAGTG ACATAGATGG CCATAAAAGC      360
TGAAGAAATC AGTGCATTAC TTCGCTCACA AATTGAAAAT TATGAGTCAG AAATGTCCGT      420
AACTGATGTA GGTACTGTAT TACAAATTGG TGATGGTATT GCATTAATTC ACGGATTAAA      480
TGACGTTATG GCTGGTGAGC TAGTGACATT CCATAACGGC GTACTTGTT TAGCCCAAAA      540
CCTTGAAGAG TCAAACGTGG GTGTGGTTAT TTAGGACCA TATACAGGTA TTAAGTGAAGG      600
TGACGAACTT AANACGTACT GGGTCGTNTC ATGGGAAGTA CCAGTAGGTG AAGAACTAAT      660
TCGGAAGAGT TGTNAATCCA TTAGGACAAC CTATTGATGG ACAAGGACCG ATTAACACAA      720
CTAAAACACG TCCAGTAGAG AAAAAAGCTA CTGGTGTAAAT GGATCGTAAA TCAGTAGATG      780
AGCCATTACA AACAGGTATC AAAGCAATTG ATGCTTTAGT ACCAATTGGT AGAGGTCAAC      840
GTGAGTTAAT CATTGGTGAC CGTCAAACAG GTAAAACAAC AATTGCAATT GACACAATTT      900
TGAACCAAAA AGATCAAGGT NCGATTTGTA TCTATGTTGC TATTGGTCAA AAAGATTCAA      960

```

CAGTAAGAGC ANATGTTGNA AAGTTAAGAC AAGCAGNCGC TTTAGACTAC ACTATTGTTG 1020
TAGCAGCATC AGCTCGTGCC 1040

(2) INFORMATION FOR SEQ ID NO:972:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 973 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:972:

CGTGCGAGCT GCTTTTGGTA AAAACGGCGG TAATATGGGT GTATCTGGAT CAGTTGCTTA 60
TATGTTTGAT CATGTGGCAA CATTTGGTAT TGAAGGAAAG TCTGTTGACG AAATACTTGA 120
AACATTAATG GAACCAAGAT GTAAGATGNA AATGATGTGA TTGACGATAA TGGATTGACA 180
ATAGTCTATG CTTGAACCAA GATCCAATTT CCAGTCGTTC CAAGATGCCG TTCGTNCACC 240
AGGTTGTTGG AAGAATTTAA AAGTTGCTTG AATTTGAAAT TGTTACCCTC CAAACAAGAT 300
ATTGAACTTT CTGAAGCGGA CCNAAGTAAC ATTTGAAAAA TTAATCGATG CATTAGAAGA 360
TTTAGAAGAT GTACAAAACG TATTCATAA TGTGGATTG AAATAATGAA ATCAGCAGAA 420
CAATGGATTG ATGAATTGCA ACTTGAATCA CATCCTGAAG GTGGTTTCTA TAGAGAGACA 480
ATTCGAGAAG TATTGAAAGA TGGACGCAGA GCGCCGTTTA GNAGTATTTA TTTTTACTT 540
ACAGATGACA ATATTTCGCA TTTTCATCGA ATTGATGCTG ATGAAGTATG GTACTATCAT 600
GCTGGTGATT CTCTAACAAT TCATATGATA AATCCGGATG GGAATATAC GACTGCAACA 660
TTGGGTACTG ATATCCAAAA TGGAGATGTA TTGCAATATG TAGTGCCTAA AGGAACAATT 720
TTTGCTTCTT CAATCGAAAT TTCAAATACT TATAGTTTAG TAGGTTGTAT GTGTCAACCG 780
GCATNTGAGT TTAAGCAGTT TGAATTGTTT AAGCAATCTG AATTAATTAC ACAATATCCG 840
CATCTTAAAT CAGTGATTGA NAAATATGCT TTAATAATAA AATGATCAAT GAAGTGGTTT 900
GAAGGTGTTT AATAAACCTT TGAGTCACTT CATTTTTATA TGTATTCTTG ATTGAATCAG 960
AATAGATTTG ATG 973

(2) INFORMATION FOR SEQ ID NO:973:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1388 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:973:

```

ATAATTGAAA TGGAGGCATT TATTATTGGA ACATTATTGT TGAATAATAA GAAGTTATTT      60
AAATAAGAAG ACCTTGGATG ATTTGTCTCN CCAAAACCAA AAAATAATTG ACCCCTGCAT      120
ATTNCGATGT GCTAAGAAGC GATAAATGAT TTATCAAATG ATTCATTATG TGTGTTAAAT      180
CATTTAATAT ATTAACGGAA GGACAAGAAG AAACATTGCA NCAAAAATTT TTGCAACGTA      240
ATAAGCATTT AAAAAACGTT GATGGGTTTA AAGCATTAGG TTTTAAAGAC CTAGAACAGC      300
TGGTAGACAC TATATCATTA TTACGCTGTG GGAAAATAGG CAAGCATTTT ATCATTGGCA      360
AAATTCAGCT GAGTACAAGC ATACACACAA GCATCGTGNC ACTTCGAAAG GTGCAGATGT      420
AAAAATAATT AATCGTGAAT TATCATACAA TATTCGTATT GAATTAGCTG ATATGGTCTA      480
GCCCCGAGATA TCAACCTCA ATCATTTGAA AGTCCTTGAA TGCTACGTCA TGGCAAAGTG      540
TAGTGCCGAG GACTTTGGTA TTTAACCCTA TTTAATTGAA AATTCTGTAA AGATAGGCGT      600
ATGATATATA TAATTCATTT ATAAAATTAC AATGTTTCATC ACAGGGAAAG TGGATGTATG      660
AAAGGAAGTT AGTTATGCAA AAGTCAGCTC TATTCGCGCC TGAAAAATAT AACATTATTT      720
CGGAAATCGA AAAATATAGC CACATACCAG ATAAAAAGGC AATTTTATAT CATAATACTG      780
AAGGCGAAGA TATATCAGTC ACTTACCAAC AGCTCATTTGA ACAGTCTAAT AAAGTAGGTA      840
ATGTTTTAGC ATCGCACGGT TTATCTAAAG GCGATAAAGT ACTCATTATG ATGCCACGAT      900
CTATTGCGAC GTATGAATTA TATATTGCTG CTTTAAATTT AGGTGTTGCA ATCATCCCAT      960
GTTCTGAAAT GCTAAGAACT AAAGATTTAC AATACCGTAT CACGCACGGT GAAATAAATG     1020
CAGTTATTGC ACTAGAGCCA TTCACAGTTG AATTTGAAAA AATTAAAGAA TATGATGCGT     1080
TANCTAAATT TGTATTGCCC GGTCAAAAAG ATGGATGGAT TTCACTTGAA GCTGAAAAAG     1140
AAAACGCAAG TAACAACTA GAAATGGCAG ATACGACGCG TGATGATATG GCGANTCTGT     1200
CATATACATC TGGTACAAC TGGCAATCCTA AAGCCCGNTA CACATTGTCA TGGATGGGGA     1260
TTTGACACATT TACAAAATGG CACCAAAACA TTGGTTATGT ATTAATGAAG ANTGACTTAG     1320
TTTGGGCAAC AAGCAGCANC AGGTGGCAA AAAATGGGTA AAACTTAAC AACAAAATCT     1380
TTTACGGT

```

(2) INFORMATION FOR SEQ ID NO:974:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 890 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:974:

```

CTGCAGATGA TTGAGCCCAA GTTCGTAGTT ACAGCTGTAA TGTAAATAT TTTTAGTGCG      60
CTTATCATCG CTAGTGTAAT CAATCCCTAT AAATCTGATG ATAGTGATGT TGAGATTGAT      120
AANTTAACTA AATCAACGGA AACGAAATCA ATTGAATGGA AAAACAGGAA AACCTAAGAA      180
AGTTGCCTTC TNCCAAATGA TAGGTGATAG TGCGATGGAT GGATTTAAAA TCGCTGTTGT      240

```

AGTAGCCGTA	ATGTTGTTAG	CATTTATTTT	ATTAATGGAA	GCAATTAATA	TCATGTTTGG	300
TAGTGTGGN	TTGNACTNTA	AACAGCTTAT	TGGCTATGTG	TTTGCACCAA	TCGCATTCTT	360
AATGGGGATT	CCATGGAGCG	AAGCTGTTCC	AGCTGGCTCT	TTAATGGCGA	CTAAATTAAT	420
TACAAATGAG	TTTGTAGCAA	TGCTTGATTT	TAAAAATGTC	CTGGGTGATG	TATCTGCTCG	480
AACACAAGGT	ATCATTTCAG	TTTACTTAGT	AAGCTTCGCT	AATGTTGGTA	CGGTTGGTAT	540
CATCGTAGGT	TCAANTCAAG	GCACTTAGTG	ATAAACAAGG	AGAAGAAAGT	TTCATCCTTT	600
NCAATGAGNC	TGTTACNTGG	CTCAACTCTA	GCNTCAATCA	TTACAGGACT	CAATACAATG	660
ACTTAGTATT	GTNAATTANT	CGAAGTATCT	AAATTAAATT	CATGGCNAAG	CTAAACCCCA	720
TCACCAAGTT	GGCGCAACAG	CGCATCATAA	CTTGGTGATG	GGATTTTATC	ATAACAATCT	780
ACTTATTCGT	AGCCGTTTTT	GANATGTATG	TTGNTGGTTT	ATCTTTTTC	CCAAATTGTT	840
AATCCCGTTA	TATCTTTTTT	ATGTTTTGAA	GGGACAATGA	AGCTAAGTAG		890

(2) INFORMATION FOR SEQ ID NO:975:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 925 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:975:

GGCAGGAGAC	TTATATTAGA	CGGCTTAGAA	GACCCGCATA	ACTTGGGATC	AATTTTAAGA	60
ACCGCCGATG	CAACGGGAGT	TGATGGTGT	ATTATTCCTA	AACGTCGTTC	AGTTACACTA	120
ACGCAAAACAG	TTGCAAAAGC	CTCAACAGGT	GCAATTGAAC	ATGTACCAGT	TATTCGAGTG	180
ACAAATTTAG	CTAAACTAT	CGATGAACTA	AAAGATAATG	GCTTTTGGGG	TAGCTGGTCA	240
CTGAAGCTAA	TAATGCAACA	GATTATAGAA	ATCTAGAAGC	GGACATGTCA	TTGGCTATTG	300
TAATTGGTAG	CGAAGGACAG	GGTATGAGTC	GCCTAGTAAG	TGATAAATGC	GATTTTTATA	360
TTAAGATTCC	AATGGTTGGA	CATGTAAACA	GTTTGAATGC	TTCGGTTGCA	GCAAGTTTAA	420
TGATGTACGA	AGTATPTCGA	AAAAGACATT	GATGTTGGAG	AAATATAATG	NAAGNCCGTT	480
ACTTAATCAT	TGATGGATAC	AATATGATAG	GACCAATCAC	CACCGCTAAG	CGCCATTCCN	540
NAAGAGAATT	TAGAAGAAGC	TAGAATGCAA	TTAATAGATC	CAATTCCAAA	TTATAATGCA	600
GTTATTTTCAG	ATGAAATTAT	TTGTGTTTTT	GATGCTTATG	ACCAATCGGG	TGTTGAAAGA	660
GAATACATGT	ATCATGGCGT	TAAAACGATT	TTTACCAAGG	AAAAAGAAAC	AGCTGATAGT	720
TTCATAGAAC	GTTATGTTTA	TGAACTTTAT	GACAAGCATA	CTAAGCATAT	TGCAGTTGTA	780
ACAAGTGATA	TGAGTGAGCA	ACATGCTATC	TTTGATCAG	GTGCATATAG	AATATCATCT	840
CGCGAAATGT	GGAGAGATTT	AAAAGAAAAT	GAAATTGATG	TGAGTAAATC	ATTAGATGAT	900
ATAAGTGAAA	ACAAGCCAAG	AATC				925

(2) INFORMATION FOR SEQ ID NO:976:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:976:

```

CAATATAAAG TGGCAAAGGA GGTAATTGAG ATGGCAACAC ATTTAAGCTT TAGAACNAGG      60
CGNACAAGAG TGTANCCCAA CATTATTGGG TTATGCCGGT GTTGGTATCA TCATTTGGTA      120
TTGTGGCTTC GTCTCAAAAC TTTAGTATTT NAGAAATTAT CTNGTTATGT CTTGTTATAT      180
ATGCCGGTGC TGCGCAATTT ATTATGTGCG CGTTGTTTAT AGCAGGTACA CCGATATCAG      240
CGATTGTACT AACTGTATTT ATCGTAAATT CAAGAATGTT CCTTTTAAGT ATGTCGCTTG      300
CACCAAACTT CAAGACATAT GGGTTTGGGA ACCGTGTTGG ATTAGGCACA TTAGTAACTG      360
ACGAAAACGTT TGGCGTCGCC ATTACACCTT ATTTAAAAGG AGAAGCTATC AATGATCGNT      420
GGATGCATGG TCTTAATATC ACAGCATATT TATTTGGGGA CAATTCATG TGTAGCTGGG      480
GCTTTATCTT GCGGAATATA TCTCAAATCC GCAAACGCTA GGGTTAGATT TNGGCTATCA      540
CGGCTATGTT TATCTTCTTG GCCATTGCGC AATTTGGATC AATTAGGCAC GAAATCGCGA      600
TTAAGAATTT ACATAGTACT CATTATTGCC GCCATAGGAA TGATGTTATC GCTAAGTATG      660
TTTATGCCTT CATATCTAGC AATATTAATT GCAGNCACAA TNTCAGCAGC GTTAGGAGTG      720
ANGATGGAAC GATGATAACT CATATGAACA TGTTAATACT TATTTTATTG TGTGGTATCG      780
TAACGCTATT AATTCGAATT ATNCCTTTTA TCATGATNTC AAAAGTGCAA TTGCCTGATG      840
TTGTGGTTCG ATGGCTATCA TTTATCCCAN TCACACTATT TACGGCACTT GTCATTGACA      900
GCATTATTCA ACAGACGCCT CATGGTGAGG GGTATACATT AAACATCCCT NACATTATCG      960
CGCTCATTCG GACGGNTATT TTATCTATAA TCACGCGGTA GTTTAACTAT TACAATTATT     1020
AGTGGGATTG TTATCAAGGC AACATTACGA TTTTCTTTAA AATACTGAAA TCATGACAGT     1080
ATTTAACTTA GGTAACGGT AGTAATCAGA AA                                     1112

```

(2) INFORMATION FOR SEQ ID NO:977:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1173 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:977:

```

CTAGCCAATT AGTAACGTCT AAAAATAACT TACAAAGTTC TGTGAACCAA GTACCATCAA      60

```


CTGCTGGTAT	GACGCAACAA	AGTATTGATA	ACTATAATGC	GAAGAAGCGT	GAAGCAGATA	120
ACTGAAATAA	CTGCAGCTCA	ACGTGTTATT	GACAATGGCG	ATGCAACTGC	ACAACAAATT	180
TCAGATGAAA	AACATCGTGT	CGATAACGCA	TTAACAGCAT	TAAACCAAGC	GAAACATGAT	240
TTAACTGCAG	ATACACATGC	CTTAGAGCAA	GCAGTGCAAC	AATTGAATCG	CACAGGTACA	300
ACGACTGGTA	AGAAGCCGGC	AAGTATTACT	GCTTACAATA	ATTTCGATTCG	TGCACTTCAA	360
AGTGACTTAA	CAAGTNC'TAA	AAATAGCGCT	AATGCTATCA	TTCAGAAGCC	AATAAGAACA	420
GTGCAAGAGG	TACATCTGCG	TTAACAAATG	TAAATCGTGT	CAATGAGCGA	TTAACGCAAG	480
CAATTAATCA	ATTAGTACCT	TTAGCTGATA	ATAGTGCTCT	AAGAATCTGC	TAAGACGAAA	540
CTTGGATGAA	GAAATCAATA	AATCAGTAAC	TTACTGATGG	TATGACACAA	TCATCAATCC	600
AAGCATATGA	AAATGCTAAA	CGTGCAGGTC	AANCAGAANC	AACAAATGCA	CAAAATGTTA	660
TTAACAATGG	TGCACGAGCG	ACAGACCAAC	AAATTGCCGC	AGAAAAACA	AAAGTAGAAG	720
AAAAATATAA	TAGCTTAAAA	CAAGCAATTG	CTGGATTAAAC	ACCAGACTTG	GCACCATTAC	780
AAACTGCAAA	AACTCAGTTG	CAAAATGATA	TTGATCAGCC	AACGAGTACG	ACTGGTATGA	840
CAAGCGCATC	TGTTGCTGCA	TTTAATGACA	AACTTTCAGC	AGCTAGAACT	AAAATTCAAG	900
AAATTGATCG	CGTACTAGCA	TCTCATCCAG	ATGTAGCAAC	GATTTCGTCAA	AACGTGACAG	960
CAGCGAATGC	TGCTAAAACA	GCACTTGGAT	CAAGCGCGCA	AATGCCTTAA	CAGGTCGGAT	1020
AAAGCACCTT	TAGAAAATGC	GAAAAATCAA	CTACAACATT	GGTATTGGAT	ACGCAAACAA	1080
GTTCAACTTG	GTATTGAACA	AAGACTCTTT	TTAATTGCAT	ACAAATGCGA	AGGTTAACAG	1140
GGTGCACCGT	TATTAGGGTC	CAACAAATCA	ATC			1173

(2) INFORMATION FOR SEQ ID NO:978:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 714 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:978:

CTAAGACGTC	AACATCAGTT	ACAACCCAAA	TCCAAGGGTC	CAANTCNTAA	TGCGTTTAGT	60
TTCCCGGAAA	ATGACCCAAC	TTGATAATCA	TTGGATGGCC	ATGTTTNAAG	ATATGAATTT	120
TGATCTAGGT	ATTATGGCAT	TGTATGCCAT	AGAAAGTGAT	CCGCTTGCTA	ATTTNCCGCG	180
TAACTCTGAC	GCTGAAATTG	CCGTCNTTGA	CGAGTCGCAT	ATAGATGCCT	ATTAAAAGTT	240
GCATATCAGT	TTAGTCTGCC	ATTGGGAAAG	GACTATGCAG	ATGCACATGA	AGAAATGGTA	300
AGGGAACATT	ATCAAAAAGA	TGTGATTAAA	CGCTTAGTAG	CTTATTTAAA	TAATGAACCT	360
ATTGGCGTTG	TAGATGTCAT	TGAAAGTGAA	AATTACATTG	AATTAGATGG	ATTTGGTGTA	420
TTAGAACAAT	TTGCACACCA	AGGAATTGGA	TCTACAATTC	AATCCGTTGA	TAGGTGAATT	480
ACGCCATATC	AAAAAATCAC	AAACCAATCA	TATTAGTTAC	AGATGGTGAA	GATACAGCAA	540
AAGATATGTA	TGCAAAGCAA	GGTTATGTCT	ATCAATCGTN	TTTGTTATCA	NATATTAATA	600
GAAGATATTG	GAAATTANCG	ATTGATGATA	GGTTTGTATT	AGAATAANAA	AGCAGTAANC	660

TGGTTTCGAG TAGAAATCAA CTTACTGCTT TTAAATTGT TTTGAGCTCG TGCC

714

(2) INFORMATION FOR SEQ ID NO:979:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 975 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:979:

CATAAAGNAA AGCGTAAATA CTTTTTTAGC CCGAATACAT TTGTATTCGG TTTTTTTGTT	60
GAAATGATTT TAAAGTGAAT TGATTAAGCG TAAATGTTG ATAAAGTAGA ATTAGAAAGG	120
GGTCATGACG TATGGCTTAT ATTTTCATTAA NCTATCATTC ACCAACAATT GGTATGCATC	180
AAAATTTGNC AGTCATTTTA CCGGAAGATC AAAGCTTCTT TAATAACGAT ATANCTGCTA	240
AACCATTAAA AACTTTAATG TTGTTACATG GATTATCAAG TGATGAAACG ACATATATGA	300
GATATACAAG CATAGAAAGG TATGCGAATG AACACAAATT AGCTGTGATT ATGCCCAATG	360
TGGATCATAG CGCATATGCT AACATGGCAT ATGGTCATAG CTATTATGAT TATATTTTGG	420
AAGTATATGA TTATGTTTAT CAAATATTTT CACTTTCCAA AAAGCGTGAT GACAATTTTA	480
TAGCAGGTCA CTCTATGGGA GGATATGGCA CAATTAAATT TGCATTAAACA CAAGGGGATA	540
AATTTGCCAA AGCTGTACCA TTATCTGCTG TGTMTGAAGC GCAAAATTTA ATGGATCTAG	600
AGTGAATGA TTTTTCAAAA GAGGCCATAA TTGGCAATCT TTCAAGTTGT TAAAGGAACT	660
GAACATGATC CGAATTATTT GCTAGACAAA GCTGGAGCTG AAGATAAACA AACCCCAAAA	720
TTGCTCATGT AGNTGTGGTA GTACACAGAC TTGANATATC ANNACAACTT AGATTTTATC	780
GATTATTTAT CACGTAAAAA TGTTCTTTAT CAATTTGAAG ATGGACCAGA GATCATGATT	840
ATGCATATTG GGACCAAGCG ATTAAGCGTG CTATAACATG GATGGTGAAT GATTAATTAT	900
TCCCTGGAAA ATATGTGGTT GCATTAATAC ACAGAGTGAG AGATACAACT ATTACGCACA	960
CTACATTCTG ATGTT	975

(2) INFORMATION FOR SEQ ID NO:980:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:980:

ATAGGAAGCA TATGNNAGAG GAGAGGCCAG TTGTTTGT	60
TTT TGTGCAGCAG CCTGCATAGA	
GAGCCTCTAA TCACTAAAGG TGAAGAGGNA CGCAGTTGGA	120
TGCTAAGGCA CAACTGCATA	
AATCCCTCTA ATCGCTAAAG CGAAAAAGTG GGATTAAAA	180
GGAGATGTGA TAATGTGAAG	
AAATCGTTAA TTGCTTTTAT TTTGATTTTT ATGCTTGTCC	240
TGAGTGGCTG TGGTATGAAA	
GATAATGATA AACAAAGGTAG CGATGATAAT GGCTCGTCTA	300
AATCGCCGTA CCATAGAANT	
GTTTCGTTAA TGCCTAGTAA TACTGAAATT TTATATGAAT	360
TAGGATTAGG TAAATACATA	
GTTGGTGTGT TCAACGGTTG ATGATTATCC AAAAGATGTG	420
AAAGAGGGTA AGAAACAATT	
TGATGCTTTG AATCTAAGTA AAGGAGGAAC TTTTAAAGGC	480
AAAGCCAGAT CTAATTCNTG	
CGCATGAGTC NCAAAAGNCA ACTGCTAATA AAGTATTGTC	540
ATCATTAGAG AAACAAGGCA	
TCAAAGTAGT GTATGTTAAA GATGCACAAT CAATTGATGA	600
AACATACAAC ACATTTAANC	
AAATTGGGAA ATTAACGCAT CATGATAAGC AGGCTGAACA	660
ACTTGTGAG GAAACTAAAG	
ATAATATCGA TAAAGTCATA GATTCAATTC CTGCTCATCA	720
TAAAAATCA AAAGTATTTA	
TTGAGGTNTC ATCAAAGCCT GAAAGANATA CAGCAGGGAA	780
GCATACATTT TTTAATGATA	
TGTTAGAAAA ATTAGAAGCC CAAAATGTTT ATAGNGACAT	834
TAATGGTTGG AACC	

(2) INFORMATION FOR SEQ ID NO:981:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1208 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:981:

CTGAAATGGT TCAAATNTTG GGATGAGAAT GGTAACGTCG	60
TAAATGAAGA CTTAGTACCT	
GATCTTACCG ATGAACAATT AGTAGAATTA ATGGAAGAA	120
TGGTATGGAC TCGTATCCTT	
GATCAACGNT CTATCTCATT AACAGACAA GGACGTTTAG	180
GTTTCTATGC ACCAACTGCT	
GGTCAAGAAG CATCACAATT AGCGTCACAA TACGCTTTAG	240
AAAAAGAAGA TTACATTTTA	
CCGGGATACA GAGATGTTCC TCAAATTATT TGGGCATGGT	300
TTACCATTAA CTGAAGCTTT	
CTTATTCTCA AGAGGTCACT NCAAGGAAA TCAATTCCTC	360
TGAAGGCGGT TAATGCATTG	
GAGCCCCACA AAATTATTAT CGGGNGCACA ATACAATCCA	420
AAGCTTGCTG GGN GTTGNA	
TTNGNACTTN AAAAACGTGG TAAAAATGCA GTTGCAATCA	480
CTTACACTGG TGACGGTGGT	
TCTTCACAAG GTGATTTCTA CGAAGGTATT AACTTNGCAG	540
CAGCTTATAA AGCACCTGCA	
ATTTTCGTTA TTCAAAACAA TAACTATGCA ATTTCAACAC	600
CAAGAAGCAA GCAAACCTGCT	
GCTGAAACAT TAGCTCAAAA AGCAATTGCT GTAGGTATTC	660
CTGGTATCCA AGTTGATGGT	
ATGGAGGCAC GTTAGCTTGT ATATCAAGCA ACTAAAGAAG	720
CACGTGAGGC CCGAGCGCAG	
TTGCAGGTGA AGGTCCAACA TTAATTGAAA CTATGACATA	780
TCGTTATGGT CCTCATACAA	
TGGCTGGTGA CGATCCAACCT CGTTACAGAA CTTCAGACGA	840
AGATGCTGAA TGGGAGAAAA	
AAGACCCATT AGTACGTTTC CGTAAATTCC TTGAAAACAA	900
AGGTTTATGG AATGAAGACA	

AAGAAAATGA AGTTATTGAA CGTGCAAAAG CTGATATTAA AGCAGCAATT AAAGAGGCTG	960
ATAACACTGA AAAACAAACT GTTACTTCTC TAATGGAAAT TATGTATGAA GATATGCCTC	1020
AAAACCTAGC AGAACAAATAT GAAATTTACA AAGAGAAGGA GTCGAAGTAA GCCATGGCAC	1080
AAATGACAAT GGTTCAGCG ATTAATGATG CGCTTAAAAC TGAACCTAAA AATGACCAAG	1140
ATGTTTAAAT TTTTGCGGAA GACGTTGGTG TTAACGGCGG TGTTTCCGTG TTAGTGAGGA	1200
CTACAAAA	1208

(2) INFORMATION FOR SEQ ID NO:982:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1025 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:982:

CAGTTATTAA ATTAGATGCA ACGACAACAA GTGTNTTAAT TACTTGTGTC ATGGCAATAA	60
TGATTCCATT AGCATTAAATG TNTGGCAAGT TAGCGGATAA AATAGGTGAA AAGAAAGNAT	120
NTCTAATTGG CACGAGACTG GTGGGCTAAC ATTATTTAGT ATCATCGCAT TTATGTTATT	180
ACATTCACAA TCATTTGTTG TAATAGTAAT CGGTATATTT ATATTAGGAT TTTCTTATC	240
AACTTACGAA GCGACAATGC CAGGGTCGTT ACCAACGATG TTTTACAGTC ATATAAGATA	300
TCGAACCTTA TCAGTAACAT TTAATATCTC TGTTCGATA TTTGGTGGTA CGACGCCATT	360
AGTTGCAACA TGGTTAGTTA CGAAAACCTGG AGATCCATTA GCACCTGCGT ATTATTTAAC	420
AGCAATCAGT GTTATTGGCT TTTTAGTTAT TACATTCTTA CATTTAAGTA CAGCAGGAAA	480
ATCTCTAAAA GGTTCGTATC CAAATGTAGA TAACGAGCAA GATAGAGCTT ATTAGCAGA	540
ACACCCAAAA GAAGCATTAT GGTGGGTAA AGAACGTAAG AATTAGAGAT TTCAATAAAA	600
AGTATAAATC AATCGTATAT AAGCACTTTA AAGCTAGTAG GTTCTGCTAA CTTTAAAGTG	660
CTTTTTAAAT TGAGAACTGT AATTAGCCGT AATAAAGTTT TTGTATATAC ATAAACCCCC	720
ACTGCAATGA TTATCGCAAT GGGGAAAGA GGGGACTTAA AGCATATTGT TTAGCTTTGG	780
AATACTTAAA ATTCTCTTTG GCTATTGAAA TTGTTAGGAT TGTAATATT GTCTTTAGAG	840
TATTTTGGTC CCAACGCAAT TAATATTTGG AGACTCTTAA CCTTCAAAT ATTTATTATA	900
GGAGGAACAA CAAACTTAAA TAGGATTGGG TGACTTATTT GTGTCAGTTA TTGCGATTGC	960
GATAACTTCT TTTCTCTATA TACATATAGT AACGCTTAT CTAATAAAAA ACATGGTCTC	1020
GTGCC	1025

(2) INFORMATION FOR SEQ ID NO:983:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1360 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:983:

```

GGAGCTNCGA AGTTGAATGC GTCAACTACA GNTAAGCCAT TCTCTNGAGC TNNGAAAGAT    60
AATGCTGAGC GTAAAGCTAA ACGACGCATN NTCTTAGGCA TTGNGTATGC ATAAC TTCTT    120
GGAGTTGGTC CGAATACGAT ACCACCGNCA CGNCATTGTG GAGCACGGAT TGTACCTTGA    180
CGAGCACGAC CTGTNCCTTT GTGTTTCCAT GGTNNACTTN CATTTNTATA CCTCCCTATA    240
TTATGGAGTG ACGATTATTT ATAACGACAA GTAAC TCGTG CCGNGTGTTA AATCGTACGG    300
AGACATCTCA ACAGTTACTT TGTCGNCAGG GTAGAATACG AATTGTAATT CATTCCTGAT    360
TTNACCACTT ACGTGAGCTA AAATCTCATG ANCATTTTCT AATTCTACTT TAAACATTGC    420
GTTCCGTAAA GTATCTAATA CAGTACCTTC TAATTCAATT ACATCTTGTT TAGCCATTGA    480
TTAACTTCCC CCTTTTGTGA ATAGTAAGGT AATCGTCAAT AGACAACTTT ATTGTTACGA    540
ATCTATCAGT GATTAATTTT ATAAGTTAAA CAAAAATTAC GGAATTAAT TATCGGTAAT    600
TGCCACTCTC ATCTATCTAA TATGATTAAA TCAAGCCTCA CTTAAAATAG ACCGCTAAAA    660
GTGGATCTCA TTACAAATGA TCNAAAATAT CAATGACATC TTTGGGTAAN GTCGCTAATA    720
TCTTTTGAAC CATCAATATT TTTCAATACA CCTTTTGGAT CATAGAAATC TAAAATAGGC    780
TTAGATTGTT TAATATTAAC ACTCAAACGG CACGAGCTAC CGNTTCAGGA TTATCATCTT    840
CTCGTTGATA CANNINAACA CCATCGATAT CACAAATACC TTCGACCTTC GGAGGATTAA    900
ATACAAGATG ATACGTTGTA CCACATGACT CACAGATTCG ACGACCTGTA AGACGGTTCA    960
TTAATTCCTC TTCCGGAACT TCGATATTGA TGACAGCATC AATGTTTCTG TCAAGCTCAG   1020
ACATAATATT ATTTAATGCC TCAGCTTGCT CGATTGTTCT TGGGAAGCCA TCTAATAAAA   1080
AGCCTTGTTN GNGCATCCGT CCTTNCAGAA ATTCTTTTCC CTTAACGATA CCTACAGTCA   1140
CTTCCATCCA GGAAC TAATT CCGNCACGGT CCCATATAAG ACTTAGCTTC CTTTACCTAA   1200
TTCAGTNCCT TCCTTCTATN GCTTTTCTTG AACATGTTCA CCAGCTTGAA ATGTTGGNGT   1260
ATTGNGNAAT TCCTTGACAA TTNCAC TTGAGTTCTT TTACCTGCGC CAGGGTNAAC   1320
CCCATCAAAA ATGATATTCA TAANGTGNCC CTCCCTAAAC                               1360

```

(2) INFORMATION FOR SEQ ID NO:984:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 684 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:984:

TATTGNCATA	TTAATCGCAA	TTTACATTCA	TATTCAACAT	AGCAATATTA	ATTTATTCTT	60
ACTCATGACC	ATTGCCATGA	TCTGTTCAAC	AATACTCACT	TTATTGCTCG	TTACAGGCTG	120
GCAATATGCGT	AACTTCATTA	CCATAGCCAG	TACAATTATC	GGAAC'TTTT	TGAGTATAGG	180
TTTAACAGAA	TTAATCATAT	ATATGACAGA	TGGTAAAGGC	ATTAAATATG	AAACGATGAA	240
CTTTTATCA	TTACCACCGA	AAGATATCTT	CCTAGCCTCA	GTGTTAATAG	GTTCACTTGG	300
CGCTATTATG	GATGTTGCAA	TTACAATTGC	TAGTGGGATG	CATGAAATTT	NACAGCGNAC	360
GNCACACATT	TCAATGAGGA	GATGGGCGCT	TGCTTGGGCG	AAACATCCGA	CAAGATATTA	420
TGGGAACAAT	GACTAACATC	TTATTATTCT	CATATTTATC	CGGTGCACTA	CCTATGTTTT	480
TACTCTTTTT	AAAAAATGCA	AATACTGTGA	CTTATACTAT	TTCGATGAAT	TGGTCGTTAG	540
AACTCGCGCG	CGCACTAACA	GGCGGTATAG	GTATCGCACT	TACAATTCCT	ATCACAATAT	600
TGTTATGGAA	ATATTTGAAA	CATAAGGAGG	CGAAACAATG	AATGCTGTAT	TATATTGGCG	660
TATTGCTCTC	TTTCTGATGA	TATT				684

(2) INFORMATION FOR SEQ ID NO:985:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 662 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:985:

CCCCACNAAG	TACNCGAAAC	GCAAACAAAC	ATCTTAAAAG	GAGGAACGAA	CAATGCAAGC	60
ATTACAAACA	TTTAATTGGA	AAGAGCTACC	AGTAAGAACA	GTGGAAATTG	AAAACGAACC	120
TTATTTTGTA	GGAAAAGATA	TTGCTGAAAT	TTTAGGATAT	GCAAGGGCAG	ACAATGCCAT	180
CAGAAATCAT	GTTGATAGCG	AGGACAAGCT	GACGCACCAA	TTTAGCGACA	GCAGGTCAAA	240
ACAGAAATGT	AACGATCAAT	CAACGAATCA	GGATTATACA	GTTTAATCTT	TTCTAGCAAA	300
TTAGAAAATG	CGAAGCGGTT	CAAACGTTGG	GTAAC'TTCGG	AAGTTT'TACC	AACATTAAGA	360
AAAAC'TGGTG	CTTACCAAGT	ACCTAGCGAC	CCAATGCAAG	CATTGAGATT	AATGTTTGAA	420
GCTACAGAAG	AAACAAAACA	AGAAATTAAA	AACGTAAAAG	ATGATGTTGA	TNGATTTGAA	480
AGAAAATCAA	AAACTGGATG	CGGGAGACTA	CAATTTCTTA	ACTAGAACTA	TCAATCAAAG	540
AGTAGCTCAC	ATNCAAAGAC	TACATGCGAT	AACAAATCAA	AAACAACGTA	GCGAATTATT	600
CNGGGATATT	AATTCAGAAG	TGAAAAAGAT	GACTGGTGCA	AGTTCAAGAA	CGAATGTTAG	660
AC						662

(2) INFORMATION FOR SEQ ID NO:986:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1112 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:986:

```

NTGATTAATT ATTTCTGGA AAATATGTGG TTGCATTAAA TACACAGAGT GAGAGATACA    60
AACTATTTAC GCACGACTAA CATTTCTGAG TGTTTAAATT AAATTTGTAT TAATATGATT    120
GGCGCAATTT GNTGATACGC AAAAATGTTT CTCGTGAAAC TTAGATTTAG CTTATAGTTT    180
TATCATCATT TGTATGACTT ACATTATAAA TTTTATTATA ATGAGGTAA CGCTTTGAAA    240
GGAGTCATCA TCANGTCGAC CAATAAAAAC GATTATGAGC ATATGTTGGT TTTATGTGTC    300
ATATAAACG TTTATTACTA CCGCTGATGA AATTATAGAG AAGTATGGTA TGAGCCGTCA    360
GCATCATCGT TTTTGTGTTT TTATCAATAA ATTACCTGGT ATTACTATTA AATCATTACT    420
AGAAATATTA GAAATTTCTA AACAAGGATC ACATGCAACA CTTCAAAAAT TAAAAGAGCA    480
AGGTCTCATT ATTGAAAAAG TTTTAGAGAC TGATCGACGT GTCAAAAAT TATATTCGAC    540
GGATAAAGGC GATCAACTCA TTGCTGAATT GAACAAGGCG CAAGATGAAT TATTGCAAAA    600
TATATATCAA CAAGTCGGT CCGATTGGTA TGATGTGATG GAAGCATTGG CTAAACGGCG    660
ACCTGGCTTT GATTTTATTA AGCATTTGAA AGATGAAAAA GAAAGCTAGC ATCAGAAATG    720
TTAAAAATCT TCGCATTCTT AAATTTAAAA AATATGTCAA AAAGTGATA ATAAAAACAT    780
ATAATTTAAT TGAACCTAGT TTCAACACAT CTTAGAAAGG AGTNTGAATG ATGAAAAAT    840
TAGCAGTTAT TTAAACATTA GTTGGCGGTT TATACTACGC ATTTAAAAAA TACCAAGAAC    900
GTNTTAACCA AGCACCTAAC ATTGAGTACT AAATTAACCA TAAAAAATTC CCGAACACCT    960
TGNTATAGTG CTCGGGNAA TTTNMNTATG CTTNACTTGA ATATTTCAA TATTATTTGT    1020
GCGCTTTCTT GTATTTTCCG ATATTACACT AATGATCTGA TCTTNGGCCC CCNAGCGTAG    1080
GTATTAACAA TCTCGCTGTA TTTTCCACCG GA                                1112

```

(2) INFORMATION FOR SEQ ID NO:987:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1080 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:987:

```

CTTATGGATT CACATCTAAG TTACATAATA TATATTAATA GGAAGTAATG TGTGTGACCC    60
CAAAGGTACC CTACATCATA TCATTATCTA ATATCGTCAC ATAACCTACT TATGCTATAA    120
TCATGTATTA TATTGTTTGG AGTGATTGTA TGAGATTTGT CTTTGATATT GATGGTACGC    180
TTTGTTTTGA CGGCTGATTA ATTGACCAGA CTATTATGTA TACATTGTNA CAATTACAAC    240

```

ATGATGGTCA	TGAACTAATA	TTTGCATCAG	NACGTCCGAT	TCGTGATTTG	TTGCCAGTTT	300
TACCATCAGT	ATTTTCATCCA	GCACACATTA	ATTTGGCGCA	ANGTTGGTTG	CTATGATTTT	360
ACAGCCNATC	CAAAGATTTT	TGTTATCCNN	NCCAATTCAT	ACAAGATACA	TATCACCATA	420
TCTTAAAAAT	AATTCAAAAAG	TATGAGTTAG	ATTATATTAT	TGATGATGAT	TGGAATTATG	480
CTGCACAACT	TGACGCTGAG	AACGCGATTT	TTGAGCGTTT	AGATCCACAT	AAGCTGGCCA	540
GTTGTATTGA	TGTTGCAAAT	ATCGACACAC	CAATCAAGAT	CATTTTATTA	AATATAGACC	600
CGGCACAAAT	TACAACTATA	TTAGACGAGC	TAAATAAATA	CCATCAAGAA	TTGGNAATGA	660
TTCAACCATTC	AAATGAGTAT	AACATTGATA	TAACAGCGCA	AAATATTAAT	AAATATACTG	720
CATTACAATA	TATTTTGTGAT	GCAGATGTTA	AATATATAGC	ATTTGGGTAA	TGACCACAAT	780
GATATTTTCA	TGTTACAACA	TGCTAGTAGG	TGGCTATATT	ATAGGACCAT	CAGAAGCATA	840
CACACACGCA	ATATTGAAAC	TTGATAAAAT	CAAATACATC	AATAATAATA	CACAAGCTAT	900
TTGCAAAGTC	TTAAAATCAT	ATAAATAAAA	GCACCCCTAT	CAAATGATAA	TCATTATCAA	960
TCGATAGGGG	CTATTTTAAT	AAAATTCGTC	CTCGAACATT	TCTTCCNCTT	CATCTAATCC	1020
AAATAATTCT	GCCATTTCCTC	CATGTTCAAT	TAACATGTTT	AAATATGCAN	CGCNCGTGCC	1080

(2) INFORMATION FOR SEQ ID NO:988:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 854 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:988:

CCTGCATTGA	TTATTTTAT	TTTCAGTTT	AATAAAAATG	AAGGTGTAAC	ACCTGCGAGT	60
ATGGTATTAA	TAGGTGTAGG	TTTACAAACA	GCATTATATG	GGTGGCTCAA	TTACAATTAT	120
GTCAAAATTT	GATGATAACC	AATCTGATTT	CATCCCTGCT	TGGTTTGCAG	GTAATATTTG	180
GGGTGACGAA	TGCCCATTIG	TCATTGCATT	TTTACCGTGG	GTGTTGATTA	TTATTCCTTA	240
CTTACTATTT	AAATCGAATA	CACTAAATAT	TATTCATACG	GGTGATAATA	TTGCACGAGG	300
TCTAGGTGTA	AGGTTAAGCA	GAGAACGTTT	AATATTATTC	TTTATCGCAG	TGATGTTATC	360
ATCTGCTGCT	GTAGCAGTAG	CAGGTTCAAT	TTCGTTTATC	GGATTAATGG	GTCCGCATAT	420
TGCCAAACGT	ATCGTTGGAC	CACGTCACCA	GTTGTTTTTA	CCAATTGCCA	TTTTAGTAGG	480
GGCATGTTTA	CTTGTTATAG	CTCGTGCCAT	TGGCCAAAAT	TTGTATTACA	ACCAGGTGGG	540
GTTCCAGCAG	GTATTGTCTG	AGCAATTATT	GGTGCACCGT	ATTTCTTATA	TTTAATGTAC	600
AAAACGAAAA	ATGTATAGTG	TCAAAGGACA	CAACTTATTG	CTATGAAAGG	CACTTTATTA	660
TAAGGCTTTT	CATAGCATTT	TTTATTTAAT	GAGCCACTCA	AGACTATTTA	TTTTTTCAAT	720
AATGAACCAT	TAAGTTATCA	AGAGGATCTT	ATCAAAAATA	TATTTGATAA	CGGTATCAGG	780
TTAATTCCTT	ATGATAGCGC	ATTCATTTAT	TCTGTTTTAT	ACTATGACTG	ATAATACCAA	840
GGAGGTCTCG	TGCC					854

(2) INFORMATION FOR SEQ ID NO:989:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 637 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:989:

```

CATCACCCAG AGCGAATAAA AGAGATTGTA GCGGCCGTTA AAGAGGNGGG TAAATATCGT    60
ATTGTAGACC ATCAACGTAA TGTCACAGTA TATGTGATGT GTAGGCATTT ATGTATCTTT    120
AGTTATGGAT GNATCTAAAA CATCAGNCGC TAGTGGTGGA GACTGTNGTA TTACAATTAT    180
CAATANAGAT GTAGATAAAG AANAAATTTA TGATGAATGG ACAAACATG GTATTAAACC    240
ATTAAAAATT AATATTTATC ATGGGCAATA AATGATTTGA TAGGGGAGCA ATCATCTAAT    300
TTAATTAGAA GATAAATGCT CCATTTTTTA TTGCCAGCCG TGTACGTAT CTTGAAAAAA    360
ATATTAAAAA GAGTAAATA GATAGAGTTA ACGAAAAAAT TAATGAAATC GACGATATAG    420
ATATGATAAA GAAAGGTGGG TAGCAATATG AAAAATACAT TCCTTATTTG TGATGAATGT    480
CAGGCAGTCA ATATAAGAAC GTTACAAAAG AAGTTGGAAG AATTAGATCC CGATGCTGAA    540
ATCGTGATAG GTTGTCAATC TTATTGTGGA CCTGGACGCC GAAAAACATT CACTTTTGGT    600
AATAACCGCC CACTGGCTGC GCTTACTGAA GAAGAAG                                637

```

(2) INFORMATION FOR SEQ ID NO:990:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 960 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:990:

```

TAATTCGCAA TAGGAGTGAT GAATATCATA AATTTTACCC TCCAAATGAA GCTAATGAAG    60
TCCTGGACCC GAGTAAGACG CATGTAGCCA AGCTAAAATA ATCCACTCTA CCTTATCTTT    120
AGTTAATAAT GTTACTAAAT GTTGTTTATA CGCTGCTTTT GAATCAAATT GTTTTGGTTC    180
ATTAATATAA ACAGGAATAT CGTGCTTGTT TGCTCTATCT ATACAAAACG CATTTTGATG    240
ATCCGTATAT AGCNCCTGTA CTTCAATATT TTCAAGTTT CCTGATTCAA CATGCTCAAC    300
TATATTTTCA AAGTFACTTC CTGAACCTGA TGCAAAAATC GCAATTTTAA CCATTGTTAT    360
ACCCCAACA ATTCAATTGC AGTTGACTCA TTTTTCACAA TATGACCAAT TTGATAAGCT    420

```

TCCACATTTT	GTTCTGCTAA	AATCTTCAAA	GCGCGTCGAT	GCATCTTTTT	CATCAACGAT	480
AACCGTATAG	CCAATACCCA	TGTTAAAAAT	GTTATACATT	TCATTTGTGT	CTATATTGCC	540
TTGTTGTTGT	AACCAATCAA	ATATTTTTTG	CGTTGGAAAT	GATGTAGTAT	CAATTCTAGC	600
AGCATATCCG	GCTGGCAATG	CACGTGGAAT	ATTTTCATAA	AAACCTCCAC	CAGTAATATG	660
ATTCATTGCC	TTAATAGAAA	CTTCTTTTTT	TAAAGCAAGT	ACAGGTNTGA	CATATAATTT	720
AGTTGGCTCT	AAAAAGACAT	CTATAAATGG	ACGATTATCG	NAGGGTGATG	CCAAATCAAT	780
GNCTGATTCA	NTAATTAATN	TGCGCACTAA	ACTGTNTCCA	TTNGANTGAA	TGNCACCTGG	840
ACGCAAGTCC	TATAACAAC	TGGCCCTCTT	NCAATTCTTG	AACCATCTTA	CAATAGNCAA	900
CCTTTTTC	CTGCTCCAAC	AGCAAATCCG	GCTACATCAT	ATTCACCTTC	GTGATACATT	960

(2) INFORMATION FOR SEQ ID NO:991:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:991:

GGCACGAGCT	CGTGCCGAAT	TCGGCAGGAG	ACTTCAAAATC	AATCGAGTGG	CATGTCAAGG	60
TCATATCAAT	ATTTTAGAAT	CTGCGACTAT	GAGAGAGGAA	ATAAATGAAA	TGGCACGAGC	120
GACGTATCAT	CGTTGATATT	CGTGATAAGC	AATTACGATA	TCAAGATATT	GCAATTTTAT	180
ATCGTGACGA	GTCTTATGCT	TATTTATTTG	ATTCATATT	ACCGCTTTAT	AATATTCCTT	240
ATAACATTGA	TACAAAGCGT	TCGATGACAC	ATCATCCGGT	CATGGAAATG	ATTCGTTTCAT	300
TGATTGAAGT	TATTCATCT	AATTGGCAAG	TGAATCCAAT	GCTACGCTTA	TTGAAGACTG	360
ATGTGTTAAC	GGCATCATAT	CTAAAAAGTG	CATACTTAGT	TGATTTACTT	GAAAATTTTG	420
TACTTGAACG	TGGTATATAC	GGTAAACGTT	GGTTAGATGA	TGAGCTATTT	AATGTCGAAC	480
ATTTTAGCAA	AATGGGGCGT	AAAGCGCATA	AACTGCACCG	AAGATGAACG	TAACACATTT	540
GAACAAGTCG	TTAAGTTAAA	GAAAGATGTC	ATTGATAAAA	TTTTACATTT	TTGAAAAGCA	600
AATGTCACAA	GCGGAAACTG	TAAAAGACTT	TGCAACTGCT	TTTTATGAAA	GTATGGAATA	660
TTCGAACTGC	CAATCATTGA	TGACAGAGCG	AGATGACTGA	TTAATGTATC	ATGAAAGCGA	720
GAATGATCAT	ATGATGCTAT	CATCCTGACG	ACT			753

(2) INFORMATION FOR SEQ ID NO:992:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 952 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:992:

```

CAATCTACTT AATCGTAGCC GTTTTGGAA ATTGTATGTT GTGGNTTAAT CCTNTTCCCA    60
CAAAATTTGT AATNCCCGTA ATAATCTTTT TTATGTGTTT TGAAGGGGGC CNATTGGAAG    120
CTAAGTATAA TAAACCANAA GACACAAGCA ACTTGTAAT GTGATGGGTA AGATACATAA    180
GAAAGGTGAG TTACCCTTTG CCAACCACCA TTATAAGACA TAAGCACAAAG ATGATACCCA    240
ATATTAATCC ACANATAACA CCGAATGTAT TCGTACGTTT AGTGNAATA CCCANCTGCA    300
NATACACCAG CTAATGGAAC ACCGAATAAT CCAGTTACCA AACAAGAATA AATCCCATAA    360
GTCATTTGTA TTAGAAGCAA TTAAGTATAG TGACATTCCN CAAACCGAAA ATACCTGCAA    420
TGATGATAAT GAAACGTGCA AAGTTAACTT CGTGTCGCTC GCTATCTTTT CCGAAGAAGC    480
GTTGCTTAAT GTCGATTGAA ATACAAGCAG ATATAGAATT TAAACTAGAT GAAATGGTAG    540
ACTGTGCAGC GCGCAAAATG GCTGCAATAA GTAATCCTGC TACAAATGGT GGCATCTCAG    600
TCAAAATGAA ATATGGCACT ACAGATGATG TATTGAAGCC TTTTGGTAAA ACAGCTTCAT    660
GTGTATAAAA TGAATACAGC ATTGTACCCA TACCATAAAA TAAGGGTGCT GAAATTAAAG    720
CTAGGATACC ATTTGTCCAT AACGATTTAT TTGTTCTTTT TAAACTATCA GAAGCTTGAT    780
AACGCTGCAC GACGTCTTGA CTCGCTGTGT ATTGATACAA GTTGTGAAA ATATTTCTTA    840
GGAAATAAT TGGAATGGCA GCTGCCGAG TATTTAGTTT CCAATTGTCT GACTAATTA    900
ATTTTTGTG CTCAATCGCA TCTGCAAAGA CAGTGCCAAA ACCGCCTTTA AG          952

```

(2) INFORMATION FOR SEQ ID NO:993:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 675 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:993:

```

TTTTCGCAGG ATTCCTTTCA AGCCTAAGAA TTGGGCCCAN TTGGGAAGAA ATGNATGGGT    60
GCCCCGTAAAC CTGCCGGACC GCATTGAACC AAGCATTCCT AAAATACCCA ACAAATATAG    120
CGCCATMNNN AAANACANCC CTGCTACCCG TAAGTTATGA ATATCTCATA ACATTCAAGC    180
TAGCAGTTCT TTTTATTTTA AAGGTTTAAA TAGCAGNCTG TACCCACGCA TAACTGTAAT    240
TAATTGTTCT NTGTCATTCT TAATTTTAT ATCCCATAA TGTGTCGACT TACCTCGATG    300
AATAATTTCA GCTGTCGAG TAACACGACC ATCTTTAGCA GAATGAATAT GGTTAGCATT    360
CATCTCTAAA CCTAATGGAA TAAATTTGGT TGTATCAATT AAATTAGCAG ATCCTAATGA    420
ACATGCTGTT TCACCTAAAG CAATCGAAGC CCCACCATGT AAATATCCAA ATGGTTGTTT    480
TACTTTATCA GTGACAGGCA TAGAAATAAC AACTAAACCA TCTTCCTGGT GATCTATTGA    540

```

CATCTCAAAT GTCTCTAATA AATGAGTCAT ATTTTCACCT CTTTATGCCT ATAGTACCAT	600
AGCAGCAATA GTACCGAAAA TCATTAAAGG AATATTATAA AACAAGAAGT TTGGTACACA	660
TGTATCGCTC GTGCC	675

(2) INFORMATION FOR SEQ ID NO:994:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 683 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:994:

AGGGGCNGTN TTTTGGAAA CCNGGTCACG ANCTCACATG GGTAAAGNTG ATCANCACCT	60
TTGGTGTTTT AGGNTTAAAA ACAATTACC TATTATCGCG CCAATTGCAC TTATCAGCT	120
TTTTAATATA TTGATTCATT TGGGCTTTGC GAGTGAACA AGTTTATCAT CAGCGTTAAT	180
ACCTGTTTTT ATTCGCTAA CCTCTACGTT ACACCTAGGA GACCAGTCTA TAGGATTTGT	240
TTTAATTCAA CAATTGTGA TTAGTTTTGG TTTCTTATTA CCTGTTAGTG CACCTCAAAA	300
TATGTTGGCT TATGGCACTG GTACTTTTAC GGGTAAAGAT TTCTTGAAGG CAGGTATACC	360
ATTGACAATT GTAGGTATA TTCTAGTGAT AGTTTTTAGT ATGACTTATT GGAAATGGTT	420
AGGTTTGCTT TAATTAAAA TATAATAAG AATCTAGGTT ATTTTAAAGT GACAAAAGC	480
TTAATAAAAT AAAAAGATAA TTGAAGGTG TTTTGTATAT GGCAATTGCT GTGTTATTAA	540
ATCGNATGTT TCGNATGGA CACNATCCAT TATTGGATA TATTATCCA CAAAAGGAG	600
ACCTTGGTGC ATGTTATTTT ATCATTCCGG GAGGGGACAT GTCTTCAGCT TCTGATTTGT	660
TAGCACATTT TCTCGCTCGT GCC	683

(2) INFORMATION FOR SEQ ID NO:995:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 955 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:995:

CTGCATCTGG TGAAGGAAAT CAANTANNIN TTATNNCTGA AGTGATTGCA TGGTGCAACN	60
TCAAATATCA CATATGGCTC AGTGGANTAT ATGGATAAAG GCTTAACAGG TCATATCATG	120

CGGCGTGGTA	TTACTGAAGC	GGATGCCTCA	ATTAATTGGG	CACTAGGTTT	AATGAATGAG	180
GGTAGCCAAA	TTATTGATAA	TACAACAAAT	TTATGTGGTG	ATCGCACAAAC	AAGNNCACTT	240
AAATCAGGAG	GTGNAGGTAC	AGGAGAACAA	AAAATTAATC	TAACATCTAA	ANTCGCACAA	300
ATATGGTAAA	GAAACAGATG	GTTATNTCCT	TAAACATGGT	GTTATGAAAG	AACATGCATC	360
ATCTTGATTT	TTAATGGGTA	TCCGGCTACA	TTANGCATGG	GGGGAACATA	ATCAAGTGCT	420
AATCAGGAAT	CACGTGTTAT	TNATGTTATC	TTGAACATGC	TCGGGGGNGA	CGCGAATCCT	480
ATTTTATTTA	ATTGANGAAG	ATGATGTACA	AGCTGGTCAT	GCTGCATCAG	TAGGCCGTGT	540
TGGATCCCAG	ATCAACTTTT	ACTATTTAAT	GAGTCGTGGT	ATTTCTCAAA	GAGAAGCGGA	600
ACGTCTTGTT	ATACAGGGTT	TCTTAGATCC	AGTAGTACGT	GAATTACCTA	TCGAAGACGT	660
TAAACGTCAA	TTGAGAGAAG	TAATTGAACG	CAAAGTTTCT	AAATAATATT	TTGAAAATAA	720
AAGTTTGTA	TAGATATAGA	CTGTCGATAT	TGGTATAAGA	CTAATACAAC	GTCAGTATTT	780
AAATGATTAG	GATTTTTTATT	TAAGAAAGGT	CGTGAATGAA	GTGGCCGAAC	ACTCATTTGA	840
CGTTNATGAA	GTAATCAAGG	ATTTTCCGAT	ATTAGATCAA	AAAGTCCATG	GCAAACGTTT	900
AGCATATCTT	GATTCAACAG	CGACAAGTCC	AACGCCTATG	CCAGTGTTAA	ATGTT	955

(2) INFORMATION FOR SEQ ID NO:996:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 685 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:996:

AAACCCCTTC	GGATTANAAA	TTGGANCCCA	GGATTCTTTT	GTTTATCACA	CAAGATTTAA	60
AAAAAGATTG	CACATTGTCT	TGCTGTCTAA	NPTAATTACA	TTAACACCTG	GTACCTGTAG	120
TGCTTGGTGT	AAGTGATGAT	CGCACACAAA	TTTATATTCA	TGCCATAGAT	TTTTCANCTA	180
AAGAGCAAGA	AGTAGAAAGT	ATTAAAACAT	CATTAGAGAA	AATTGTAAGA	GAGGTGGGCG	240
AAATATAATG	AATCATAATG	TTATTATCGT	TATTGCATTA	ATCATAGTTG	TCATTTCTAT	300
GTTAGCTATG	CTCATTGCGG	TTGTGCTAGG	CCCATCACTT	GCCGATCGTG	TTGTGCGATT	360
AGATGCGATT	GGTCTTCAAT	TAATGGCAGT	TAGAGCATTA	TTCAGTATTT	TATTAAATAT	420
TAAATACATG	ATTGTGTTA	TTATGATGAT	TGGTATATTA	GCCTTTTATG	GTACTGCACT	480
ATTCTCTAAA	TTTATGGACA	AAGGTAAGGT	GATTGAACAT	GATCAAAATC	ATACTGATTA	540
GTCTTGCACT	TATCTTTGGT	ATCATCGGCG	CTTTAATTAG	CGCCCTAGCA	GCTATAGGAT	600
TATTGAGACT	TGAAGATGTA	TATTCACGTN	CACATGCTGG	CGGAAAAGCA	TCAACATTAG	660
GTGCAATGTC	AATACTATTT	GGGAC				685

(2) INFORMATION FOR SEQ ID NO:997:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 686 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:997:

```

GGCACGAGCT ATTTGGACAT TC'TTAAGTAC ANTCTGGAAC ACGATAATTA CAATCGCTAC      60
TACGATTTGG AATTTGTTAG TCACTGTAAT AACTACAGTA TTTACCACAA TTATGACTAT      120
CGCAATGACA ATTTGGAACG CTATTTGGAC GTTCTNACAA ACGTTGTGGA ACACTATAGT      180
TACTGTGGCA ACTAAGGTTT GGAACGCTAT CACTACAGCT ATATCTACTG CATTACAAGC      240
GGCATGGAGT TTTATTTCTA ATATATGGAA TACGATTTGG AGTTTCTTAT CTAGTATATT      300
AACGACAATT TGGAATAAAG TTGTAAGCAT ATTCACACAA GTTGTATCAA CTATATCAGA      360
CAAAATGTCT CAAGCTTGGA ACTTCATTGT CACTAAAGGT ATGCAATGGG TATCTACTAT      420
AACAAGTACG CTAATTAACT TTGTTAATAG AGTTATTCAA GGATTCGGTA ATGGTTGTTA      480
ACANAGTTAG TCAAGGTATG ACANATGCAG TAAATAAAAT AAAAAGCTTT ATAGGAGATT      540
TTGTGTCTGC AGGTGCAGAT ATGATCCGTG GNTTAATTAG AGGTATTGGA CAAATGGCTG      600
GCCAATTAGT AGATGCAGCT AAAAATGTTG CTAAGAAAGC TTTAGATGCA GCTAAAAGTG      660
CTTTGGGTAT TCACTCACCN TCACGT                                           686

```

(2) INFORMATION FOR SEQ ID NO:998:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 882 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:998:

```

ATTAATTTAT GGGCCCAAAA GACCATGAAT ACTTGAAATT GAAGTCGCCC AAACCCAATT      60
GCACCAAAGA TCCCAGGATT GAAACATCAC GGTTTAAGAT ATGTCAATTA TTATCCACCN      120
AACTTACCCC CAAACNGCAT TAACCACAAC ATGATATGGG AAATTACTAA TAATGGAAGA      180
TGGGAATACC TAAATACATT TGTTCCAAGC TAAGAAATTN ACTTTTCTTT GTCGTTTTCG      240
AAGGCGCTCT AAGCTTATCC AAATTGGGGC TAAGCATATT ATTACAGGCG TATGTGAAAC      300
AGACTTTTCA GGCTACCCAG ACTGTCCGGA TAGTTTATA AAATCAATGA ACGTAACATT      360
AAGCCTAGCT ATGGACAAAG ATTTTGTTCAT TCATACTCCT TTAATGTGGT TAAACAAAGC      420
AGAAACGTGG AAATTAAGTG ATGAACTCGA AGTTTTAGAT TATATTCGTA CAAAAACATT      480
AACATGCTAT AACGGTATCA TTGGGGATGG CTGTGGTGAA TGTCCAGCTT GTCATTTACG      540

```

TCAACGTGGA	CTAAATCAAT	ATCTTGAAAG	TAAAGGAGCG	CNTTAAAAGG	TTACAACAAA	600
TCTATCCTAG	TACAACGCAT	CCATATCAAT	TCGAATTAAA	TAAAGATTTN	AATTTCTCGG	660
CTGCACATCA	CATTCCTTGT	GAAGAAGCAG	GTATTTGGCA	AAATGTCCAT	GGTCATACTT	720
ACTNTGGTTA	ATTTAACAAT	TGNCGGGTGG	ATAAACTAGA	TGACACTGGC	TTCTTAGGNG	780
ACTTTTAGCC	CATNTGGAAA	NGATGATACA	CGGTAAATTT	GACCATCAAC	TGTTAAATAA	840
CTTACCTGCT	TTTAAAAACA	AACTCCCTCA	ACTGAAATCG	GG		882

(2) INFORMATION FOR SEQ ID NO:999:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:999:

CTAGATTGGT	GTTATATTNT	TGATATGATA	AGAAGAGATG	TAAGAGTAGG	GATAAATACA	60
ATTGAGGTGA	ACCCATGTTA	ACGACAGAAA	AACTAGTTGA	AACATTAAAG	TTAGATTTAA	120
TCGCTGGTGA	AGAAGGACTA	TCGAAGCCAA	TTAAAAATGC	TGATATATCA	AGACCAGGCT	180
TAGAGATGGC	AGGTTATTTN	NCACATTATG	CGTCAGATAG	AATACAATA	TTAGGAACAA	240
CGGAACATATC	GTTTTACAAT	TTATTACCAG	ATAAGGATCG	CGCAGGTCGT	ATGCCGTAAAC	300
TATGCAGACC	AGAAACGCCT	GCAATTATTG	TGACACGTGG	ATTGCAGCCA	CCAGAAGAAT	360
TAGTTGAAGC	TGCAAAAGAA	TTAAATACCC	CAC TTATAGT	TGCTAAAGAT	GCGACTACAA	420
GTTTAATGAG	TCGCTTAACA	ACGTTTTTAG	AGCATGCACT	TGCAAAGACG	ACATCTTTAC	480
ATGGTGTTTT	AGTAGATGTT	TACGGTGTTG	GGTGTA CTTA	ATTACCGGTG	ATTCAAGGGA	540
ATAGGGTAAA	AGTGGAGACT	GCGTTGGGA	ATTAGGTTAA	ACGGTGGGCA	TTAGATTACG	600
TAGCAGATTG	ATAATGTNGA	AATACGTCAA	ATTAATAAAG	ATGAACTTAA	TAGGGAAACC	660
ACCAAAGGTA	ATAGAACATC	TATTTAGAAA	TACGGTGGAC	TAGGTATTAT	CAATGTTATG	720
ACTTTATTTG	GCGCGGGTTC	AATATTA ACT	GAAAAACGAA	TTAGATTAAA	TATTAATTTG	780
GAAAACTGGG	ACAAGCAAAA	GTTATATGAC	CGCTCGTGCC			820

(2) INFORMATION FOR SEQ ID NO:1000:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 554 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1000:

GGCACGAGCG ATNNGTTTCGN CTGATCTACN AGTTAACTTC AGATATTNAA GAGATTCATC	60
ATCAACTGGG AAGCAATCCG CAAGTNGCTC CATACTCTGG TGCCATGTTT GCAATTGTNG	120
NACGGTCTGC TAGTGGNAAA TGTGTACAC CTGGACCAA GAANTCCACA AATTTACCAA	180
AAACACCTTT TCTACGTAGC TCTTGAGTTA CTCTTAACGC ATAAATCAGT TGCTGTTGCG	240
CCTTGTGGTA ATGAATNTAC TAGTCGTACA CCAATAACCT CTGGAATTGG GAAATAAGAA	300
GGTTGTCCAA GCATTCCAGC TTCAGNTTCA ATACCACCAA CACCCCATCC TAGTACGCNA	360
ANNCCATGTA TCATTGTTGT ATGTTGAATC AGTNCCAACT AAATGTTATC TGGAAATGCA	420
GTTTTTTCAC CATCTACATC CACGAACATG TTACAACACT GTGCTAAATA TTCTTAAGTT	480
AACCTGGTGA AGTATTCCAA TTGCAGGAAG AACTGCATCG GTAATTATCA AATGCTTTCC	540
GTGCCCCAAT TTAA	554

(2) INFORMATION FOR SEQ ID NO:1001:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 752 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1001:

ACTTTACNTC CAATTGGTAC CAACATGGTC ATGGAGCTAT GAAACAAGCT AATGGTCCAA	60
ACCTGCTGGT TTCTCCAAAC GTTGCAGGTT GCAAGACTAC ACTACTTCAA TACACCCAAG	120
GTTCAAGATG TACAATCAGT AAGCTACAAT GCACAATCAA GTAACTCANA CGTTGAAGCT	180
GTTTCAAGCT CCAACTTACC ATAACCTACAG CACTTCAACT ACTTCAAGTT CAGTGAGATT	240
AAGCAATGGT AATACTGCAG GTGCTACTGG TTCATCAGCA GCTCAAATCA TGGCTCAACG	300
TACTGGTGTT TCAGCTTCTA CATGGGCTGC AATCATCGCT CGTGAATCAA ATGGTCAAGT	360
AAATGCTTAC AACCCATCAG GTGCTTCAGG TTTATTCCAA ACTATGCCAG GTTGGGGTCC	420
GACAAACACT GGTGACCAAC AAATCAACGC AGNTGTTAAA GCATACAAAG CACAAGGTTT	480
AGGTGCTTGG GGATTCTAAT TCCTTCATAA TANATAAAAG TAATGTTTAG ACATTAAATA	540
TATAGCTCTT CCCATAGAAA TTGGAGAGAG TTTTNTTATT AATTAAAAAT ACATTCTTA	600
AAAAGTGGAT ATTGANGTTA GGGAAATTTA TTGGGACTTT ATTGTATTAC TGCTAAAAAT	660
ACTTGGTCTT TATTAANGGT GCAANGTGGG GAATAAACT TCATGTGAGG CTGGTNCTGN	720
GTACAACTAG ATACNAACTA AACGCTCGTG CC	752

(2) INFORMATION FOR SEQ ID NO:1002:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 747 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1002:

```

ANCTACCTTG TCACTTTTNT AGAAAACATA TTAGTAATAA GTTCTTCATA TGTATGTGTA    60
TTCATATTCA TCAATGCGCT AGTAGCACCT ATTGCAACCA TGTTTGGCAC GAATGCTCGT    120
ACCTAATTC TTAGCGGTTG CTGTAAAAGG TAATTCAATA AGCTGTGCAT GACATCCTTC    180
TGGTTTCACA GGGTTAGCCT TGGCATCAGC TAAAATAATA CTGTCTTCTC TCATTTTCATG    240
ATGGTTAACA TCAATTGTTT CTGGGTCAAA TGCAATCAAA ATATCTAAAT CATCACTAAT    300
TGCATGAACA GCGTCGTAG AAACCTAAT TTTATTATTC GTATGTCCAC CTTTGATACG    360
ACTTGAAAAA TGTCTATATC CATATAAATA ATATCCTTTT CTATTCATAG CCGTAGCGAA    420
NATTTCCCCA GTTGATTCAA TACCTTCGCC TTGTTGACCG CCAACTTTC ACGATAATTG    480
TGGTTTCATA GTTATATGCC TCCTATGGAT ATATTTTATA TTAAATGATA AAAAAAGAA    540
CCACCGATTT ACTATGTAAA CAGTGGTACT ATATTAAATT CATACTAATG GACGAATAGG    600
GTCCAATTCC GAATGTTTTA CTTACGTAA TTTTAAAAT GTTTGNAAAT GGATGGTCAT    660
CATTTATCAA TATACGTTTC ATGTGCTTTG TTTTACCTTC TTTGTCTAAA TCAATAACAA    720
CACCAGATAA TACACTTCTA CCTTCAG                                     747

```

(2) INFORMATION FOR SEQ ID NO:1003:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 672 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1003:

```

AATTTTGTG ACCCTAAAC CAAGACAATG CGTAATGCTG CTGATTAAT ATTCATTTG    60
GCACGAGTAC TAATATTATC CAAATGATG AATTAGGTCG TACCATTTTA AATGAACNTG    120
GTAAAAAAGC GGAACAAGGT GTAGAAGTTA AAATCTTTTA TGATGACATG GGTCTCGTG    180
GACTGCGTAA AAAAGGCTTA CGCCCGTTTC GCAATAAAGG TGGACATGCT GAAGCATTTT    240
TCCCATCAAA ATTACCTTTA ATTAACCTGC GTATGAACAA TCGAAACCAT CGAAAAATTG    300
TTGTAATAGA TGGGCAAATT GGATATGTTG GTGGTTTTAA TGTGGTGAT GAGTACTTAG    360
GTAAATCAAA AAAATTCGGC TATTGGCGAG ATACGCATTT ACGAATTGTC GGGGATGCAG    420
TGAATGCATT GCAATTACGA TTTATTCTAG ATTGGAATTC CACAAGCCAC ACGTGACCAC    480

```

ATCTCCTATG ATGATCGTTA TTCCCANAT GTNAATTCTG GTGGAACAAN TGGCGTTCAA	540
ATAGCTTCTA GTGGTCCTGA CGAAGAATGG NAACAGATTA AATACGGCCA TNTGAAAATG	600
ATTTTCATCTG CTAAGAAATC CATTTATATT CAATCTCCCT ATNTCATACC TGATCAAGCC	660
CTTTTAGATT CT	672

(2) INFORMATION FOR SEQ ID NO:1004:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1011 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1004:

GAGGCAACCC GACCTATATT CAAAGAACCC TCCAGGACCA GCTTGTGTAA ATCTTGAAAA	60
TGTTATCGGA TGGATAATAA AACCTTCTTG ACCTTTGTCTG TCNCGGGGAA ATATCAAGCC	120
ATTTGTAAAA CCNAAGATAA TTCCAACAAC GCAATACGTG CACCCAGGTG GCTCAATTCA	180
ATTTTGNNCC GGAATACCCA TGGCCTGTTT TTCTTTAATT AACCACCACT TGTCACATCAT	240
TTCGGAAGTA TAAATCGTTA CCCTTCACGG AGTACCGTTC AACCTACACC GGCGGAATAC	300
AAGAAATACC CACCGTGCTC TTGAGCGAT GTTGTAAATT AATTCTTGGA TTAATACTGT	360
TTTACCTACA CCGGCACCAC CGAACAATCC GATTTTACCA CCTTTAATAT AAGGTGCTAG	420
TAAATCTACT ACTTTAATAC CTGTTTCTAA AATTGAACT TCTGTTGAAA GTTCATCGAA	480
TGCTGGTGCT TGACGATGGA TAGGATCGCG GCGAACAGAA TCACTAATTT CTTCTTTAAG	540
GTCAATTGTT TCACCTAGTA CATTAATAC ACGACCTAAT GTTTCGTAC CAACAGGGAC	600
ACTAATTTCT TTGCCTGTAT CTTTACATC CATGCCTCTT TGGACACCAT CAGNTGAATC	660
CATCGCAATT GTNCGANCAN CGTCGTCACC TAATTGCAGC GCAACTTCTA ATGTTAGTTG	720
TATTGTACCT TCTTCTTTAG GCACATCAAT AACCAAGGCG TTATTAATTT TAGGAACCTC	780
GTTATGTTCA NATCGAACAG CAATTACAGG ACCCATAACT TGAGTTACAC GGCCAATTCC	840
CATGCTATTT TCCTCCTTTT AAATATTATT CCAAGCGCTT GCGGAACCCA CCAACAATTT	900
CAGTAATTTG TTGCGTTAAT TTCTGCTTGT CTCGCTCTGT TATATTCCAA ATGATAATCA	960
TCAAATAAGT TCAGTTGCAT TATCAGTGGC ATTTTCATCG CAGTCCATAC T	1011

(2) INFORMATION FOR SEQ ID NO:1005:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 615 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1005:

```

AATGTATTGT AGAAGCTGAG CACTTAAAAA GAGAGCGCGT AGAAGCTAAG TATAGAAAAA    60
TGATNTTGGG GGCTAAAAAA TAATGTTAAA TCCACCTTTA ANCCAATTAA CGTCACAAAT    120
TAAATCAAAG TATTTAATTG CAACAACTGC AGCGAAAAGA GCGCGTGAAA TTGATGAACA    180
ACCTGAAACT GAATTATTAA GTGAATATCA TTCATTANA CCAGTTGGTA GAGCGTTAGA    240
AGAAATTGCT GACGGTAAAA TTCGCCCTGT TATTCAAGT GATTATTATG GTAAAGAATA    300
GTTTCGACCA TTAATAATAT GTGAAGCTAG ACGTACATCA AATACGTCAA GGCATATCCA    360
AATCAAACGC ACCTATGTAG GTGTGTTTNN NTTAGNCTTA TCCAATGATT GATGTTATAA    420
TAATACTAAA TTGGCTATCT ATAAAAAAGT AATGAGCATT TGTCGCATA TGATGATGTA    480
AAGCGTAAAT GTCATAGTGA TATTTAAGGG AGATTGAATA TGAAGAAAAT ATTATTAGCC    540
GTTACAGGTG GCATTGCGGC ATATAAAGCA ATTGATTTGA CAAGTAAGTT AACACAATCT    600
GGGTATGAAG TTCGC                                     615

```

(2) INFORMATION FOR SEQ ID NO:1006:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1006:

```

TTTGTCTTTG GAATGGGCTC GTTTTTTTTA ACCTAATAAG AAATGATAGG GCATTTGAGA    60
TTGGAAGGNC ATTTTGGCTT TGTGCAAATA ATACAATAAG CTAAATGTCT NTTTTGTGTT    120
TTGTGAAAAT ATGATGGATG GCTTGTGTGG GCAAGTTTGC TAATTTAATA AGATATGCAT    180
TTTTCAATTT AGGAGTTGGC CATGCATCTA CACTTTATAA TGGTGAGAGC GTGGTGAGGT    240
ATTGTTAATC ACGCAATTGT AGCGAGGAGT TATTGCTACA TATGTCGTTA TGGCCTATTG    300
ATTTTCTAAA ATAGCTGTAT CAGATCATGT GACNAAATAA AAATAATTG TTGAAAGCCT    360
TTACATAACT TGTCTAGACA AGTTATACTC GTTTTAAGAC ATTAAGGGAG TGAAATATAT    420
GGCTGTAAAA AGAGAAGATG TAAAAGCCAT CGTAAGNCGC TATTGGGGGA NAAGAAAATC    480
NTGAAGCTGC ANCGCATTGT GTAACNCGAT TACGTTTNGT GCTTAANGAT GAAANCANAG    540
TTGATAAAGA CGCATTAAGG AACAACGCGT TGGTCAAGGG GCAGTTCAAA GCAGACCATC    600
AATATCAAAT TGTCATTGGT CCAGGANAG TCGATGAAGT GTATAAGCAG TTTATTGATG    660
AAACAGGTGC TCAAGAAGCT TCGAAAGATG AAGCGAAACA AGCAGCTGCG AAAAAAGGGA    720
ATCCAGTACA ACGTTTGATC AAATTGTTAG GGGAGATTTT TATACCAATA TTACCTGCCA    780
TTGTGACAAC TGGTTTGTTA ATGGGGATTC AATAATTTAC TTACAATGAA AGGTTTATTT    840
GGTCCCAAAA GCATTATTG AGATGTATCC CGCAAATTGC TGATATTTCA AACATCCATT    900

```

AATGTGATTG	CGAGTTACCG	CATTTATTTC	CTTACCANCA	TTAATTGGTT	GGAGTAATAT	960
GCTGTGTATT	TGGTGGTAGT	CCGATCCTAG	GCATAGTCTT	AGGTTTGATT	TTAATGCATC	1020
CGCAATTAGT	ATCTCAGTAT	GATTTGGCAA	AAGGGAATAT	TCCGACGTGG	AAC TTATTTG	1080
GCTTAGAGAT	TAAGCAGTTG	AATTACCAAG	GTCAAGTGT	GCCTGTTTTA	ATTGCAGCTT	1140
ATGTTCTAGC	TAAAATTTGA	AAAAGGATTA	AATAAAGTCG	TTCACGATTC	GATAAAAATG	1200
TTGGTCGTTG	GACCGTAACG	CTTTTAGTTA	CTGGATTTTT	AGCATTATT	ATCATTGGAC	1260
CAGTTGCATT	ATTGATTGGT	ACAGGTATTA	CTTCTGGTGT	TACATTTATA	TTCC	1314

(2) INFORMATION FOR SEQ ID NO:1007:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1011 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1007:

CTATAATTGT	TAACGTTGTT	AATAATGTAA	AAAGTGCAAT	TTCATTTGGT	GTTTTATTTC	60
TTTCCGCCCC	TTCAACTAAG	GCAATCATTT	TATCTAAAAA	AGATGTAGCC	CGCTTCCACT	120
CTCAAAGACG	TATTTCTNAC	CCAATCAAGA	TGTTACCAAG	TGTACCGCCA	ATGACTCCAT	180
CAAAATCGNC	ACCTGATTCT	TTTATCACAG	GTGCAGACTC	ACCAGAAATT	GNAGATTCAT	240
CANCGGTTGC	TAATCCATTT	ATTACAACGC	CATCAGCAGG	GATTGTTTCT	CCATTTTCNA	300
CCCGAATATT	GTGTCCGGCT	TTTAACTCTG	TGGCGTACAC	TATCCGATAC	GCACCATTTT	360
CTTCTATCAA	TCGAGNAGNT	AAATGTGATT	GTGCTTGTCT	TAAACTATCA	GCTTGCCTT	420
TTCCACGACC	TACAGCAAAG	GCTTCTGAAA	AATTAGCAAA	CAATATAGTT	ATTAATAATA	480
TGATAAAAAT	TGTAATCAAA	TAACCTCGNT	CGNCAGACAG	CTAGNTCCAA	ATATGTCAGG	540
AAAACATATT	AATATCAACG	GTTAAAACCA	TTCCANCCTC	AACGACAAAC	ATTATCCGAT	600
TTNNNTATTA	ATTGGNNTAG	GATTCAAGCT	TATAAAAACT	CAATNTACAA	AGCTTCTTAT	660
CAACATTGTG	TGATTGAAAT	ATTTATTNAC	ATGATGNATT	TTTTCCATCC	CTTTACTTTA	720
TTTTAAAGTT	AAAAATTAC	CAATAGGACC	AAGTAATAGC	ACTGGAATAA	ATGTCAAACC	780
ACTTAGTAAA	ACGATAAATA	CGATTAGTGA	TACGCCAAAA	TAAGGTTTAT	CAATCGCTAT	840
TGTATTTTTA	TCTTGATGGT	ATGATTTTTT	ATTCACTAAA	CTTGATGCAA	TCATTAATTG	900
CAAAAATAAT	TGGTATATTA	CGAGAAAGCA	ACATAATGAC	TTCTGTAGA	GATATTCCAG	960
AATGTGTATC	ATCTTACAGT	CCTTCAAACC	CTGATCCATT	GTTCGGAGGA	G	1011

(2) INFORMATION FOR SEQ ID NO:1008:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1118 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1008:

```

GGCACGAGAC TCAAANCACT GAAGCATTAA CAAAATAATA CTATATTACT GTCTAATCAT    60
AGACATGTTG TATTTAACTA ACAGTTCATT AAAGTAGAAT TTATTTCACT TTCAATGAAC    120
TGTTTTTTAT TTACGTTTGA CTAATTTACA ACCTTTTCAA TAGTAGTTTT CATGCCACGA    180
GCTATCCTAA CCCACAGATT AGTGATTTCT ATACAATTCC TCTTTTGTCT TTACATTTTC    240
TTAAATATT TGCAGTGTG AGTATAAATT TTTGTTTCT TCCTACCTTT TTCGTTATGA    300
TTAAAGTTAT AAATATTATT ATGTACAACG ATTCAATCGC TCTATTTTTC AACTTTCAAC    360
ATATTATTAA TTCGAAAGG ACCACTTTAA AATTTAACNG GCCACAACAA ATCAAATCAA    420
TTAATCACTT TTTCCAAAAT AATCATATAA GGAGGTTCTT TTCATTATGA ATATCATTGA    480
GCAAAAATTT TATGACAGTA AAGCTTTTTT CAATACACAA CAACTAAAG TTATTAGTTT    540
TAGAAAGAT CAATTAAAGA AGTTAAGCAA AGCTATTAAA TCATACGAGA GCGATATTTT    600
AGAAGCACTA TATACAGATT TAGGAAAAAA TAAAGGCACG AAGCTTATGC TACTGAAATT    660
GGCATAACTT TGAAGGTAT CAAAATGCC CGNAAGGAAC TTAAAACTG GACTAAAACA    720
AAAAATGTAG ACACACCTTT ATATTTATTT CCAACAAAAA GCTATATCAA AAAAGAACCT    780
TATGGAACAG TTTTGATCAT TGCACCATTT AACTATCCTT TTCAACTAGT ATTCGAACCT    840
TTAATCGGTG CTATTGCAGC AGGTAATACA GCAATTATTA AACCATCTGA GTTGACACCA    900
AATGTTGCAC GAGTGATTAA ACGATTAAAT AATGAAACAT TTGATGCAAA TTACATTGAA    960
GTTATTGAGG GAGGAATTGA AGAAACGCAA ACGTTAATTC ACTTACCTTT TGAATATGTC   1020
TCTTACAGGA GTGAAATTGT AGGCAAATCG TTTATCAAGC TGCAGCGAAA TTAGTCCTG   1080
TGACATAGAA TGGTGGGGAA ATCTCCAGTC ATCGNGGG                               1118

```

(2) INFORMATION FOR SEQ ID NO:1009:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 686 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1009:

```

AAAGAGTTCG CCTTAAAGG TAACGTCTTA GATTTAGCAA TTGCTGTTGT GATGGGTGCA    60
GCTCACACAA GATTATATCT NCATTAGTAG AAAATATCAT CATGNCATTA ATTGGTAAAA    120
TTCNCGGATC AGTTGATTGT GCTAAAGAAT GGACANTCTG GGGTATTAAA TACGGTTTAT    180
TTATCCAATC TGTTATCGAC TTTATTATCA TCGCGTGTGC TTTATTCATC TGTGTTAAGA    240

```

```

TTGCAAATAC ATTAATGAAG AAAGAAGAAG CCGAAGAAGA AGCAGTTGTG GAAGAAAATG 300
TTGTGTTATT AACTGAAATC AGAGATTTAT TCGTGAGAA AAAATAATTC TAAATAAAAA 360
GAGATGGGCT AAGGTTGCTC TATACATTCC AAAGCACCAT CTCTATTNN TATGGTNNNA 420
ATCTCTTG TG ANTCCTGGCG AACTCTGATA TTGGATCTTG ATTACACTTC TAAAACTAAA 480
GGTNTTCTTA TTATCTCTTA AATTCGCTAC AAACCATGTG AAATCTATGA TTGGAATCCC 540
AACCATTCTA CCAGGAAAAT TATTTGATTA AAATTGATGA TTGGCATCCT AATAAAGGGT 600
CTTTAACGCT NTTGCAAGCG GCCAATTTAC TTGATCTAAT GTACNACGAA TCCTTCATCA 660
ATAAATATTG ATTCTAGTGA AATACC 686

```

(2) INFORMATION FOR SEQ ID NO:1010:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1010:

```

GGCACGAGCT TTTAAAGAAG ATGGACGTTT TATTCCAACA ATTGCATTTT ATAGTCCGAA 60
TGCATTAGGC GCTATCCAAC TTAAAAGCCA CCTACCATT CTGATAACT TACAGTTTTT 120
ACAAAAATAT ATATCATGAA TTATCAANCG GATTATTTGG ATGTCAGGGA TG TAGATGCG 180
CCCTCATATT GGTACAAAAA ATATAAATTA TCAGCATGAT TTGGACGCTT TAATTCAAAA 240
ATTGTAAGCT GTTAGGAGGT CCACAAATGG TAGAACAAAT AAAAGATAAA CTAGGACGTC 300
CCATCCCTGA CTTACGGTTA TCTGTGACAG ATCGGTGTAA CTTTTAGGTG TGATTATTGC 360
ATGCCCTAAA GAGGTATTTT GGAGATGATT TCCGTATTTT TACCCTAAAN ATGAACTTGT 420
TAACGTTTGA TGAAATGGCT AGAATCGCTA AGGTATATGC AGAATTAGGT GTAAAAA 480
TACGCATTAC AGGTGGAGAA CCATTGATGC GACGCGATTT AGAGCCATGT ACTTATAGCT 540
AAATTAAATC AAATCGATGG TATTGAAGAT ATTGGTTTGA CTACAAATGG TTTGTTATTA 600
AAAAAGCATG GACAAAAGTT ATATGATGCT GGGCTACGCA GAATTAATGT CAGTTTGGAT 660
GCTATTGATG ATACGCTATT TCAATCAATC AATAATCGTA ATATTAAAGC GACTACGATT 720
TTAGAACAAA TTGATTACGC GGCACGAGCT CGTGCC 756

```

(2) INFORMATION FOR SEQ ID NO:1011:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1011:

GGCACGAGCG	CACGATGGGC	ACCGTGAGTT	ATACCTATGT	AACTGACATA	CCTAGTAGTG	60
CTTATGCTTA	TCTAATGCCT	TATCGTAAGT	TAAGTTGGGG	TAAGCGATAT	GTTTAATCCG	120
TTTGATGAGT	TTCCGCACAC	AATTGAAATT	GGAGAGGTTG	AAGTTGCAGG	AACATTTTCCT	180
AAAGAATACG	AGCGTTTAA	AAGTAACGAA	ACAATTAAAG	GATTTATGGA	TACGCCTACA	240
TCAAGCGAGA	CACTCAAATT	TCATCAAATG	AGCAAAGACT	TCGACCGTAA	CCTATATACG	300
CCGTATCACA	TACCAATAAC	AAACAAACT	TTATTTAATT	ACGAGGGTAA	AACGTACGAA	360
GTTGTAGTGC	GAACCGTCG	ACCAAGGCGG	ACAACATGAA	ATCAATTTAA	CTAGATTGAG	420
GTGCGATCTA	TTGGCAAAGG	TTTC				444

(2) INFORMATION FOR SEQ ID NO:1012:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1056 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1012:

CAAATCATCA	TATGCGCACA	ACTTGCTACT	GTACTCATAG	CATTTACATA	AATAGGGTTT	60
CACGAGCGTC	ATCATTAT	CTATTTCGTC	GTGTCCTTT	GTATTAATCA	TCTCTCGACT	120
TGTTACAATA	CCTACTAATT	TATACGACTC	ATTGACTACC	GGAAATCTTG	TATGGCCAGT	180
TCGATTGCGC	ATACGCTTAT	AATCTGCTAT	TTTCATCGTA	TCAAACAGCA	CAGACAAATC	240
ATCTAATGGC	GTCAATTATAT	CTTGAACAT	TAAGATATCT	TTTCGTATTT	TCTTGATTAA	300
AAAGTGCTTT	GTTGATAATA	TTTGCAACTA	GGAATGTATC	ATAACTCGGA	TGATAGAACA	360
GGGTAAATCA	TGTTCAATTC	GGCAAAATTA	ATAACTTTAT	TAGGATGGGC	TTAAATCCAC	420
CAGGTAATTA	ATATAGGCCG	NACCTCTTTN	NTAANGCTNC	AACCTGGCAC	ATCTTCGCGA	480
TTTCCGACAA	TCAATAATGT	CTTTGGACCA	ATATATTTTA	AAATATCTTT	GAGTTCCATG	540
GCTCCAATGG	CAAATTTAGA	TACCATCTTA	GTGATACCTN	TATGGCAACC	TAACACTTGG	600
CCATCAATAA	TATTGAAAAT	TTCATTAAAA	GTTAAATGTT	CAATTTTATA	ACGATTACGT	660
TTTTCGATTTC	GAACCGTACC	AACACGATCT	ATCGTTGCGA	CCATGCCCAT	TTTATCAGCA	720
TCTTTAATTG	CACGATATGC	TGTCCCTTCA	GATACGTTTA	AAAATTTAGC	GATTTTACGC	780
ACCGAAATTT	TAGAGCCTAT	AGATAACGAT	TCAATATAAT	CTAAAATTTG	TTTATGTTTT	840
GTCAATCTTT	ACCTCTTCCT	TTTCGAACAG	TATTAACTAC	ATTATAACTT	TATTTTGGAT	900
AAAAAGCATT	GAAGTGAAT	GAAATAATGA	TCGTTTCACC	TATTTTATTT	TTTGAAAATA	960
TACAACAANA	CACAAAGGAT	CACAAAATCT	TTAATTTTAA	ATGGAAAAAT	CCATTATTAT	1020
TTATTAGAAT	TGTAAGTGAG	GAGGGATTGT	ACTAAT			1056

(2) INFORMATION FOR SEQ ID NO:1013:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 690 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1013:

```

ATGCCTCNAA ATGTGCACTT GGGGTGNNCC CGATGCTAAA TGNAATAGAC AAGATGAGCG      60
GGATCGTTAG CNTTACTACC CAAAGATAAT CCTTCAGTG AAAGATGATA GTGCGAAANC      120
NACACCANTC TGTACATAAT CAGTACCAGC GTGAANAAGT GCAATATGTG GACTAATGAC      180
CATATATGAC CCGNNTTGTT CNGNACATTG TTTTAANNNG ANTTGCANCT GTATAATCTG      240
ANTAGACAAT GCCATCATTG ANTAAAGGNT GCACAGCCAC TNCAANTNCG GANTCAANTG      300
ATAATGGNTG TTCANTTATA NTGATNCGAT GTTCAGGACA ATAAATCTGC GAGTGACTTG      360
CCATCAGTTG CCATTTTCAT GACTCGNTGT TCTCTTGAGT CATTGATAAT TTGATTCAAT      420
TTTTGACGAG NTTGTTGATT GATAAATGGA TCGACATGAA TAACTGGTAC AGCTGATATT      480
TCACAAGGTA CTCGTTGAAA TGACATAANC AATGTTATCT TGCAATAATC GACTTTCCTC      540
CAATTGATAA ATGGAATAGG CATCCCAAAT GTGAAACTCA GGATACAGAT GATTTAGTTT      600
TGATTTTAAA AGTTGCGACG TGCCTATACC AGAACCACAT AGTAAGACAA CCTTAATCAT      660
TGATTGTTTA TGTGTTGCAA CACGCTCTAG                                     690

```

(2) INFORMATION FOR SEQ ID NO:1014:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1019 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1014:

```

GGCACGAGCT GATACATTAG ATATCACACC AAAATTAATG TTACAAGGTT CTGTTGACCT      60
ATTAAATGAA GTTGCAACTT CTAAAATCAC AGGTGAAGAA GAAATTTATT CACATACAGA      120
TTTATATGAT TTAAAGCGA ACGTTGAAGG CGCACAAAAA ATTTATGACT TATTTAAACC      180
TATTTTAGAG AAAAAAGATA AAAAATTAAG TGATGATATT CAAATGAAC TCGATAAAGT      240
GAATCAATTA TTGGATAAAT ATAAAGATAA CAACGGCGGT TATGAGTCAT TTGAAAAAGT      300

```


ATCGAAGAAA GACCGTAAAG CATTTGCGGA TCCTGTTAAT GCATTAGGGA GAGCCACTAA	360
GTAAATGGC CTGTGATTAC TTGAATGACA AATTATTGAA CAAGTTAACG GATAGTACNC	420
AATTTTCAAG ACGTACATTT TTGNAAATGT TAGGTATTGG CGGGTGCCGG TGTTC AATT	480
GGCGCAAGTG GTGTTGGTAG CATGTGGTCT TTCAAATCAA TGTTC AATAC ACCAGAAGAT	540
CCGGA AAAAG ATGCGTATGA ATTTTATGGT AAAGTNCAAC CAGGCATTAC CACACCCACC	600
CAAAAAACAT GCAATTTTCGT TGC GTTAGAT TTGAAGTCAA AAGATAGAGA TGCAATTAAG	660
GCAATGTTTA AAAAGTGGAC GGT TATGGCT GATCGTATGA TGGATGGTGA TACAGTTGGC	720
AAGACGAGTA ACAATCCTTT AATGCCACCA GTAGATACCG GTGAATCGAT AGGATTAGGT	780
GCAAGCAAGT TAACGATTAC CTTTGGGATT AGTAAGTCTT TGATGAAGAA AAATGGGTTA	840
TCTAAGTAAA ATTCCCGATG CCTTTAAAGA TTTACCGCAT TTTCCGAATG ATCAGTTAAT	900
AGACGATTAC AGCGATGGTG ATATTATGAT TCAAGCATGC TCAAATGATT CGCAAGTATC	960
CTTTCATGCG GTTCATAATT TAGTTCGTCC ATTTTCGAGAT ATTGTTAAGG TCTCGTGCC	1019

(2) INFORMATION FOR SEQ ID NO:1015:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1015:

NANACTGGTA ATTTACTTGT CCACTTGANA AGAATCCCCT ACCTCAATTT TAATTGAAGC	60
CGAAGAAAGT AAAATACCTG AAATCAAAAA TATGCTTACT CATTTTATG CCGNTCATAT	120
TGAGCATCGA CGCTGGGGCG CACCANTCCC TGNCATTGAA ATTGTAAAAC TTGGTATTAA	180
TAAAGCAAGA GGCATTGAGC AAGTTAGACA ATTTTANAT ATTGACCGAA ATAATATTAT	240
TGCATTCGGT GATGAAGATA ATGATATTGA AATGATTGAG TACGCCCCGCC ATGGTGTTGC	300
TATGGAAAAT GGTGTGCAAG AACTTAAAGA TGTAGCGAAC AATATTACAT TCAACAATAA	360
TGAAGATGGC ATTGGGTGCA TATTTGAATG ATTTCTTTAA TTTAAATATT AGATATTACT	420
GNTAATTTAT AACTAATCAT TNTATAATAT TTCAAAACAA TAGGAGGTAA GTTACGATGC	480
CCAAAATAGT CGTAGTCGGA GCAGTCGCTG GCGGTGCAAC ATGTGCCAGC CAAATTCGAC	540
GTTTAGATAA AGAAAGTGAC ATTATTATTT TTGAAAAAGA TCGTGATATG AGCTCGTGCC	600

(2) INFORMATION FOR SEQ ID NO:1016:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1016:

CTCNGCCCTG CCATGCCAAT CNGTCCCNT ACAAATATTT TTAATTATTT TAAAAAATGA	60
TGCNCTAAAT TAGGCACGAG CTTAGNAGNT CTATTGTCAG CGTCATATGT TGGATTTCATC	120
TCAGCAATAC TAACTGAAGA CACCTTATCA CTTGGAATAA TACGTTTTGC TAATTCAAGA	180
ACAGTATGTG GATACAAACC TAACACTGNC GGCGCACTTA CCCCAGGCGC AAACGCACTA	240
TCAATGACAT CCATACAAAT CGTAAACATA ATGACATCAT GTTCATGTAC AAAACGTTCA	300
ATCATATCTT TAATTGTTGG TGATACGTGA CTCAATAATT CATCTGCAA GACATAATCA	360
ATCTTTTTCT CTTAGCATA ATCAAATNAN CTTTGCGTAT TACCACCTTG AGCAAATNCC	420
AAGCACTAAA TAATCTGTGC TTTCATCTTC TTCTAAATT TGGCTAAAGC TCGTTCCAGA	480
TGTAGATTGT TGT	493

(2) INFORMATION FOR SEQ ID NO:1017:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 637 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1017:

GGGATTCCGT GGAGGCATCA TGTGGATTGA ATCTAAGTCA TTTACTAAAA CATTCGGAAT	60
GGGTATTCTT GATGCTCGTA TGCCTCCAAA CTCATTTCCT TAAACCTCTT GTAAAACTG	120
TGTCCACATT TTATCAGGTG ACGGTGCCC ACTATATACC AACGTATTAG CAAACATGCC	180
TAGCATTTCG TCCGTGCCTT TATGCATACG CGCACTCATC AACTACCGA CAACAACATC	240
ATCTTTTCGA GCATATCTGC TTAACAACGT CATGACCACA CTCATAAAGA ACATAAAATC	300
AGTAATTTGA TGCTTTTCTA CATACTTTTG AAGTAGCTGT CTCATTGTGT GATTCAATTGT	360
AAATGACATC ATTGCTCCAT TTGTCGTTTT AATATTTGGT CTAACATAGT CTGTCGGTAA	420
GCTTAAATA GGTACTTCAT CTTCTGAATT GAGATAACCA ACATTGTCTA TGTTTCCGTC	480
ATATCACGAA TGCACATCC ACCCACTATA GTCTCTATAT TGCAATTTAA GTGGTAACAA	540
TAATTTATGT TGATAAAGTG CGTTAAGATC ATTCATTAAT TGTATATTAC TCATACCGTC	600
CATTAATGAT ATGATGTGTA TCTATAAACA GTATGCA	637

(2) INFORMATION FOR SEQ ID NO:1018:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1032 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1018:

```

GGGAGATAAA TATTGCCAAT CAGGACAGAC CATGAAATCT ATGTCAGAGC AAATGTATAA    60
AATAGACAAG TTTCCCTCAA GATACGAATC ACCATCATAAC AATGTTTGGT GGTACATTGA    120
TGGCTAATAT TGATGAAATT GCAGCAATCA CAGCTATGAA ACAATGCTGG TGC GCAAGTA    180
GTTACCGCAT CTACAGACTC AGTAGATTTC TTAAAGCCGA TTAAACAGG GGACATATTA    240
CAATACGTAG CGATGGTTTC ATACGCTGGG ACTAGTTCAA TGGAAAGTGGT CGNTCACATT    300
AGANTTGTCTG ATGTATTTAA TAACAAGCAT GATTTAGCTC CATTAAGTTA CTTAACATTT    360
GTTGCGTTAG ATGATGAAGG CACACCTAAA CATGTACCTG GTGTATATCC AGAAGATGAT    420
GTTGTAAAAT GGTTTTATGA TACAGCACCA CAACGTGTTG AACGAAGAAA AGCACGTCGC    480
ATTGAAAGTA AACAAACAAN TGAATATTTA GCTCAAGTGC AACATATTAG AGACTAAAAA    540
TATAAAGACA GATTGTTAAG GATGAATTGA ACTGTTATGT TCGAATATTC CACCTACAAT    600
CTGTCCTTTT GATTATGCAC GTTTATGCTT TTAGTTAAAA TTAAACCTTT TTATTATAGA    660
CTATTAGTCC GATTGCCTNA NTGACCTTNA TTATNAANGT AGAGTACTGN CAGAAATTAA    720
TTGTTTTTTT TTNAATAATA GCATNAAAAT ATGCGGAGAC TACTTATCGA TAAAGTGCTT    780
CTCCGCATAA TTAAGAGTTT TAAAAATTGN NTAATNTGTG GGTGNANGNG CATATGACGC    840
TCATTATCTT TAAANTCCAT NTTCGGATAG TATCGTGCCA TATTTGTAAC AAGAACATGT    900
GGTCCTAAAC ANCTAACTC GGNACAATGA CAATNCANAT GATTNAGCAA GATCAGAGGA    960
TANCCATTTA TCAAATACAT CTAGTTAATT AATCTTTGNG TATATTCCGA AATAGTACCT   1020
AGTATCATCT CC                                     1032
  
```

(2) INFORMATION FOR SEQ ID NO:1019:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 840 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1019:

```

CCATCGAAGA GTATCGACAC CATTTAGAGC ATTTAGACCG CATAAGAATT AGCTTTTTTCA    60
CATATCATAG GTCTGATGCA GACATTGAAA TTGTTGAAGA AGACTTTGAT TTATAAGTTT    120
AAAGCAATTC CTGTAATTAA TACCACAATG AGATAAAGTA ATATTGAATC TCGAAATTAA    180
ATTTAAAAAA GCAGTAAGAT TATTTTCAAT GAAGAAAAATC TCTTACTGCT TTTCTATGTT    240
  
```

ATGACCCAC	CATCCTGTTA	CAAATCTTCC	CTACAAGATT	GTNCTGAAGT	CAAACAAC TA	300
ATACTTTATA	AGTTTGAAT	GCTATATAAA	TGCTCGCAAG	CAACTTGGTT	TGGAATCAAG	360
GCACGATGGG	TNCCCGTTTC	AACAAATATT	GTCCCATTTT	CAATTACGAC	AANTTNGGCA	420
GCA T N T T G T A	ATAGTGGACA	AAGCGATGCG	CTACGATAAG	TGTCGGTCGA	TCTTTAATCA	480
ACACATCTAA	TGCTTCTTGA	ATTANTGGAT	TCACTTTCTA	AATCAAGTGC	ACTTGTTGCT	540
TCATCCAAGA	TAAGAATTGG	CGGATTATTT	AAAAATATTC	TAGCAATCGA	TAATCTTTGT	600
TTTTGACCAC	CTGATAATTT	AACACCTCGT	TCACCTACTT	CAGTGT CATA	TCCCTGTGGC	660
AAGTTCATAA	TAAAGTCATG	TGCATTAGCC	ATTTTCGCCG	CTTCAACTAC	TTCTTCATCT	720
GT TGCTGN TG	GACGACCANG	TAAAATATTT	TCCTTAACTG	TATCAGAGAA	TAAAATATTA	780
TCCTGTTGGC	ACCCAATCCT	ATTTGATTTT	TTAAACTTCC	CGTTAAAAAA	TCTNTAATAT	840

(2) INFORMATION FOR SEQ ID NO:1020:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 774 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1020:

AATTTTAAAG	ACCCCNCGCA	TAAATANCCA	TCCCACCTAC	TTATCCAAAA	GTTANGTGG A	60
TGGTTTTTCA	ATTAA AATTA	ATATTAGTGT	AANCCAATCA	AAGATTTAAT	CNAATATGCC	120
CCTGCTCAAA	ACATTTCTC	ATTTAATTTG	CTTTACTTTC	AATTTAATAT	CATTATCCAC	180
AACACTTGGC	GTGTCATCGT	TATTATTTTCG	CATCTTTGAC	ACGTTTATCA	TCATTAGGAN	240
TCGGCACC GA	ATAAAATTGC	GATAAATGCC	ATGATTCCCA	TTAATACGTT	AACCCAAAGT	300
GCAATCATCG	CACCTGTATG	AATGCTCGTT	GCAGCAACTG	CACCAACATA	TACAGCACCA	360
CTAATTGCGA	CACCGAATGC	GCCACCAAGT	GATGAAGCCA	TTTTATAAAT	ACCTGAAGCA	420
ACGCCAACTT	TATCTAACGG	TGCATTCGAA	ATAGCTGTAT	CTGTAGAAGG	TGTTGCATAA	480
ATACCTAAGC	CTAGTCCGAA	ACATAAATAT	CCTACGACAC	AACTGATAAC	ATAAAATATG	540
CCTGGTAAGA	ATACTANTGA	AATAAGTGCA	ATNCCAATGA	CCACAATGNA	TGTACCTNAT	600
AACATTGGTC	GCTTAGAACC	CANTTNTGGT	NATAATAATT	TTTCACCAAC	TCGAATCATC	660
AATAACAACA	TGATTAAATA	AGTAANTGAT	NAGTATCCTG	CCTGCCATNC	TGTATAACCT	720
AAACCTTGTT	GCACGCATGT	ATTCGCTACA	ATTNATGTAC	CTACAACNCC	GTTG	774

(2) INFORMATION FOR SEQ ID NO:1021:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 773 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1021:

CTCTGATTCA	ACAAAATGAT	TATTCTTTAC	GTAACTACC	TTTTTTTATT	TGAGATGAAG	60
CATATGCTTT	TAATAATATT	GTCCCAATAA	TACCAACTGA	AATAATATTT	AATACTGCAG	120
AGATAACACC	TTGTGTATAA	ACCTTGTTAG	CCGGTTCGTT	ATAAATCAAA	ATATCTAATG	180
TTGGTGCAAT	AAGTGCCCAG	CAAATAATAT	TCGCAATAAT	TTGACCGATA	TTAAAATAAA	240
TCATCGATTT	CCTAGAAAAT	AGGCATGAAG	AAAGATTTAA	TTTTAGGGCC	AATCCATCCA	300
TATTAAACAG	GCGATAATTC	CTGAACAAAT	AACCCAACCTC	CACCAAGCAC	TACCCGTATG	360
TCGGGGAAAT	CTTTAATAGC	GTGNCCAAC	AATCCAGGCA	TTAAACCAGC	AAAAGGCCCA	420
AATATTGCAG	ATATTAATGC	TAAAAATGCA	TAAGATGTTT	CTATATTCGT	ATTAGGAAAA	480
CCTGTTGGTA	TTACAACAAA	ACGCCCTAAA	ATCACAAATA	CCGCNGCTCC	TATACCAATC	540
GCAACAACAG	TTTTAACTGA	AATATCNTGT	TTTTTCATCT	TCATTACTCC	TTACATAAAA	600
AATTCATTAA	ATTGATGGTG	CTTTAGATAA	ATGAATCGTC	CAATCATTTT	CAGTACCAAT	660
ATGATATAAA	TCTGAAAATG	AGTCTCGATT	GACTGCTACA	CCAATATTTA	CTAGCGAGTT	720
AACATACACA	AGAGGTTTAC	CCACATTAAC	ATCTGCAAAC	GATCGCTCGT	GCC	773

(2) INFORMATION FOR SEQ ID NO:1022:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 784 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1022:

CCTGCAAATG	TTACACCTGT	TCTCGCCAGG	ACGGTTGACT	GAGAACTTG	TTGTACGTTT	60
TAAAGACTTT	TCAGAAAGTG	AAAGTCTAGG	TGACATATCA	GAAATTTCCCT	GTAAATAATT	120
CTTTGAGTTC	CTTAGATTTT	TCATCTGANC	CAAGGCTGCC	AACGAATTCA	ACGTTGCCCT	180
CCATAAGTTC	TAATAATTGT	TTAAGTTGTT	GTTTTAAATC	AGCATTAAGC	ATGGNTGTAA	240
TGCCTCCTAA	GATTTTACCT	ACTAAATCTA	AACCAGGTTG	CAATGTTTTA	CCGCCTTCTT	300
CCCATTTAGC	TGGGCATACT	TCNCCAGGGT	TTTTACGAAC	ATATTGAGCT	GCTTTGATTT	360
TGTGAGCTAA	TGTACTAGCG	TCACGSCCAA	TTCCGTCAGC	GTTAATTTCA	GATGCTTGTA	420
CAACACCGTC	TGGGTCGATA	ATGAATGTAC	CACGTTGAGC	TAAACCAGTA	GCTTCATGCC	480
GAANACATCA	AAATTACGAG	TGATTGTTTG	TGATGGGTCA	CCAATCATAG	TGTAAGTGAT	540
TTTGCTAATT	GCATCTGAAT	GGTCATGCCA	TGCTTTGTGT	ACGAAGTGAG	TATCAGTTGA	600
TACTGAGAAT	ACATTTACGC	CTAATTTTTG	TAATTTCTCA	TATTGGTTTT	GTAAGTCTTC	660

TAATTCAGTT	GGACAAACGA	ATGAGAAGTC	AGCAGGATAG	AAGCATACTA	CGCTCCAAGA	720
ACCTTTTAAA	TCTTCTTGTG	TAACCTCTTT	AAATNGATCT	TTTTTTGGAT	CGAAAGCTCG	780
TGCC						784

(2) INFORMATION FOR SEQ ID NO:1023:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1164 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1023:

CCGACTTCTT	CTAAAGACCC	TTCAATCTTA	TCTTTATTTG	TCCATTTAGC	TACAACATCT	60
TTCGTAGGAT	TCATACCATA	TGAACGTCCT	TCAAAAATTG	CGCCTCTTGA	GTCACACATA	120
ACCATATTTT	TTACACCATA	CGCGTATAGT	AATTTAACAA	TGGNTATTCC	TGCTGCACCA	180
GCACCATTGA	GTACAACTTN	NATTTTAGCA	ATATCTTTGG	TAACAACTCT	CAATGCATTT	240
ACCAAACCTG	CCATTGTTAC	AATTGCTGTA	CCATGTTGAT	CGTCATGGAA	TACCGGAATA	300
TTAGTTTCTT	TTTCAATCG	GTACTTCAAT	TTCAGAACAA	CGTGGTGCCG	AAATATCCTC	360
TAAATTAATA	CCACCATAAT	TAGGTTCTAA	CGACTTAACT	GTTTAAATGA	TTTCTTCGGT	420
ATCAGTTGTA	TTTAACGCAA	TAGGCACCCC	ATTGATACCA	GCGAAGCTTT	TGAATAATAC	480
TGCTTTACCT	TCCATTACAG	GAATACTTGC	TTCAGGTCCA	ATGTTACCTA	AACCTAATAC	540
CGCTGTTCCA	TCAGTAATAA	CTGCAACTGT	ATTCCTTTTA	ATTGTGTAAT	CATATACTTT	600
TCTTTTATCT	TCATAAATAT	CTTTACACGG	TTCAACAACG	CCAGGTGAGT	ATGCTAAACT	660
TAATTCCTCT	TTATTAGTAA	CTTTACATT	TGGTTTAACT	TCTAATTTAC	CTTGATTACG	720
TTTGTGCATT	TCCAATGCTT	CATCTCTTAA	TGACATGAAA	TCAGCCCCTA	ATTCAATATT	780
TATTTTTAAA	AAATAACTTG	GATAAAACGC	ATTACATTAT	AAAAGTAAAA	ATATTGGGTA	840
AATCTGAATG	AGTAAGAATT	TATGGTTTTG	GATTATGTAA	CACAAATAGC	GATAAACGAT	900
AATAAAATAA	TATTTATAAA	GATACATTAA	ACCCATACTT	ATCTTAAAGA	TATTACCCCT	960
TAATTATTAT	AATGGATAGC	AAAAACAATA	TATCAAAAAG	TTATTATTTT	CCGCACGATA	1020
TATCCGACAA	AAATTCCTTT	ACTCAATTTA	TNGTATACTG	GTTNGGGGGC	TAATTATTCT	1080
TNATTGGATT	TAACAATAAT	TGTAAAGTGA	AACTCCATAA	AAATAATAAG	CATTAAAAAC	1140
TTATATTNAA	CGCAAACCTGA	TGGG				1164

(2) INFORMATION FOR SEQ ID NO:1024:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1018 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: lin ar

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1024:

```

CTCAGTTTGT TGTTTAATTT CTTACACATA ATAATATTCA TTCGCATTTA CTTTATCACT    60
TTTAGGATGA ATAAGCACGA CAATATTTTC ATCATTTTCT GTAAAAGGTA AACTTTTTCG    120
CTTACTTCTA TAATCTAATA TTTGCTGTTC ATTCATCGCA ATATCTTGAA TAATTAATTG    180
CGGTGATTGA TTACCATTC CATTGCTGAT TTGAACAGAT CCTAATATAT TAATTGGCTG    240
TTCATCTTGT AACTCAGGTT CTAAGTGTCC ATTTGGCCAA AATAGCACGA GCGNGATAT    300
TACTTTCACC AAGTGTCAAT TTTAGATGAT TTTNTGGTTG ACCGATCGCC TTAAGTGAAG    360
AAATCTGATA AATCATCCAT TTCAAAAATA GGTCTTAGAA AAATCTTGTN CCGAAGGGTC    420
TTAAACGATT CAATATCACG AATATTTTTC ATCGTTATAT CATTTTCTGT TAATAATACG    480
TCTACTGGCT TTACGGGATC TAACGAAGTT GTTTTAGATA ATTCTTTCAT CCATTTATTT    540
AAACCTTCAG CTAACGATTC TATATTTACA ATATCCATCG GACATACCTG NAGNCATATG    600
ATGGCCGNCC AAATTTAGCG ATTAACCTCT GATGGTGCTG ATAGTATTTT AAACATCGAC    660
ACTTGCATCA ATTGCATCTT GCGGAACCT TTTGGCATGA TTTTGCTCCC TATCAATATT    720
TAAAATTAAT GGTGGGCAA GCAAATGTTT CGACAATTTG CGAAGCAACA ATACCTAAGA    780
CACCTACATG CCAATTTTCT TTTGCTTAAA AGTAAAAATA AATCTCCCCT TTTAACTTCC    840
GGTTCTGCAA TAGCCATTGC TTCTTCTGTG ATAGTTGCTA CAATATCTTT TCTTTCACGG    900
TTAAATGTT CAACTTGTTC TGCTAAAAAT GCAGCTTCTT CTTCGTCGTC AGTCATCAAC    960
AATTCGCAAG CTAATGATGC GTCATCTAAA CGACCTACAG CATTAAGTCT AGGTCCAG    1018

```

(2) INFORMATION FOR SEQ ID NO:1025:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 678 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1025:

```

CCCAACCGTG CATGTGTGCC GTCGCATCTT GTTCCAACCT TCAATATAGG CCACGTTTGA    60
CCAATCGGTA CGAGTGCACC AAAGTGCAGT TCAATAGTAC CATGCTCTTT TCCATGCTTC    120
TATATGCGCA CGTGTACGA TGAATCATTG TTGTTGCTA CTCTGTTGAN AAAGTCCTAA    180
AAACCAATTA NCCGGCNAAT ACCCCAATTC CTTTAAATC CAATTGTCCT TTCTAAATAA    240
CGGTTTGTTC TCCGACCAA GTGGATTGGT TGATCCCAAT GTGAGTACCA TATTGCGTTA    300
CAATATTCCA ACGTTGCACA TAGAAACCAT GATCTTTAAC CGTGAATAAA GTTGAAACTT    360
CACCTTTTTC AAATCACTA AAACGTGGTA TTTCTGGATC AAATGTATGC GTTAAATCAA    420

```

CCCAAGTTGC TTGTTTTAAA GTATTTAATT GTTGCCATAA AGGATATTGT GTCATAAAAT	480
CACCCGTTTT TAGTTTATTA TATGATAAAT GCTGCGATTA TTCTTGGCGT TTAGCTTTAA	540
CAGCATTAC AAGTACAGTC AATGCATCTT TAACTTCTTC TTCTTTTCGC TCGTGCCAAC	600
CACAGTCAGG GTTTACCCAG NATAATTGAG CGGCCGATTT GTTGTGTGA ACGATTGATT	660
GCTGTAGTAA TTTCTTCT	678

(2) INFORMATION FOR SEQ ID NO:1026:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 547 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1026:

CTGAAGATGA TGAAATGATT TTTAATATTC CGGCACGAGA CTATTGAGTA TAAATATGGA	60
CAAGCGATTT ATGGAGTCGG AGCAGGTATT ACAATTGATT CTAAGCCAAA AGATGAAGTA	120
AATGAATTTT ACGCAAAAAC CAAGATTTTG GAGATGTTAT AATGCAATTA TTTGAAACAA	180
TGANAATTGA TAATGGACAT ATCCCTAGAC TTACTTATCA TACTAATCGC ATAAAATGTT	240
CTTCTGAGCG ATTAAACTTT AAATTTGATG AACATGCATG GCGAAATGAA TTAAACGATG	300
TAACAACAAA GTATCACAGT GGTCATATA GACTTAAAAT CGTATTAAAT GCTGAAAGCA	360
AATTTGAAAC GATAGTGTC CCTTTACCTG AGAAAAGTAG TTTTACAGCA AAATTTCAAG	420
TGTTGCCCCA AAGTTAGTTA ATCCAACCTT TATANNGAAA TAAAACGACN GAACGAAAGC	480
ATTTAGCACA CAATCNATGA AACGATTTAA TATTGCTACT TCCAGAGACG GCAGTCCCTT	540
GATTTGA	547

(2) INFORMATION FOR SEQ ID NO:1027:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 457 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1027:

GCCTGTGGTT CCAATCATTT CANTTATCGG TTGTCCTTAC NTTTTAATAT TTAAGTTANA	60
AAAAGGAGGA CGCTCCAATA TGATTAGTTC CAAATAATAA ACGCAGACAA TTGATAGCAC	120

TGCCTGTTTT	TAAGCATTCT	ACTATTTCTA	GGTTGTACTT	GGAGTATTAC	CTCAGGTGAA	180
TACAACATAC	CTGTTGAAAG	ATTTTCAAAA	ACTTTAATTG	GACAAGGTGA	TGCCATTGAT	240
GAGTTAATCT	TATTAGATTT	CAGGTTACCT	CGGATGATGA	TTACTATTTT	GGCTGGCGCA	300
GCGCTTAGTA	TTAGTGGTGC	AATAGTGCAA	AGTGTCACAA	AAAATCCAAT	AGCTGAACCA	360
GGTATATTAG	GTATTAACGC	AGGTGGCGGA	TTTGCAATCG	CATTATTTAT	TGCAATTGGT	420
AAAATTAATG	CTGACAACTT	TGTTTAGGTC	TCGTGCC			457

(2) INFORMATION FOR SEQ ID NO:1028:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1028:

CTGCCATTGG	ATACTTGTGG	TGCCATGTCC	CCGGGTATGA	TAGGCTATTG	GTTGGAACT	60
GAAATCAATC	GCATTTTAAC	TGAAATGAAT	AGTGATAGAA	CTGTAGGCAC	AATCGTTACA	120
ACGTGTGGAA	GTAGATAAAG	ATGATCCACG	GATTCAATAA	ACCCAACCAA	ACCAATTGGT	180
CCTTTTTATN	CGAAAGAAGA	AGTTGGAAGA	ATTACAAAAA	GAACAGCCAG	ACTCAGTCTT	240
TAAAGAAGAT	GCAGGACGTG	GTTATAGAAA	AGTAGTTGCG	TCACCACTAC	CTCAATCTAT	300
ACTAGAACAC	CAGTTAATTC	GAACTTTAGC	AGACGGTAAA	AATATTGTCA	TTGCATGCCG	360
TGGTGGCGGT	ATTCCAGTTA	TAAAAAAGA	AAATACCTAT	GGAAGNTGTT	GAAGCGGTTA	420
TAGATAAAGA	TTTTGCTAGT	GAGAAATTAN	CAACGCTGAT	TGAAGCAGAT	ACCTTAATGA	480
TTCTTACGAA	TGTAGAAAAT	GTATTTATTA	ACTTTAATGA	ACCTAATCAA	CAACAAATCG	540
ATGATATTGA	TGTAGCAACA	CTGAAAAAAT	ACGCTCGTGC	C		581

(2) INFORMATION FOR SEQ ID NO:1029:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 933 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1029:

CTACATTATT	ACTTACGCTT	AAAATGCPTT	AAATTTAAGA	AATGATATAA	GTTAGGTGCC	60
------------	------------	------------	------------	------------	------------	----

CAGGTACTAA	AGTTTAGTAG	GAATCCATCA	TGTCCAACAT	TATCAGGCAC	GAAGAAATGA	120
CGATGATATT	TAAAACGTTT	ACCTAATGCA	CGAACTTGAT	CGTCCGGATA	TAGCAAATCA	180
TCTATGAACC	CCATCGNTAA	GACTTTCGTT	TCTAAATTTT	TAAAAATATG	CGTTACGTCT	240
GTGCGACCTC	GGTCAATGTT	GTGACTATCC	AATACATCTA	GCAGTGTCAG	ATAACNATTC	300
AAATCAAAAT	GTTCTTTAAA	TTTATTACCT	TGATGTTGTT	GGTATGCGAC	TNCTTCATCC	360
GGCGTGAAAC	GTTCATCATA	ACTTTTGTGAT	GATCGATATG	TCAAAAAACC	TAATTGGCGT	420
GCAATACTTA	GACCTTCCTT	ACCACCAAGA	TGAATGGCTT	GCCTTGCAAT	TTCATTGAAA	480
GCTCTACTAT	AAGATGATGT	TCGACTTGTT	GCAGCAAGGA	TAATGGCTTT	NTCTACTTCA	540
AACTGTTGAT	TGTAAGTAG	CTCCATTGAT	TGCATACCTC	CAAGGACTTC	CCCCTATNAA	600
AATATTAATC	TTATCATAAA	CAAGGGCTTG	TATACCTCGC	ATCATGCGCT	CTGACTATAT	660
CTCTTAATGT	TAATTTTTTA	GGAAAATGAG	GGTCGTTTAA	AGGTGAACTT	GAGCCGAAAG	720
GACTACCAAT	AACATCAAAT	GTTAAAAATT	GATAATCGNG	AATGGGTATT	TTTCCCCCCA	780
TCANTAATTT	CTCGTCACCA	ACCCGGATAA	TCANCTTGTT	CCATATTGTT	AANTGATTGG	840
CAGGNTAATG	CATGACAAAC	TACAACTAAT	GGTTGTCCAT	GATAACCAAC	ATGNTCATAT	900
CTCAAACGCA	AGTATCTATG	ATTCCCCAGG	TCT			933

(2) INFORMATION FOR SEQ ID NO:1030:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 547 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1030:

GGCACGAGCG	ACAGGTTTTT	TAGGTGCTTA	TCTGATTGAA	GCACTACAAG	GCATACAGTC	60
ATCGCATTTA	TTGTTTCATA	CGTGCTGATA	ATGAGGAAAT	AGCATGGTAT	AAGTTGATGA	120
CGAATTTAAA	TGATTATTTT	TCAGAAGAGA	CGGTTGAAAT	GATGTTATCA	AACATTGAAG	180
TCATTGTTGG	TGATTTTCGAG	TGTATGGATG	ATGTTGTTTT	ACCTGAAAAC	ATGGATACNA	240
TTATTCATGC	ANGTGCTCGT	ACGGATCACT	TTGGTGATGA	TGATGAATTT	GAAAAAGTAA	300
ATGTTCAAGG	TACTGTTGAT	GTCATACNTG	TGGCACAACA	ACATCATGCA	AGGTTAATAT	360
ATGTGTCTAC	GATAAGTGTG	GGAACTTATT	TTGATATAGA	CACAGAAGAT	GTGACATTTT	420
CAGAAGCGGA	TGTCTATAAA	GGGCAACTAC	TAACATCACC	ATATACACGG	AGCAAATTTT	480
ATAGTGAATT	AAATATTAGA	AGCTGTAAAT	AATGGCTTAG	ATGTCGATTG	TACTGTTGGT	540
ATTTGAC						547

(2) INFORMATION FOR SEQ ID NO:1031:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1031:

```

AAGTATTAAC AAGACCATGA AATTATGGAT GCAGCTGATT ATTGGAAGTT AACCCAACCA      60
ATTAAATTTG GCACGAGCGG ATGTAATTAC CAAATACCTA GGTGTTGCAA GAAGATGCAT      120
CNAATTAAAG CAGCTATTGA AGAAGCTCAT AAAANTAATA AACAATTACT AGTTGATATG      180
ATTGCTGTTT AAGATTTAAG AAAAACGTGC AAAACAATA GATGAAATGG GTGCTGATTA      240
TATTGCAGTA CACACTGGTT ATGATTTACA AGCAGAAGGG CNATCACCAT TAGAAAGTTT      300
AAGAACCGTT AAATCTGTTA TTAAAAATTC TAAAGTTGCA GTAGCAGGTG GAANTAAACC      360
AGATACAATT AAAGATATTG TCGCTGAANG TCCTGATCTT GTTATTGTTG GTGGCGGAAT      420
CGCAATGCA  GATGATCCAG TAGAATGCTG CAAAACAATG TCGCGCGTGC CNTCGT          476

```

(2) INFORMATION FOR SEQ ID NO:1032:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1032:

```

AGCCGCTGGT GTCAATTTGT GAGATTATGA ATGATGACGG CACCGATGGC GAAAGGACCA      60
AGATTTACCA AAATTTTAA AAGAAAAACA TCAATTAAAG ATGATTACGA TTGATGATTT      120
AATTGAATAT CGTAAAAAAT TAGAACCAGA AATTGAATTT AAGCCCAAAA GTGAAAATGC      180
CTACAGATTT CGGAACATTT GATATGTATG GTTTTAAAGC GACATACACA GATGAAGAGA      240
TAGTTGTACT GACAAAAGGT GCAATTCGAC AACATGAAAA TGTACGCTTA CATTCTGCGT      300
GCCTTACAGG CGATATTTTC CATAGTCAAC GTTGTGATTG TGGTGCTCAA CTTGAATCGT      360
CTATGAAGTA TATCAATGAA CATGGTGGCA TGATTATTTA TCTACCTCAA GAAGGTCGTG      420
GCATAGGATT GTTAAACAAA TTACGCTCGT GCCACGAGGA T                          461

```

(2) INFORMATION FOR SEQ ID NO:1033:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 696 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1033:

```

AAATTTCCAA GGCCAATTGC CATACCATT TTTGTTTCAGT ACATATTTAA ATAAAATTCC      60
TTTGTAGTAA TTCTGTTTCT AATGTTTCTT ATCGCTTGTA GCAAAGTCGT TTTTATAAAT      120
TTCGATTGGA GGTAAACCTT GAGATTGAGG TGTGTCTCTA ATCAATACGT ATGAAATTGC      180
GCCAATGATA AGTGATAAGA GTGCAGGGTA AATGAATACA CCTTCGAAAC CTTTAAATA      240
ACCAAAGTTG ATAAATGCTG TTGTTGTAAT ACCCCAAGCA GCAATAGGTG CCATAATACC      300
TCCACCAACA TTATGCGCAA CGTTCCAAAG GGCAGTCTTA CTTCCGCTCG TGCACCTACA      360
CTAAACCAGT GAACGAGAAC ACGGCCTGAA GGTGGCCAGC CCATACCTTG AAACCATCCA      420
TTTAAGAATA ATAGGACAAA CATAATACCG ATACCTGATG TAAAGAACGG TACAAATCCC      480
ATTAACAAAT TGACGATAGC AGTGAGTGCT AATCCAAGAA CTAAGAATAT CCGAGCATTG      540
CTCCGATCAC TTACAGTACC CATAAAGAAC TTACTAAATC CATATGCGAT GGAAACAGCA      600
GAAAGTGCAA AACCTAGTTC CGCTTTTGTA AAACCTTGCT CTTGCAATGC TGGCATCGCT      660
AATGAAAAGT TTTTACGTAA TAAATAGTCT CGTGCC

```

(2) INFORMATION FOR SEQ ID NO:1034:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 888 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1034:

```

ATCTGAGAGT TNCAATTTCA CCAATGATGC AGTACGGGTG TGTCTCTGTA ATCGACAATA      60
TTGCGGTAAT TATTAATATC TGAAACCGTT GCCTTACCCT TATCAATTAA ACGCTCAAAGT      120
GTAGATGTTT CGATTACCTT TTGCAAATAT CCNTTCTAAA CGTTTGAGTT CTNTTTGTAT      180
TTTGTATTAT TAGGTTCTGA ATTTAATAAA AATAACAATT CTCCATAGTA TTGGTTTAAT      240
ACTGGGCGAT AATTTGTATC GTTTTGTCT GATTAACTT TCGTTTTTAA AATGCTTGTA      300
TCACTTTTTG AACAATGAAA ATTTTGCAA GATTGATAAG TCATACCTTT AAAAGTAGTA      360
TCTTCGGCAG ATGGTGTAAT TTAAAGGTAA AAACAATTTG CGCTAAGATT AAACATAATTA      420
ATACCATGAA AGATGCAATA AAACAATAAA TCATTACGGT ATTGGAATGC TTGTCCTTTT      480
GTAATGATAA ATGGTAATGT AAGTGCCATT GAAAGTGAAA ATTGTACTCG TGAATACCAC      540
ACATCGTCAT AATAAATGCG TAACGCACAC GAGAAGGTGG TGTTCATGT GAATCATGTT      600
CTTCGTCTAG ATAAGATTGT ATATTTTTCG GGAAATAAAA ATCTTTGTAC CAGAAATAAA      660

```

CCCAAACAAA	TCGACATGCA	TAAATTGCAA	TAGCGATTAA	TATAGTGATC	ACTATTAAAA	720
TGAAAAGTTG	TCAGGCTCTG	TTTGAAAAAT	ATCTATGACT	ACAGTAGGAA	TCATAAAACC	780
TAATACAACA	AATACAAAAC	CATTTAAGGC	ATAACTAAAT	GTGTTCCAAA	TTTGATGGTA	840
ATTCATTTGT	AGTTCCGTTT	GTGCTCTAAT	TAAACGGTCG	CTCGTGCC		888

(2) INFORMATION FOR SEQ ID NO:1035:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 563 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1035:

CTAGTTTTAA	CACTGGAACA	TTGAGCGTTT	TGCTACTTGT	AAATACTAAT	GGAATCAGTA	60
AGACTAAACC	TACTTCAAAG	AACAATGCAA	TACCGACGAT	AAATGCTGCA	ACCAAGCATT	120
GCCCATTGTA	CATGTTTTTG	ACCAAATTTT	TGANTCAACG	TGTCTGCAAT	TCGAGTTGCA	180
CCACCACCAT	CAGCAAGTAA	TTTCCCAAGT	ATGGCACCTA	AACCGAATAT	TAGTGCAATG	240
TGNCCGAGCG	TNCTGCCCAT	CCCTTTCTCA	ATCGTCTCCA	TAATTTTAGT	CAATGGTATA	300
CCTAGCATTA	ACGCTGTAAT	CATCGATGTG	ATAATTAATG	AAATAAATGT	TATTTAATTT	360
AAACCCAATA	ATTAATACTA	ATAAAATAAC	GATACCTAAA	ACAACACTGA	TTAACGGCCA	420
TATTTTCGTTA	AACATGACAT	TCCCTCTTTT	CTCTTTTCAA	TAGAATGTAA	CACCGTCGTC	480
GCGCACGTAC	CTTCCAGATA	ATATATAGTA	GTCATGGCAC	AACAACTTTA	TCTAAGATGC	540
TTGAGTGACG	TATTATTGTG	TTT				563

(2) INFORMATION FOR SEQ ID NO:1036:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1036:

CCGATATCAA	ATATATGTNG	AAATAGCTCT	AATTTTTTCAT	TACTTTTCTT	ATCACTACTT	60
AATTCCTTGG	CCTGTTTAAT	AGGATCTCAC	AACATGTGAT	TGATGATACT	TTGTGTATGT	120
TTAGATATAA	TTTTACGTTC	TCTTTTCGCTT	AACCCTGGCA	ATTTACGATC	AATACTGTCC	180

ATCGTTTCTG	CTTGAATTGC	CATAGCTTTC	ACACGTAAAG	CTCTAATCAC	TGGAACAACA	240
CCCAACATAC	TAATCCACTC	ATTGTGTGCA	TGTATTTCTG	CAGGAATTTG	TTCCGAAATT	300
GTTGCAGCCG	CTAATTGTCG	CTCACGTAAG	TNTGCATCAA	CTTAAACCTT	TTAAGTCATC	360
AACAACATAA	TTAAAGATGT	TGGTGATGG	CACTTAATAC	AGGTTCCAAT	ATCTCGAGGA	420
ACTGCAATAT	CAATCAATAC	TAGTGATCTT	GCTTCTATT	CTCTGCAACT	CCTTCTATCA	480
ATTCATTTGG	TATGATATAG	ATGG				504

(2) INFORMATION FOR SEQ ID NO:1037:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1037:

CATCCAAAGA	CATNTAGTAC	TNGATGACTT	NCGNTTAATA	TGTAAANCAC	GAGCGTGCAA	60
TTTGCTCAGT	TACNTCTGAC	ACTGCTGCTG	NCCCCANAGA	TTTATAACCA	TGGAATATCC	120
CTCTCCATNT	CGCTAATACA	GGAATAAAGA	TAACAACCAT	ACTAATGATT	NNTATAATCC	180
ANGTAATATC	ATCGACTGAC	CANCCGGTTT	TATCATGAAT	GTTTCTAGC	TNATNGTAAT	240
TCAGAAATAT	AAGGTGCTAA	GNAATNCAGT	CACGTGCCAA	GAAACCTAAA	ACACCGGTAA	300
TACTCATTAC	AATAAACTC	GATTTATAAA	ATTTCTGACT	TACTTTATAT	GCCCCAATAG	360
CATTATATCT	CGCAACATAT	TTCGAAGCTG	CTTAATGGTA	CACCTGCTGT	CG	412

(2) INFORMATION FOR SEQ ID NO:1038:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 632 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1038:

GGCACGAGCT	CATAATATCA	AAAAAGGTGC	AGAAGAAATG	GTTGAACCGG	CAGGCGATAA	60
AATCAAAGAT	GGTGCATCTT	GGTTANGCGA	TAAATCGGC	GATGTGTGGG	ATTATGTACA	120
ACATCCAGGG	AAACTAGTAA	ATAAGTAAT	GTCAGGTTTA	AATATTAATT	TTGGAGGCGG	180
AGCTAACGCT	ACAGTAAAAA	TTGCTAAAGG	CACGAGCGTA	CTCATTGCTC	AAAAAGAAAT	240

TAGTAGACAA AGTAAAATCG TGGTTTGAAG ATTTTGGTGG CGGAGGCGAT GGAAGCTATC	300
TATTTGACCA TCCAATTTGG CAAAGGTTTG GGAGTTACAC AGGTGGACTT AACTTTAATG	360
GCGGTCCTCA CTATGGTATC GACTTTGGTA TGCCTACAGG AACGAACATT TATGCTGTTA	420
AAGGCGGTAT AGCTGATAAA GTATGGACTG ATTACGGTGG CGGTAATCCT ATACAAATTA	480
AAACCGGTGC CTAACGAATG GAACTGGTAT ATGCATTTAT CTAAGCAATT AGCAAGACAA	540
GGCCAACGTA TTAAAGCTGG TCAACTGATA GGGAAATCAG GTGCTACAGG TAATTTTCGTT	600
AGAGGAGCAC ACTTACATTT CCAATTGATG CC	632

(2) INFORMATION FOR SEQ ID NO:1039:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1039:

GAATTCGGCA CGAGCTAGCC CAGCCATTAG AGCCATTAGC TCAGTTGGTA GAGCATCTGA	60
CTTTTAATCA GAGGGTCAGA GGTTCAATC CTCTATGGCT CACTACTTGC ACTTTCATT	120
TGTGGGAAGT GCTTTTTTTT ATGAAGTAAT AAGATAAACA GATTATATGT GTAGCTATTG	180
CTTGATAATG GTAAGCGCAT ACATTATTCT TTAATTACAT AGAGCAAAGG GGGACGCTTA	240
TGACAAAGAC AAAAGCAATT GATATTATAG GTGCACCATC AACATTTGGA CAAAGAAAAT	300
TAGGTGTTGA TTTAGGACCA ACAGCAATTA GATATGCTGG ATTAATCTCA AGATTAANGC	360
AATTAGCACC TTGATGTATT AGACAAGGGG GGATATTAAG GNACCTGCTG TGAACATTGA	420
AAATTTTATA G	431

(2) INFORMATION FOR SEQ ID NO:1040:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1040:

CTAGGCACAA TAAGCTATGT AAAATATATA GCCTAGTTAA GTATGCAAAG GGAGCGTTAG	60
ATTTATGCAG ATAAAATTAC CAAAACCTTT CTTTTTTGAA GAAGGCAAAC GTGCCGTGTT	120

ATTATTACAT	GGATTTACAG	GCAATTCGTC	TGATGTACGT	CAATTAGGTC	GATTTTACAT	180
AAAAAAGGGA	TATACTTCGT	ATGCACCACA	ATATGAAGGT	CACGCGGCAC	CACCAGAGGA	240
AATACTGAAA	TCTAGTCCTT	TCGNTTGGTT	TAAAGATGCG	TTAGATGGNT	ATGATTATCT	300
NGTTGAACAA	GGTTATGATG	AAATTGTTGG	GTGCTGGTCT	ATCATTANNA	GGGTGGGGAT	360
TTTGCCTTTT	AAAATTAAAG	CTTAAATAGA	AATGTTAAGG	GTATTGTAAC	CATGTGTGCA	420
CCAATGGGTG	GCAAACTGA	AAGTGCCA				448

(2) INFORMATION FOR SEQ ID NO:1041:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 690 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1041:

CTAGATGATA	CTGAACCAAA	AATTTATGCA	GTTCGTGGTC	CATCTGGCAT	TGGTAAAACT	60
ACTGTTTTAA	ATATGATTGC	CGGATTACGT	AAAGCAGATG	AAGCTATTAT	CGAAGTGAAT	120
GGGCAATTGC	TTACTGATAC	GACAAAAAAC	GTGAATGTTA	AAATNCAACA	ACGACGTNTT	180
GGATATCTGT	TTCAAGACTA	CCAATTGTTT	CCTAATATGA	CGGTTTATAA	AAATATTACT	240
TTTATGGCCT	GAANCCCATC	TAAACNACAT	CGATCAATTA	ATTCAAACCT	TAAACNATTA	300
ATCATNTGAT	GAAACAATAT	CCTATGACAT	TGTCAGGTGG	AGAGGCACAA	CGTGTAGCAC	360
TTGCACGTGC	ACTTAGCACG	AAACCAGATT	TAATTTTATT	AGATGAACCT	TTTTCTAGTT	420
TGGATGATAC	TACACAAGAT	GAGAGTATTA	CATTAGTTAA	ACGTATTTTC	ANCGANTGGC	480
ANATACCAAT	CATATTTGTG	ACACATTCAN	ACTATGAAGC	AGANCACATG	GCTCATGAAA	540
TTATTACAAT	TGGGTAATCA	TTTATTTGCC	ATTAAAGAGT	TTAGAACGTA	TTTAAATTCG	600
TAGAAGTGAA	TGCTTCTATC	AGCATTTTAA	TGATGTTTAA	AACTCTTTTT	TAGGGGCAGT	660
TTTTTTTGAGA	GACATTGACG	CGCTCGTGCC				690

(2) INFORMATION FOR SEQ ID NO:1042:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1042:

CCCATATATT	AGTTAAAATC	AAGGTCAGGA	TAATGACAAT	GCTTTTAAAG	TTTtagctac	60
ATCCAATACA	TATTATAAAA	ATAAAACACA	TTTGAACGG	AGTATACAAT	GATTCTAGTC	120
ATAGATAATA	ATGATTCATT	TACATATAAT	TTAATAGACT	ATATTAAGAC	TCAAACGAAA	180
CTAACAGTTC	AAGTTGTTGG	TATTGATAAT	CTGCTGATAG	AAGACGTCAT	TAATATGAAG	240
CAAAAGCAAT	TGTTATTTTCG	GCTGGGCCGG	GTATCCGGA	TGATTATCCT	ATCTTGAATG	300
AAGTGTTAGA	ACAATTTAAT	CAGGCACGAG	TACCTATACT	AGGTGTATGT	TTAGGATTTTC	360
AATGTATCGC	GTCTTATTTT	GGGGGAGAAT	ATCAATCACG	GCTATCATCC	TGTNCACGGA	420
CATACTACAC	AGGTACGCCA	TACCAATGAA	GGTATTTTTC	AAGGACTGCC	TCAAAATTTTC	480
AATGTAATGC	GTTATCATTC	ATTAATTGCT	GACGGAGCGA	CTTTTCCAAA	TTGCTTAAAG	540
ATTACAGCAA	AAAACGATGA	AGCGATTATT	ATGCGATTTG	AGCATATTAG	ATTTCCGGTT	600
TTTGGTGTGC	AATATCATCC	TGAATCTATT	TTGAGTGAAT	ACGGTTATCG	ACAAGTTTGA	660
ATTATTTTTA	TCGAAGGTAG	GTTGATTACT	GTGAGAAATA	GAATATAATT	ATCGCTACTA	720
TTTAACTGAA	AATGAATATA	AGCAATACCA	TATTCAATTA	AAGGATTTAT	CAAGAAGTAT	780
GTTGCTACTA	AGTTGGCTGA	TGTGGGAGAA	GTGATACACT	TTGCACAAGC	GCCA	834

(2) INFORMATION FOR SEQ ID NO:1043:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 592 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1043:

GGCAGGAGCG	CTTGTTGTGC	ATCGACTAAG	TTCAATTCAA	TTTCTCTAGG	ATTTTTAAAA	60
CTTCTTTTAA	CAGCGTCTTT	AGTTATTTTCG	TTGAAAACAA	GCGTGCCGAT	TTTCTTTAGA	120
ATCTTCAAGC	TCTAAAATTT	TTGATAAATG	CCAAGCAATT	GCTTCACCTT	CACGGTCGGG	180
GTCACCTGCG	AGAAAGACGT	TTTTCGCTTT	TTTTCATGT	TTTTTCAATT	CTTTTACAAC	240
AGGACCTTTT	CCGCGTATTG	TTATATATTT	TGGGTCGGAA	TTATCTTCAG	TGTCGACACC	300
CATTTGACTT	CTTGGTAAGT	CTCTTGACGT	GTCCCATGGA	AGCTATAACT	TTATATTTCT	360
TACCCTAAAT	ACTTTTCAAT	GGTTTTTGGC	TTTTGGCAGG	GCCAATCAAC	AATGAATAAA	420
TTATCTGCCA	ATGTCATTTT	CCCCTCGCTA	ATCTAATTAC	TAAAGATAAT	GATAAACGCT	480
TAATTTTGCT	TTTGTCAACG	TTTATATCT	AAACAAATCA	TTTCCCTGTC	TATTTTATA	540
GATTTATAAA	ATAATACAAG	GTACAAAGAA	TATGAGCACT	CGTATTTAGT	TT	592

(2) INFORMATION FOR SEQ ID NO:1044:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 803 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1044:

```

CCCNACATAN TTAGATATCT GTCNTCCNAT AAGAAATNCT AGAATTAGTT CAGAAGCTAN      60
ATCNGGACCA AGGTTGNACA ATTGTCATGG TTCTTCATGA TATCANCCAA GCGATTCGTT      120
TCTCAGATCA TCTTATTGCG ATGAAAGAAG GGGATATCAT CGCTACAGGT TCAACAGAAG      180
ACGTATTAAC ACAGGAAATA TTAGAAAAAG TTTTAAATAT TGATGTTGTT TTAAGAAAAG      240
ATCCTAAAAC TGGAAAACCT TTACTGGTAA CTTATGACTT ATGTCGCACG AGCTTATCT      300
TAATTAAGTA AGTTAATATG ATAAAAAGGA CAATTAACAT GACAAATAGA GAGAACCCAA      360
CGCCATTGAA GTTTTNTCC TATNTTAGAG GTTTAAGTAT GATACTACTA ATCACACTAT      420
TTATTTCTAC ATTAATAGGT GACGCCAAAA TTCAAGCCTC TACAATTATA GAGGCTATTT      480
TTAATTATAA TCCTAGCAAT CAACAGCAAA ACATCATCAA TGAGATTAGG ATTCCCAGAA      540
ATATAGCAGC AGTAATTGTA GGTATGGCGC TTGCAGTTTC TGGTGCGATT ATACAAGGTG      600
TTACTCGTAA TGGTCTTGCT GATCCGGCGC TCATAGGTTT AAATTCAGGT GCTTCATTG      660
CTTTAGCATT AACATATGCA GTTTTACCAA ACACTTCATT TTTAATATTG ATGTTTGCTG      720
GATTTTAGGT GCTATTCTAG GAAGTGCTAT GTATAATGAT AGGCCGATCT AGACGTGATG      780
GATTTAATCC GATGCGTATA TTT                                     803

```

(2) INFORMATION FOR SEQ ID NO:1045:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 577 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1045:

```

GGCACGAGCT AATGCGAAGC GTGATCAAAT CANTTCAAAT CCAGATTTAA CACCTGAGCA      60
AAAAGCAAAA GCGCTCAAAG AAATTGACGA AGCTGAAAAA CGAGCACTAC AAAACGTTGA      120
GAATGCTCAA ACTATAGATC AATTAAATCG AGGATTAAAC TTAGGTTTAG ATGACATTAG      180
AAATACCACA TGTATGGGAG GTTGATGAAC ACACCTGCTG TAAATGANAT TTTTGAAGCA      240
ACACCTGAGC AAATCCTAGT TAATGGTGAA CTCATTGTAC ATCGTGATGA CATCATTACA      300
GAACAAGATA TTCTGCACA CATAAACCTA ATTGATCAGC TTTCAGCAGA AGTTATTGAT      360
ACACCATCAA CTGCAACGAT TTCTGATAGC TTAACAGCAA AAGTTGAAGT TACATTGCTT      420
GAGGGATCAA AGTGATTGGT AATGTTCTCG TAAAAGTTGT GAAAAGATTG TCAGTAGTCA      480

```

ACAACAGGCA ATGATCAATC GAAATGCGGA CACAAAGTTG GTGAATCAAT ATAGTGTGAC 540
ATTACACTGG ACAAAAGGAG CTGCAATGAG AGTTAAT 577

(2) INFORMATION FOR SEQ ID NO:1046:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 688 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1046:

TTATTGGACC CGGAAAATAT TACCCAGGTT AAACCCTATT CAGTNCAGCT ATTTCCCTAT 60
CCCTATGGTC ATGGGTGTGG AGGTGTTCCC GCACCATGAT GTCAAACAAT ANCCACATAT 120
CCCTGCTACA GAAATTATGA GACATTGNCC GACACATCCG AACAATCAAC ATAAAGGTTA 180
TGCTGGACAT CACTTATPCA TTAAGCTTGN CAATTATCAT CAAACGGATA TTCCAGAAG 240
CATATGTACC ATTTTACAA AAATAACAAT CCTAATATTC GTAGACGGCA CTGGTAAATC 300
CTTAGAAGAT CTAAAGGTA TTATCGATCA AGGTCAACCT GTGTTAATAT ACCATACTAA 360
TCTTGGCTCT AAACCATTAC TACGTGTTTT CCGCTTTGAT AACAAGCCAG CGAAACAAGT 420
TTCAAATATT CACGTAACGG TACTCATTGG GTACGATGAT TACTATTACT ATTATATCGA 480
TCCACTTTGG AGTCATATTC GTCGTGGCCT AGTTTTACCT GCCATCATT CAAATCGCAA 540
ACAAATTATT AAAATTCGTA AAGAGAAAAT GGAATACAGC TTTAATTCAC CAGGAAGAAA 600
ATGCATTTAT GTGCAACCAC ATTCATATAC AATTGAAAAT CAACAACAAA ATAAACACAC 660
GTAAGTAAAC ACATTACTCG CTCGTGCC 688

(2) INFORMATION FOR SEQ ID NO:1047:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1047:

CCGTATCGTC AGCATTTAAT TCCTGAATTT GATGAGTGAA ACAATTGCTA GTCAACATAA 60
TGCCTATCCA ACTGTAATTA GTGGTGCTGG ACCAACTATT TTAATATTTA GTCGTAAAGA 120
AATAGTGGGA ATTGGTTTCG TCCTTTAAAT AGTCAGGTAG TATCATGCCA TTCGGAATTG 180

GTCGATATTA ATATCAGTGG TGTAAAGGA CCGAATTGTA TACCAATAGA CGCTTTATAT	240
TGTAAAATAG TATTAAATGC AGAATAGAGA GGAGATTTAA TGCGATATGA CAAATTATAA	300
AGTTGTCGTT TTAGATATGG ATGACACATT GCTAAATTCA GATAATGTGA TATCAGAAGA	360
AACTGCAAAT TATTTAACAG CAATTCAAGA TGAAGGTTAT TATGTTGTTT TAGCATCTGG	420
TAGACCTACT GAAGGTATGA TTCCAAGTGC TAGAGATTTA AAATTACCTG AACATCATAG	480
CTAGATTATG CCGCTAGTGA CAACGGTAGT AAAACGATTA ACATGACTAA TGAAGAAAGTA	540
GAAGTAAGTA AATCGATTGG TAAGCAAGAT TTCGATGAAA TTGTAGATTA TTGTCGAGAC	600
AGAGGCTTTT TCGTTCTTAC ATATCATGAT GGTCAAATTA TTTACGACAG CGAACATGAG	660
TATATGAATA TTGAAGCAGA ATTAACAGGT TTACCGATGA AACGTGTTGA TGATATCAAA	720
GCGTATATTC AAGGCGATGT CTCGTGCC	748

(2) INFORMATION FOR SEQ ID NO:1048:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1048:

TTTGTAACA ATAACCTTAG GTAANAAACC TTGTTCTAAA TTGTACCCGT CNCCCNACGC	60
TCTTTGTC TG ANCCATACAA GNNACGTAAT TGGTGTGGTT TACCTGGTTT CCTCGTTCGT	120
AAACGCCATC CTTTCATCATA ATCTTCATTA AAAACAATTT TGCGAATCTC TTTAGGGAAC	180
GCATGCATTG GTAATGAGAT TTTACCTTCT CCATCTGTAT TCCCTGATTC AATTGGACCG	240
CCATCAGCAT AAGCTGTTTT TAGTTCTCCA CCAGTTTCAA CACCAATTTT TTGTAATCCT	300
CTTGTTTTNG TAATATCACT ATATTTTAAT TCCGCGCCTT CTTTCGTTAA TTTAGCGAAA	360
CCTAAACCAG TAATGTTAAT ATACGCCTTT GGCGCACTTG CATGTTTTAC TGCCATTTAA	420
TTTTCTCCT TATAAAAAAT GCCCTCGTAA ACGCTCGTGC C	461

(2) INFORMATION FOR SEQ ID NO:1049:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 712 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1049:

ATTGACATCC	ACTCCAAGAA	NCAATTAAAA	TAATGCCTAC	ATTACTTTCT	AAAAGATCCT	60
GATAATATTC	AAGNCTACTT	GTATTTACAA	TCATTATATG	AAAATGAAAN	AAATTATCCA	120
GATGCCATTG	AGACGGGTAA	AGAAGGATTA	CGACTAAGTC	AATTTTATAA	AGAGTTAATG	180
TATACAAC TG	GATGTTTGGA	AATAGAACAC	GGCGATGCTA	ATGAAGGTGT	ATTATTGTTA	240
AAACAAGCAT	TAGAGGTTGA	TAATGCTTAC	CCAAGAACCT	TTATTGATTT	TAAAGCGGAT	300
TTATATTCGT	AATGGAAGGA	AGATTATGAA	GCAATCATTG	AATTATTAAC	ATAGGTAGAT	360
GAAGGAAGAT	TTGGATCCTA	CATTCATGTG	GCATTTAGCG	TCGCCTATG	GTCAAGAAGA	420
GCGAGATAAA	GAAGCTCAAC	ATTTCTTTGA	ATTAGCATAT	CCAACGATGA	AAACAAATAT	480
TGATTTTATG	AGTGATTATT	ATTTCTATTT	AATTGAAATT	GGTCAAAAGG	AACAAGCAAT	540
TACTATTTTA	AATCAATTGT	TGGAAGTAGA	GCCAAGTAAC	GAAAATTGGC	ATGACGAATT	600
ATCAAGATTG	CAATCTTAAA	ATGGGGTATT	TGATGTCAGA	GACACTCAAT	CAAATTAAAG	660
AAAGTTTTAT	TGAATATTTA	CTTTTCAAT	ATCGATTTAA	GTCGCTCGTG	CC	712

(2) INFORMATION FOR SEQ ID NO:1050:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 680 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1050:

CCCAANATCT	AAAATATTTG	ATTCCATCTT	TGCAGTGATT	TTTNACCAAT	NTCCNANCCA	60
TTTTTCAATA	TGGTTGATNC	TTGAGTCAAT	TGATCGTACA	CTAGGCTCAA	TTTCTGCATA	120
TTGCGACATA	ATTAATACGC	AACCTGACCA	TATGATTCTA	ATGGTGCATC	TTGATATAAC	180
TTTTCAATAT	TATAATAATT	TCTTTCGTCT	TTATGGAAAA	CATGTACCAC	AACATCGAGC	240
TAAGTCAATT	AATATCCAAC	GCGCTTCATT	GTATCCTTCC	ATACGTTTTA	CTTCTATATT	300
TTGTTTCATTG	GCTACTTCTT	TCACCGCTCT	AGCAATCGCT	TGAAC TNGTC	GTTCA TTATT	360
TCCGTGCGTT	ACAACAAAAT	AATCNGTCAT	ATCGCTGATA	CCTTTCATTT	CTAAAGAAAT	420
CGTATCTTCG	CCTTTTTTAT	TNTCAATGNC	ATCCACAGCA	ATGGCTAATA	ATTCTTGTGA	480
ATTCATTTAA	TCATCCTTTA	TTCTTTCGTC	ACTATAGTTA	TAATAATTTA	AACAGTCAAT	540
CGTCTTATTA	TATACGTAA	TATCTTTCTG	TTATTAAAAA	TAGTACTGTG	CGTTTTAGAA	600
ATTTCATAAA	TTGTCTTATC	CTAAACTACC	TTGATTGTAT	GCCATATCTC	GAAATATCAT	660
CAACTCCTGG	GATTGTCTCC					680

(2) INFORMATION FOR SEQ ID NO:1051:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1051:

```

AATGAAGATG TGTATANTGT AGGGACACCG AATGTTGGGA AATCTACATT GATTGNTAAA      60
CTGANTGAAG CTAGTGTGG TGAAGAAGAT GTAGTAACAA CTTCAAGATT TCCCTGGANC      120
NACTTTAGAT ATGATAGATA TTCCTTTAGA TGAATCATCA TTTATGTATG ATACACCAGG      180
TATTATTCAA GATCATCACA TGACGCATTT AGTTAGTGTG AAAGAATTGN AAATTATTAT      240
GCCTAAGAAA GAAATNAAAC AACCGGTATA TCAATTAAAT GAGGCGCAGA CATTATTCTT      300
CGGCGGGCTA CGAGCGCATA GATTATGTAT CAGGTGGTAA ACGTCCGTTA GTTTGTTTCT      360
TTTCTAATGA CTGAATATA CATCGTACTA AANCGGAGAA GGCTAAGGAT TTATGGCGTA      420
ATCAACTTGG CGATTTATTA ACGCCACCTG GAAATCCACA AAATTTTGAT CTTAATGAGT      480
TAAAGGCTGT TAGACTTGAA ACAGGCAAAG AGAAACGTGA TGTATGATC TCTGGTCTAG      540
GCTTTATAAC TATAGGACCA GGAGCTAAAG TAATCGTTCG TGTTCCTAAA AATGTTGATG      600
TTGTATTAAG AAATTCCTAT TTATAAGGTG ATTTAAAAAA TGAAATTTGC AGTTATCGGA      660
AATCCTATTT CACATTCCTT GTTCGCCCCG TTATGCCTAG AGCAAATTTT AATTCCTTTA      720
GGAATTAGAA TGAACTTTA TGAAGCTTTT AAATATTCCA ATTGAAGATT TTCATTTAAT      780
TAAAGAAATT ATTCCGAAAA AAAGAATTAG ATGGCTTTAA TATCACAATC C              831

```

(2) INFORMATION FOR SEQ ID NO:1052:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1052:

```

GGCACGAGCG ATAGTCGCTA CTACTTCCAC ATGTGTCATA GTAAATCCCT CATTTTCAGAT      60
ACTCATTATT TTTATTGTAA ACAACAACTT TTTATCCTTC AATCAAACAA TGCTATAAAT      120
GAAAATGATT AAGGTATTTT CGAATGGGTA AAGCATAAAT GTATTTTAAA TTAGGAGGTT      180
ATAAGAATGG CAATACATTA TGAACTAAA GCGACGAATG TTGGCGGACG TAAAGGACAT      240
GTTTATACTG ATGATCGAGC GTTAGATATT GATATCGTTC CGCCTGCTCA AGCAGATGGT      300
AAAGCTACTA ACCCCGAACA ATTATTTGCA GCAGGTTATG CATCTTGCTT CAACGGTGCT      360
TTCGACCTAA TTTTAAAGCA AAACAAGTGC GTGATGCTCA TCCAGAAGGT AACACTAACA      420
GTGAGACTAG AAGATGATCA GACTCAGAAA GTCCTAATTA NGTGGTTCAA TTGATCGCAC      480

```

AATTAAAATG T

491

(2) INFORMATION FOR SEQ ID NO:1053:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1053:

```

GGCACGAGAC ACCTGCATAT ATATATGCAA TACCAGTTGC ATCCTTAGCA TTATTAATCG      60
CAATCACATT GTTTGTTAGA AAAAAATCTA AAGGCAATGT GGAATAATGA GAAATGTTAA      120
ACAAATTGCT ACAAATCTA TTATAGCTAT TATTAGCTTA TGTATACTTA CATATACAAC      180
AATGATTGGT AGCGTGTGG CTGATGAGAT AAAATATCCA TCAGCCAAAT TTAATCAACC      240
TGAAGCAAAA GATAAACAG AATTAACTAC ATCAATTTTT GATGAAAAGA TAAAAGAGAA      300
TAAAGCGTTA GAGTTACTAA TTTTAAATCA AGAAAATAAA AATGTAACG AGGAACAACA      360
ACTAGTTGAC GAAAAGGCGC AATTGATTTT AGATATGACT GGTAAAATTT ACTTGCAAGT      420
AAAGCTAAAA GGTCAAATAG ATAAAGAACA ACTTGTTTTT CAAAATGACA AAAATGAAGA      480
ATTTCTTTTT GTTATAAAG ATGAAAAGGA TGACCCATAG TAAGAATTTT AATTGAACAG      540
CATATGGATA AA                                         552

```

(2) INFORMATION FOR SEQ ID NO:1054:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1054:

```

GGCACGAGAC TGTTTCGAAA TTGTGTAAAT CCCTTGATGT AACTTTGAAC GAATTTTTTG      60
GAATCAATGA AAAAGAGGGG GTCAAATAAA TGTCTAGAAC AAAATTGCAA GACTTCCCAT      120
CAAAAGAAAA TACAGTTACA GAACCGAAGC AAGTTGTAGT AAATCCGTTG TTTGCGAAAC      180
CTAATGCACT AGCTGGTATT TTTGGAATTT CATACAGTTC GGTGAATCGC ATTTTAAAAG      240
AATGGGAAAA AGATTCTAAA GGTGTTGATG ATTTATATTA TTCACTATCA TCAACATTGA      300
TTGTTATCAG TATTCGCGA TTCNAGGAGT ACATGAAGGT GCGTCCTAAA AAATGGATGT      360

```

TTGAGGTAAA GCAATGAAAA TATACTTAAC NTTATATCTG CTTTAGTTTC

410

(2) INFORMATION FOR SEQ ID NO:1055:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1055:

```

GGCACGAGCG AGCGTAAACA TCTGTAATAA TTGGCATGTT TATAATCTCC TTTAAATAGT      60
TATTCTATAA TTATTATAGC TTTATTCTTT CATTTAACAA AATGATATTA CTATTATTTA      120
CAAAAAATAA GTGTCATTAA GCGTTTACTT AACATCTTTT ACAATATTAG TGTTTAATTA      180
AAGATTCACC TGTCATGTCT ACAGGTTGTT CTACATTAA TAAATCTAAT AATGTAGGTG      240
CTAAGTCACC TAAGCGACCA GTTCTCGAA GTGTAACGCC TTCTTTTGTT ACAATCACTG      300
GTACTGGGTT CGTTGTATGC GTAGTCATTG GTTGATCATC ATCCGTCAAT ACTTGATCAG      360
AGTTACCATG GTCAGCAGTA ATAATTGCAT AACCGTCCAT GTCTAAAATC TTATCAACGA      420
CTTCACCTAA ACATTCATCA ACCGCTTCGA TTGGTTTGAT TGTCGGCTCA AGCATACCAC      480
TATGTCCACC ATATCAGGTT AGCAAAGTTT AAATATTAAG TCCAAGTCAC TNTATTTAAC      540
TCTCTAATAA TGCATCTT

```

(2) INFORMATION FOR SEQ ID NO:1056:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1056:

```

GGCACGAGCT AGAGGATCAA GAGAATTAA ATGGCGATTG CCNNACAAGA TGACNATNCG      60
AATCAGTNCC ATTGGTGCCN TANGTCTGGG ATTTGGTGCG TCANTNGCTG GTGGTTGTTT      120
TATCGGTAAC GTTTGGTTG AAACGGCAAC GATGACTTGG CAAGGATGGA TTGCGCTAGC      180
ATCCATGATA GNTGGTGTAT GGACAATGAG TCATTTTNTC NTTGTTTCGTC CAATGAAAAA      240
NGTACAACAA CNATCCGCAA TAGGTTAAAC AGCAAACGCN AATAGTATAG AAGATTATTA      300
TGCCCATGAT GTTGATCAAA TAATAAGTGA TTG

```


(2) INFORMATION FOR SEQ ID NO:1057:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1057:

```

GGCACGAGCT CGTGCCGAAT TCGGCACGAG ACATTACATC ATTAATTTCA ACCATCTTCT    60
TATTGATTAT GGTTCATTC TTCTTAATTT ATATGTTAAA AGACCATGAA AAATTTATCC    120
CAGCTGTTGC TAAATTTTTC AAAGGTGAAC GTAAAGTATT TTTCGTAGAT TTATTAACGT    180
ATTTAACTT TACATTAATA TCTTACATTC AAGGTCAAGT AACTGTCAGT GTTATTTTAG    240
GTATATTCTT ATATATCGGT TATTCAATTA TTGACTTACC ATATATTCCT TTATTAGTTC    300
TATTTGCTGG TGTCGCAAAC TTAATTCCTT TCTTAGGTTT ATGGTTATCA TTGTCACCTG    360
CAGCAAATAC TCCGGTATTA ATAGATAGTC CTACTACATT TATATGGGTT TGTATCATTA    420
CATTAATTGC ACACCAACTT GAAGGTAATA TCATTACGCC AAATGTTAAT GGGTAAATCT    480
TTAAGTATCC ATCCTTTAAC AATTATCGTT GTTA                                514

```

(2) INFORMATION FOR SEQ ID NO:1058:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 592 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1058:

```

GGCACGAGCG CCCGTCTACA TCGTTCAAAG CCCATTGAGT ATAAGACAGT CCATGAGGTG    60
TTGCGGCCCTC GTCAATGGCT TCTACAACGT TCTCAAGAGG TACGTATTTT GATTTAAAAA    120
ATGGATTGTT TTTATCTTTG AGCGGTTGTT TTAATTCCTT GCGAAATGCA ACCATAGCTT    180
TATTTATTTT AACAACGTGTT TCTGATTTAT TCATCACTTA ATCACCAGAC TTTCTGTTAC    240
CTTTAATTCA ACGCCAGGAA TATCTTTCCC AGCTTTCAAA TCATCGATTA GTTGCTTAGA    300
ATTAAGTTTC GGGGCTTGTG ATAGCCAATA ATCCTTTGGA ATAAGTTTTT CATCGATAAT    360
ATTTTTACTA GCTCCGTTTT TGCGTTTAAA AATATGATTA GTAGCTGTGC GGTAACATC    420
TACTTCTTGT GTTCTTAACA TTTCTTTTAA GTAATCTCTT AATCGATCAG TTAAATTTTG    480

```

TTTTTGTTTT	TTTAAATTTT	GAAGTCGTTA	TCTCTTATCT	ATGACATCTA	TGTCACTAAG	540
TTCACGTCTC	CATGACATGT	TATCTACTTG	ACATCATTCT	GCTGATAATC	TA	592

(2) INFORMATION FOR SEQ ID NO:1059:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1059:

GGCACGAGCT	ATAAATGATG	AAGTTGATTT	AGATGAAAAT	TAATCTTGGA	TATTTAATAC	60
TTTGTTGATT	TCATCAAGAT	CAACATGGTA	CATTGGATTG	CCATTCAACA	AAATAAACGG	120
AGTTGAAAAA	GCATCAAAAT	CTATCATTTT	GTTTCGATAT	TGTTGATTGT	TGATATTTCT	180
CTCTTCAAAA	TCAATTTGAT	GCTCATTTAG	ATAATTTTTT	ACAAATGTAC	AAGGTGGACA	240
ATCATTCTGC	GTATAAACGA	TTATTTCTGA	CATGTTATCA	TGCTCCTTCG	TGCTTTATTC	300
TAATGTAATA	TACACAATTA	TACATTGAAA	TTCCAAATTT	GTGAACACAT	TGTGAAGTGA	360
CATAAATTAT	ACACAATTTT	CATAGCGCCA	TAATGTTTTT	TAAAAATACA	CATTATAGCA	420
ATTATAATTA	GTTCCATGTG	TTGGTCCATC	AAAAAAGAAA	AGGTGATGTT	TTTTAATGGA	480
TACAGTTGAA	TCCGTCCGTT	TTGAC				505

(2) INFORMATION FOR SEQ ID NO:1060:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1125 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1060:

ATCCTTTTATT	TNTAAGGCGT	TTCATCAAGC	TAACACTTCA	TTATCTTTAG	TCGCTTTAAT	60
GCCCTTCTAT	TAAACTCGGA	ACTAAAAATG	GATTGNCCTT	TCAACCACCC	GANCACTAAA	120
ACATTGTCNT	TTTTGATGGC	CNATTAAGAC	ACAATTTCCC	GCTGTTTGCT	TCAAAGTAGC	180
TTGCTTCTTG	NATTNATTTT	CAATATCTTT	CTTGTTAAAA	ACAAGANTGT	TGCACAGTTT	240
GATTGGCATC	TTTATTTAGA	NCAATGGCAT	CTGCTTGCCA	CTTATCAATG	CCTTCTTTAT	300
TCATATTGAT	AAGACCATTG	GCCAATCCAG	ATAATAAAAA	TAGCAAGTAA	CTAATCATCG	360

TTAACACACC	AATAATTAGT	CCAAACTTCA	ATTTGTTGCG	CCGTATTTCA	TTCCAAGCTA	420
AAAACATGCA	TTTCTCTCCC	TACTACTATG	ATTTAAACAT	TGTTTATATT	CTTAGATGCA	480
CGTACGTCGT	GTTCGCTCT	GTAATGTTAT	ACATACACTT	ATCCTTCATT	ATACCCGANC	540
TTTTTATATT	AAAACCAAAT	TTATGGAAAA	TGCAANNANT	TGTCTATTAT	TTTTGTGCGG	600
TACATTTAAA	ATTAAGGATC	AATTTAAAAA	CGCCTACATA	TACCTTTAAG	TACATGAAGA	660
CGTCCAATTC	ATATATTATT	TAAC TTCGCC	TGTTTTAGGA	TCGGATTGCT	TAATAGCATT	720
TTTACGTAAT	TTATCTTTTG	CTTTGTCACT	TGCTTTATAG	TTATTGTTGT	AAATCGTAGC	780
TTCCCAACTA	CCATACATTG	GGTTAGGGAA	AATGATATAT	TTCTTACCGA	AATCGTCTTT	840
ATGTTTTTCA	ATTAATGCTT	CACGAGATTC	AGCTGTAGCT	TCTTTTGGAT	CTGTAAAGTC	900
TAATAAATTA	TCTCCAAATA	GCATGACAAG	TTTATGATCC	TTTTGAACCA	TTTGTCTGCG	960
TGATTCTTTA	CTCTTATCAT	CTTTACCTTT	TAGTAAAATA	TGACTCTTCT	TAGCTTGAGG	1020
GATACCTTGT	TGTTTTAAGT	TCTTTTGTGT	TGCCTTTAAA	TCTTTTTCTT	TATCTCTATC	1080
AGAAATATAG	TAGATATCGA	CACCTTTTTT	GTCAGCATAT	TTCAA		1125

(2) INFORMATION FOR SEQ ID NO:1061:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1746 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1061:

CGTCCTTCAG	TCATTTTTTAA	NNATTTGCTT	AATTTTCATCC	AATTTGTTAA	ATTGTTCAAG	60
ANNAAAATAT	TACCCCTCCG	AAATACGGGA	TTGTCACTGT	CTTGTAACCC	ATGCTTTTCGC	120
TTTNCGCCAA	GATGTNCAAC	TTGNTGAAGT	AAATAATTGT	TACCCATACA	TCTCACTCTC	180
CTATTTGAGT	GAATAAAATT	CATTGCTTAA	AATTTAGTTA	TAAGATCAAG	ANAAAACATT	240
TTTTTCTAAA	ATTCTTAATC	GTTACTATTT	ATTATAACTA	TCTAACATTA	AAATTAAATG	300
AGANAAACCT	AATTTTTTCAG	ATAAGTTTCT	ACACTTATAA	AAAAGATTAT	TAATCCTTTG	360
TTAGTAGTAA	GTTATACGTA	TATTCTAACA	CATCTTACAT	TTTTAAGAAA	TACTGTTATA	420
ATGATAATTA	TTAAAATATT	ACTAAGAAAG	TAGGCATTTA	AATGGAGACA	TTATTTTCAG	480
GCATCCAACC	TAGTGGAATT	CCTACTATTG	GAAATTATAT	TGGCGCACTA	AAACAATTTG	540
TTGATGTGCA	AAATGACTAT	GATTGTTATT	TCTGTATCGT	AGATCAACAT	GCAATTACAA	600
TGCCACAAGA	TCGTTTAAAA	TTACGTAAAC	AGACCAGACA	ATTAGCAGCG	ATTTATTTAG	660
CTTCTGGTAT	AGATCCAGAC	AAAGCAACAT	TGTTTCATACA	ATCTGAAGTC	CCTGCACACG	720
TACAAGCAGG	ATGGATGTTA	ACTACGATTG	CTTCTGTTGG	AGAATTAGAG	CGTATGACGC	780
AATACAAAGA	TAAAGCTCAG	AAAGCAGTTG	AAGGTATACC	AGCTGGTCTA	TTAACATATC	840
CACCTTTAAT	GGCAGCTGAT	ATTGTTCTTT	ACAATACTAA	TATCGTTCCA	GTTGGAGATG	900
ACCAAAAAGCA	GCATATCGAA	NTGACTCCGT	AACCCTTGTA	GATAGATTTA	ATAGTCGCAA	960
TAATGATGTG	CTTGTGAAAC	CCTGAAATTC	GTATGCCTAA	AAGTTGGTGG	ACGTGTCATG	1020

AGTTTACAAG	ACCCAACAAG	AAAAATGAGT	AAGAGTGATG	ATAATGCTAA	AAACTTCATT	1080
TCATTATTGG	ACGAGCCGAA	TGTTGCAGCT	AAAAAAATTA	AAAGCGCAGT	AACTGATTCA	1140
GATGGTATTA	TTAAATTTGA	TCGTGACAAC	AAGCCAGGTA	TAACAAATTT	AATTTCAATA	1200
TACGCTGGAT	TAACCGACAT	GCCAATTAAA	GATATTGAGG	CAAAATATGA	AGGGGAAGGT	1260
TATGGTAAAT	TTAAAGGTGA	CCTTGCTGAA	ATAGTTAAAG	CATTTTTAGT	AGAATTCCAA	1320
GNAAAAATAC	GAAAGTTTCT	ATAACTCAGA	TAAACTTGAT	GATATTTTAG	ATCAAGGTAG	1380
AGATAAAGCA	CACAAAGTTT	CATTTAAAAC	TGTCAAAAAA	ATGGAAAAAG	CGATGGGATT	1440
AGGACGTAAG	AGATAAAATA	AAGAGGTACT	AGAATTAACT	AGTGCCTCTT	TTATTATTTA	1500
ACGTCTACCT	CTAGGATTAA	AAGCATCTTT	AAGCCCTCCC	CCTACAAAGT	TTATACTTAA	1560
TATAGTTAAT	GTAATCATT	TAGCAGGTGG	CATCCATATC	CACGGTTTAC	CACTTATAAC	1620
ATCCCTTCT	TGAGCATCAC	TCAACATATT	ACCCCAAGAT	GGTATTGCTT	TTACTAACTC	1680
CGAATCCTAA	AAAGCTCAAT	CCTGATTCCA	CTACAATCAT	ACCGGGAAAT	TACAATGTTG	1740
GGTTGG						1746

(2) INFORMATION FOR SEQ ID NO:1062:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1909 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1062:

ACTGGGTCCT	ATTTATTGTC	AGGTAAAGAT	GTCTCAATCA	ACTATGGAAT	ATATGTATGG	60
GAGATATTGT	AAACTTTTCC	AAGAGGTTCC	ACGGGTTAAT	ACTAATATCT	TTATCATAAT	120
CGATCAAGAC	ATAAAGATCC	AGAGGCGGAC	TTTAATGCAA	CATATGTTTC	TTTTGAAACG	180
TTGTTAGCAG	AAAGTGATTT	TATCATCTGT	GCAGCGCCAC	TTACACAAGA	AACACATCAT	240
AAATTTAATG	CTGAAGCATT	TGAGCACATG	TGAAATGATG	CAATTTTAT	TAATATCGGT	300
AGAGGGCACA	TTGTAGATGA	AACAGCATT	ATCGATGCAC	TAGACAATAA	AGAAATTTTA	360
GCATGTGGTT	TAGATGTATT	AGCAAATGAG	CCGATTGATC	ATACACATCC	ATTAATGGGA	420
CGTGATAATG	TTCTGATTAC	ACCACACATT	GGTAGCGCAT	CAGTAACAAC	ACGGGACAAT	480
ATGATTCAAT	TATGTATTAA	TAATATAGAA	GCGGTTATGA	CAAATCAGGT	ACCACATACC	540
CCAGTAAATT	GAAAATAAGT	ATGGTTTTTA	ATCATTGGTA	AAACAAGCAA	AGCAATTGTT	600
AAATATGTTA	TGCTTGACTT	GCGAATGTAT	ATATTTGCGC	TGATGATAAT	TCAATAACAT	660
TATAAACTCG	TCATATTAAT	GTGATGAGTT	TATTTGATTT	TGACGTATAT	AACAAAATTG	720
TTATATAGAC	TGTAATTGTT	TATTGTTTAA	ATAACCTTTA	AAATGAATGA	TGTTCTCAAC	780
AAAGTGTATC	ATTTACAATA	ATTGAGTGAT	GACAACCAAT	TACTATGTTG	AATCTATAAA	840
ATTAAAAATG	AATTTCAATTA	TGAATATCGA	TATAATGAAT	TGTAAAAAAC	AAATTTTAAA	900
ACGTATTTTA	TATTGAACGG	TCTTTATAAA	GGCGTTTTTA	CTAAGAACTT	TAAGAGGTGC	960
AATATGAAAT	CTAAAAGTAA	ACAGCCACCT	AATAAATATG	TTGAAGCATT	CAAACCATAT	1020

TTATTAACAC	TATGTATTT	GGCAATATTT	ATTACTTTAT	ATTTAATTTA	TGGCAGTGGC	1080
GACACACACA	ATAACTTCAT	TTATAATGAG	TTCTAATGAG	GGAGACTTAA	TATGACAGAT	1140
ATTATTAAACA	AGCTGCAAGC	GTTCGCGGAT	GCAAATCCAC	AAAGCATTGC	TGTTAGACAC	1200
ACAACCTGATG	AATTAACCTTA	TCAACAGTTA	ATGGATGAGT	CTAGTAAATT	AGCACATCGA	1260
TTACAAGGTA	GTAAGAAACC	GATGATTTTA	TTCGGTCACA	TGTCACCATA	TATGATTGTT	1320
GGGATGATTG	GTGCCATTAA	AGCAGGATGT	GGATATGTAC	CTGTAGACAC	CTCCAATTCC	1380
TGGAAGACCG	TATTAATAATG	ATTATTAACA	AGGGTCCAAC	CNAGAGTTTG	TATTTAATAC	1440
GACTTGTTGA	TCATTTGAAA	GTTAAAGAGG	CCGAAGTAAT	TACCAATTTG	AAGATATTAA	1500
AACATCTCNA	AGACCCAGTA	ATTTTTTGAT	AGTCAAGATT	AAAGATACCG	ACACAGAATA	1560
CACAATCTTT	ACATCTGGTT	CTACTGGGGA	ACCTAAAGGT	GTTCAAATTG	AATATGCAAG	1620
TTTAGTTCAA	TTTACTGAGT	GGATGTTAGA	ACTTAATAAA	TCAGGAAATA	AACAACAATG	1680
GCTTAACCAA	GCGCCATTTT	CATTTGATTT	ATCTGTAATG	GCTATTTATC	CATGTTTAGC	1740
ATCAGGCGGT	ACATTAAATC	TTGTAGATAA	AAACATGATT	AATAAACCTA	AATTATTAAA	1800
TGAAATGCTA	ACAGCAACAC	CGATTAACAT	TTGGGTATCA	ACACCATCAT	TTATGGAAAT	1860
GTGTTTATTA	TTACCAACGC	TTAATGAAGA	ACAATATGGT	AGTCTTAAC		1909

(2) INFORMATION FOR SEQ ID NO:1063:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1063:

CCATCGACTA	AGCAATGGTA	TTTGTTTCATT	AAATCCTCAT	GTGATCGTT	TAACGTTAAG	60
CTGTCGCATG	GAAATCGATG	CTAGTGGTCG	CGTTGTAAAA	CATGAAATTT	NTGATAGTGT	120
TATACATTCT	GATTATCGAA	TGACGTATGA	TGCGGTAAAT	CAGATTATTA	CTGAAAAGGA	180
TCCTAACATT	CGCGAACAAT	ATAAGAAAT	TACGCCTATG	TTAGATTTAG	CACAAGATTT	240
ATCTAATCGN	TTGATTCAAA	TGAGAAAACG	ACGTGGGGTG	AAATCGATTT	TGGATATTAG	300
NGAAGCAAAA	GTATTAGTTA	ACGAAGTCGG	GTATACCAAC	AGATGTTCAA	TTAAGACAAC	360
GTGGCGAGGG	TGAACGTCTA	ATTGAATCAT	TTATGTTAAT	TGCAAATGAA	ACAGTTGCTG	420
AACATTTTAG	TAAGTTAAAT	GTACCTTTTA	TTTACCGAGT	GCATGAGCAA	CCTAAATCAG	480
ATCGCTTAAG	ACAATTCTTT	GATTTTATTA	CAAACCTTGG	CATCATGATT	AAGGGCACTG	540
GCGAAGATAT	TCATCCAACA	ACACTTCAAA	AGGTTCAAGA	AGAAGTAGAA	GGTCGACCTG	600
AACAAATGGT	CATTTCACA	ATGATGTTAC	GTTCAATGCA	ACAAGCGCAT	TATGATGATG	660
TGAACCTGGG	ACATTGTGGC	TTATCAGCTG	AATATTATAC	GCATTTNACA	TCACCAATTA	720
GACGTTATCC	TGATTTAACA	GNTCATCGTT	TAATCCGTAA	GTATTTAATT	GAGAAATCAA	780
TGGATAACAA	AGAAGTGAAG	CGTTGGGAAG	ACAAATTGCC	TGAGTTAGCT	GAACATACTT	840
CTAAACGTGA	ACGTCTGTCT	ATTGAGGCAG	AACGTGATAC	TGATGAATTG	AAAAAAGCAG	900

AATATATGAT	TCAACATATT	GGTGATGAAT	TTGAAGGTAT	TGTCAGCTCA	GTAGCTAACT	960
TCGGTATNTT	CATTGAATTG	NCAAATACGA	TAGAAGGTAT	GGNTCATATT	GCGAATATGA	1020
CTGATGATTA	TTACCGCGTT	GAAGAGCGTC	AAATGGCATT	AATTGGGTGA	GCGTCAAGCT	1080
AAAGTATTTA	GAATTGGTGA	CACAGTTAAG	GTTAAAGTGA	CGCATGTTGA	TGTAGATGAA	1140
CGATTAATTG	ATTTTCAAAT	TGTTGGAATG	CCTTTACCTA	AAAATGACCG	CTCACAGCGA	1200
CCAGCAAGAG	GTAAAACGAT	TCAAGCTAAA	ACGCGTGGCA	AATCTTTAGA	TAAATCGAAA	1260
TCTGATGATA	AGGGTCGGTA	AGAAAAAAGG	TAAGCAACGT	AAGGTAAAAA	CCAACGTAAT	1320
AATGATAATC	AGGTAATAGT	AAGCATAG				1348

(2) INFORMATION FOR SEQ ID NO:1064:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1283 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1064:

CCGTCATTAA	TGATATGATG	TGTATCTATA	AACAGGTATG	CATGTAAGGG	ACTTCTAATG	60
TATCTCACTC	TAATTTGACT	TGGCTTTTCC	AAATTAAAAG	GTGCCACAAA	TTGGCGCATA	120
ATTTCTTGTT	CATCCGTAAA	ATGCGTGTTA	ACTTCTTCAA	AGTCAGCTAC	AACATCTGCC	180
ACAATACGTT	GTCGAACCTC	ATCATCTACA	ACAATATATT	GTGTTCCGTAG	AATCTCATGT	240
CGCGCTATCA	AATGCTGAAC	TGCTTGTTGC	AATTGAGCTA	CATTAAGTCC	TGATGATAAC	300
CGCCATAAAA	AAGGTACGGT	TATACAACCG	TATCTTTATG	GGTNGGGATT	TCCATAATAA	360
ATACAATACG	CTTTTGGGGC	AGGAGCTCCA	AGCAACATAA	TCAACTTTNN	ACTTATAGNT	420
TCTTGGAATC	ACTTCATAGT	TTTGTTCTTG	AACCTTAGCA	ATCGCTCGTG	CTAGTTCAAA	480
TACAGTTGGC	TTTNGTAATA	AATCACCAAT	TTGTAATCGT	TTCCCAGTAG	ATGCCCTCTAT	540
CCGATTCACC	ACTAACGTTG	CTTTTAATGA	ATGGCCACCT	AATTCAAAGA	AATTATCATG	600
AATACCTACT	TGATTCACAT	GTAAAATATC	TGCACAAATT	TGGCATAGCA	AGTGTTCCGT	660
ATCTGTACTC	GGTGCTACAT	AGGCATCCGT	ATCGACATAG	TCCATGATAG	GCAATGCCTT	720
CTTATCTAAT	TTCCCATTA	TAGTAATAGG	AATTGCTCA	ATATGCATGA	AATTAAGTGG	780
TATCATGTAC	TCCGGTAAGG	TCATACGTAA	TTGTGATTTA	ATCTTATTAT	GTGATAATGT	840
ATGCATCGCT	TCATAATAAG	CAACGATATA	CTGATCTTGA	TCATGATTTT	GAACAAGAAC	900
AACTGCTTTA	TGAATACCTT	GTATACGCTC	GAGCGCATGC	TCAACCTCTG	ACAACCTCAAT	960
CCTAAACCCT	CGAATCTTAA	CTTGTTTGTC	CTTTCGATAT	AAATAATCTA	TGTTGCCATC	1020
GGGTAACAAA	CGAACGATAT	CACCACTTCT	ATACATCAGN	TGATTTATAT	TTGAATCTTT	1080
GATAAATTTA	TCTGCTGTCA	ATTCTGNGTG	ATTTAAATAA	CCTGCAGGTA	ACCCAAAGGC	1140
ACTTGTACAT	AATTCTCCAG	GAATACCAAC	GGCACACGAN	GGTCGGCTNG	ATGATATAAA	1200
CATGAGTACC	CAGAATCGGG	NTTACCAATA	GGAATACGAT	TGGACTTGGG	TAGGTATATT	1260
ATCGCGTGGG	AATGTGNTTT	CAA				1283

(2) INFORMATION FOR SEQ ID NO:1065:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1065:

```

CTGAAAACT TAACTCATT TAACTATGTA CGTAAAGGTT TAGAATATGA AGAAAAACGC      60
CAAGAAGAAG AATTGTTAAA TGGTGGAGAA ATCGGACAAG AAACACGTCG ATTTGATGAA      120
TCTACAGGTA AAACAATTTT AATGCGTGTT AAAGAAGGTT CTGATGATTA CCGNCTACTTC      180
CCAGAGCCTG ACATTGTACC TTTATATATT GATGATGCTT GGAAAGAGCG TGTTTCGTCAG      240
ACAATTCCTG AATTACCAGA TGAGCGTAAG GCTAAGTATG TAAATGAATT AGGTTTACTG      300
CATACGATGC NCNCGTATTA ACNTTGACTA AAGAAATGTC AGATTTCTTT GAATCAACAA      360
TTGGAACNAG GGTGCAGATT GTTAAATTTA ACATCTAACT GGGTTAATGG GTGGCGTNAA      420
CGAATATTTA AATAAAAAATC AANTAGAATT ATTAGATACT AAATTAACAC CAGAAAATTT      480
AGCAGGTATG ATTAAACTTA TCGAAGACGG AACAAATGAGC AGTAAAATTG CGAAGAAAGT      540
CTTCCCAGAG TTAGGCAGCT AAAGGGTGGG TAATGCTAAA CAGATTATGG GANGATAATG      600
GCTNAGTTCA AATTTCTTGA TGAAGCAAC AATCTTCTAA AATTGGGTAN ATGGAAGCAT      660
TAGACAAATA ACGAACAATC NGTGAAGAT TACAAAAATG GTAAAGGCAA AGCTATGGGG      720
CTTCTTAGTT GGTCAAATTA TGAAAGCGTC TAAAGGTCAA GCTAATCCAC AATTAGTAAA      780
TCAACTATTA AAACAAGAAT TAGATAAAAG ATAATTTANA TCATCAAAC TGAAGATTT      840
AAAAAATAAA CCCTTGATTG CTGACTTAGA TGCAATCGAG GGTTTATTTA TATCTATAGA      900
AGTCATATTA CTTTAACTT TATTCATTGN ACATGTTAAT GGTAAAAATA TTAATTTTAT      960
TAATGCGTTA GCTTTAATTA TATTAAGGCA AACTGTATAA TAAAAAGGTA TAAACATTT      1020
GTGTATAAAG ACAACATTAT ATTTACAACA TCATTTTAAA GGTAATATAG CATAACTGAC      1080
GAAGTCTATA TAATGAAGAA CGGCAAAAAA TGCTGAATAA ATAACAAGCT TTGTACATAT      1140
TGAGATAGTA TTTGTTTAAG ATACAAGTTG GTCCTTAACG ATATTAAGAA TGATGAAATA      1200
AGACTGAGCC TGGGTCATAA ATTCAATGTC CTAGGCACTA CAATGTTAAT ATTGGCAGTA      1260
GTTGACTGAA AGAAAATACG CTTGTAACAA GCTTNMNTCA ATTCTAGTGG GGCCCCAACA      1320
TAGAAGCTGA CTTTCTGTCA GCTTACAATA ATGTGCAAGT NGGGGTGGGG CCCCAAACAA      1380
AGAGAATTTT GAAAGGAAAT TCTACAGACA ATGCAAGTTG GGGTAGAACG AAATAAATTT      1440
TGTTAAATAT TATTTCTGTC CCACTCCCTA TTAGACGAAA CAAAGATGAA GTCAAAATAT      1500
ATGAATTTTA AGTAGAAGGA TAAGATATGA ACAAACGTGC TAGAATCATT TATAACCCGA      1560
CATCAGGTAA AGAGCTAATT TAAAAGAGAA TTACCTGATG CCTTAATAAA ATTAGAAAAA      1620
GCGGGATATG AAACGAGTGC ATATGCAACC GAGAAAATAG GTGATGCCAC ACTTGAAGCA      1680
GAAAGAGCTA TGCATGAAAA TTATGATGTA TTAATCGCTG CAGGTGGTGA TGGAACATTA      1740
AATGAAGTAG TTAATGGTAT CGCAGAAAAG CCTAATCGTC CTAAGCTAGG TGTCATTCCCT      1800

```

ATGGGTACTG TTAATGACTT TGGACGTGCA TTGCATATAC CTAATGACAT CATGGGGGCA	1860
CTTGATGTCA TCATTGAAGG TCATTCTACT AAAGTAGATA TTGGTAAAAT GAATAATCGA	1920
TACTTTATTA ATTTAGCTGC AGGCGGACAA TTGACGCAAG TCTCTTATGA AACACCGAGT	1980
AAATTGAAAT CTATTGTTGG TCCATTTGCT TATTACATCA AAGGTTTCGA AATGTTACCT	2040
CAAATGAAAG CTGTAGATT T AAGAATTGAA TATGATGGTA ATGTTTNCCA AGGAGAAGCA	2100
TTATTATTCT TTNTAGGCTT AACAAATCCA ATGGCAGGAT TCGAAAAATT AGTGCCCGGA	2160
CGCTAAGTTA GATGACGGCT ATTTCTACGT TNAATNTATA G	2201

(2) INFORMATION FOR SEQ ID NO:1066:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1066:

GGCACGAGCT ATCATAAGAA AAAAGAATGT GATTGGAAAT TACTCAATCA ATTAACTAAA	60
CGTGCATATA CGAATCGTGT GTTTATCACT CATTATCAA ATATCATTTA CTTGCCTAAA	120
AATACTCGTG TTAACCTTTTC AGGTGACGAA AAAATGGCAT TGCTAAAAAT TAGNAGNAGC	180
ATCAAAGATA TATTTTATGG CACGAGTACT TTAAAGAGAG AAGATGATTC TGTAGAAACT	240
TTACGTTTCGA CTATAAAAGC ACTTGAAATT AGTGGTGAAA ATCAAATTAA AAGTCATATA	300
CTATACGAAG TTCTAATGNT TTATCGACTG CTAGACAGCA GATATGCTTA ATTTAAGTAC	360
CTTATGCTAA TTGGCACCAT GGGAGTGGGA CAGAAATGAT ATTTTCGTAA AATTTATTTTC	420
GACGCCCCAC CCCAACTCGC ATTGCCTGTA GAATTTCTTT TCGAAATTCT CTGTGTTGGG	480
ACCCACACCC CAACTTGCAT TGTCTGTAGA AATTGGGAAT CCAATTTCTC TTTGTTGGGG	540
CCCCTGACTA GAATTGAAAA AAGCNTNGTT ACAAGCGCAT TTTCGCTCAG TCAACTACTG	600
NCCAATATAA CTTCCGNGGA GCATAGAACA TTGATTTATG TCCCCGCCTC TNNTTATCGG	660
ATATAGCATG TCCCTTTTNN AAATTACAAG CATAAATATT CAGACTCNAA TATAGCCACA	720
CGCCTAAACT NCGGAGGGAT GTGGCTGTCT TTTNTGATTG TAATTATGTA TCAGATTTAA	780
ATCATTAATA TAAAGAGGCT AATTCATTAA TAAATTTAGT AAAATCTGAT TTAGCAATAT	840
TTATCCTTAA TGAAATACCA GATTCTGTTG CCATGTTTGA ATGCCTTAAA CCAGAATCAA	900
AATCAATATA AATACAAAGC AGTTC TTGAT TAAAATCAAT AATTGTAAAA TGTAATCAG	960
GTTCNATAAA ATATATTNCA GNAACAGGAT TGCCGNAATC CATATTGTTT CAAATTGGCC	1020
ATGTCACTAT CAAAAAGTGC AAANTCAAAT TTAAC TTCTT GATCTTCGAA AGTTGCACTA	1080
GTGTCGAAAT AATAAATTTT ATTATCTTCT TCGATAACTA CATCTTTTAA AATAAATGTT	1140
ATCGATNCTT TGCCATGTAA ATAAGATGCA TCTCTTANAA TCACTTTAGT GGNCTTCATC	1200
GTCAAATTC TTTTCATCATT CATTTTTTCA TGTTGCATAA GCACCATTAC TAG	1253

(2) INFORMATION FOR SEQ ID NO:1067:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 908 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1067:

CATATTTGAT AATAAGCCT CGCTCTAATA TCCCAGGGAT TTTTNAGAGG CGGAAGACCC	60
TAAAATAANN TGGATGTACC AATTTTTTTG ACATTAGTCC ATCATTTGCA TATTTTTTTG	120
CAGTTGATGG ATTATTTTAT TTTTGCCAAA AACAATTTTT TTAACCTAAN NACCCAACTA	180
TACTTAGTTT TTTNACCAAG AACATTTGAG CCCGAGACAT AAATCAATGT CATAGGCTCC	240
ACAATGTTAT ATTAGCTGTA GTTAACCGAA CGAAATGCGC TTATAACTAG TTTTTTCAAT	300
TCTGGTCGGG GGTCCCAACA TAGAAGCTTA TGGAAATTCA GCTTACAATA ATGAGCAGGT	360
TGGGGTGGGC TCCAACACAG AGAATTTCGA TAAGAAATTC CACAAATAAT ACAAGTTGGC	420
CCACTCCCAT TCTGTAATAA ATATAGGAGG TCATTGTTAT GCAAATAGAA CTTACTGATG	480
CAGCAGTAAC TTGGTTTAAA AATGAACTTG AGTTGCCTGA AAATAATAAA GTGCTCGTGT	540
TTTTTGTAAG ATATGGTGGC GAATTCACAC TCAAGCAAGG ATTTAGTCCT GCTTTTACAG	600
TTGAACCAAA GGAAGATGTT GATATTGGCT ATGAACAACA ATATGACGAT TTAAATGTTG	660
TCGTAGCGGA AAAAGATTTG TGGTACTTTG AAGATGACCA CATTATTGTA AATGTAGNTG	720
ATCACGAAGA TGAAATTTCT TATTCCACAA AATAACTAAA ATAAAACGAA CTTGTTTACA	780
CATTCTGATG TGTCTGAAC CTCGGAAGTT GACTCTGCC TTAGCACATC TGATGTTGTN	840
TGAACAANTT CGNNTGNNGG TATATATTAG CTTATCTTCA CGCTAATTAC ATAATGTTAA	900
CGTATGGG	908

(2) INFORMATION FOR SEQ ID NO:1068:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1709 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1068:

GGCACTAACT TCATTGAGC ATCCTCCTAT CAATTGCTAT ATAAATTAGT ACCCTTTTGC	60
CACTTAATTA TAACAAATTC TCAAATTTTA AAAATTGAAA ATCTAGTTAA TGTATTAGCT	120
CGATTTTGAA ATCTAATAAT AATTGGCATA AAATGGAAGT AATATTATGT GAGGAGTGTT	180

```

ATGAAATGAC AAAAATATCA AAAATAATAG ACGAACTGAA CAATCAACAA GCTGATGCAG 240
CATGGATTAC AACACCGTTG AATGTATATT ATTTTACTGG ATACCGTAGC GAACCCATGA 300
AAGATTATTT GCATTATTGA TTAAGAAAGA TGGTAAACAA GGTACTATTT TGTCCAAANA 360
TTGGAAGTCG GAAGAAATCA AAGCATCACC CTTACACAGT TGAAATCGTT GGATATTTAA 420
GACACTTGAA ATCCTTTTTC ACTTTATCCA CAACNCAATC AATAAATTAC CTAATTGTAA 480
GCGGAGCACC TTAACAAGTA GCACCGCCAC AAACAATTAA TCTCTGTTTC NATGTCAATT 540
CATTCGGAGA TGTGAGTTA ACAATCACAC AATTAAGAGA TATTAAATCC GAAGATGAAA 600
TTAGCACAAT ACGTAAAGCT GCTGAGTTAG CAGATAAGTG TATCGAAATA GGTGTTTCTT 660
ATTTAAAGA AGGTGTGACT GNACGTGAAG TAGTCAACCA TATTGAGCAA ACTATCANAC 720
AATATGGCGT CAATGAAATG AGTTTTGATA CGATGGTTTT ATTTGGAGAT CATNCCGCAT 780
CACCTCATGG CACACCAGGA GATCGCAGAT TAAAAAGCAA TGAATATGTA CTATTTGATT 840
TAGGTGTAAT TTATGAGCAT TATTGTAGCG ATATGACACG TACCATTAAA TTTTGGTGAA 900
CCTAGCAAAG AAGCACNAGA AATTTATAAT ATTGTATTAG AAGCAGAAAC ATCTGCAATC 960
CAAGCAATTA AACCTGGAAT ACCTTTAAAA GATATCGATC ATATCGCTAG AAATATTATT 1020
TCAGANNAAG GTTATGGTGA ATATTTCCCT CATCGCTTAG GTCATGGTTT AGGATTACAA 1080
GAACATGAAT ATCAAGATGT TTCAAGTACT AATTCTAATT TGTTAGAAGC TGGCATGGTT 1140
ATTACAATCG AACCAGGTAT TTATGTACCA GGTGTTGCAG GTGTAAGAAT TGAAGATGAC 1200
ATACTTGTC AATGAAGG ATATGAAGTA TTAACACATT ACGAAAAATA AGGAGTGGGA 1260
TAAAAATGAA AAGCTTGTTA CAAGCACATT CTCATTCAGT CAAACACTGC CAATATAACA 1320
TTGTAGCGCC TAAGACATAA ATTTTATCC AAGTCTAAAT GCAATATGTA ACAAACAAGC 1380
TAGAAACACA TATGCAGGTA TGTTTCATCAG TAACATGTAA TGAATCAAAT CAATATCATT 1440
CATGTTGAT GATTTCTTCG CATGTTTCT AGCTTTAATT TATCATTATT TAATTTTAAT 1500
AACCAAGGAG ATGATAACGT CAGTCTTTAG TACGCTGTAA TCCATTCCCT TTTCATCAAA 1560
TTCAAATTAT AATTGTAATG CTTCTTCTAC AGATTTATAT TCCATTTCAA ATGCCTCTGC 1620
AACGCCTTTA TTGGTTACGT GACCTTTGTA AGTATTTAAA CCTAATGATA ATGGTTGATT 1680
TGATTTAAAT GCTTCTCTAT ACCCTTTAG 1709

```

(2) INFORMATION FOR SEQ ID NO:1069:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1069:

```

AAAGAGGAAG ATGTGAACCA CCACTAGTAT TGAATCTAAA GATTGAGGAC GTTCCTTTAT 60
TAATTGGCTA NNNAAGNNAN ATCNNAAGA TAGCCAATCC AAAGCCAAA AGTCAGCATC 120
AAGAAATACT TCTANNAAGG TAGCAGCTNN NNAGAAGNGN NAGAAATCTA AGANAAATNN 180
NAAATAATTT GTTCTTTGTC TAAATAGAGG AGCACCATT GACATCATAT CAGTCGGTGC 240

```

TCCTTTTATT	TATTCTTTTT	AATTAATTTA	TACAAANCCN	ATTCCCTGTT	GAGCGTGTG	300
AATCGCCTTC	CNTTGTTTTG	TTCTCNCGGT	ANCCCATTTA	ACCAAATNAT	AAACCANAT	360
CTTNTTCCAA	ATATTTCTAT	TTGATCAAAA	TAAGGTTTGA	AATTTGCGTT	TTTCACATAA	420
CCAGCTCGTG	CCAATGCTAT	CGTGCAATTA	GCTTTGAGTC	TGTATATAAT	AGTGCGTTTT	480
GAACATTTAA	TTACGTGCA	TGTTCTAGTG	CATAAATACA	TGCAGCCCAT	TCTGCAGTGT	540
GGTATCCAT	TTGCGCTAAC	TCATGTGTAT	ATGTATNATG	CTGCTTATCT	TCTTTGATTA	600
CAATGGCACA	NGTACTTATG	CCTGGATTTC	CTNTTCGTCG	CAGCATCAAA	ATTTATGTGC	660
GCCATAATAA	ACCTACTTTC	TATTCAATAC	TTAGTTAAAG	TTACTATTAC	TGTAATACAA	720
AATATGTTGG	GTAATCCATT	AAAAAACACG	CATCACTTAA	ATAAGTAAAC	ACGTTGTAA	780
AAATACTTCG	CTTGATTCAA	AAGATGATTT	TCTAAATACG	TAGTNC'TTGT	AAAATACTTC	840
CTAAANAAAT	CATCTTCAGG	CTGGGGACAT	AAATCAATGT	TCTATGCTCC	TNCCGAAGTT	900
ATATTGGCAG	TAGTTGACTG	ANCGAAAATG	CGCTTGTAAC	AAGCTTTTTT	CAATTCTAGT	960
CAGGGGCCCC	AACACAGAAG	CTGNCGAAAA	GTCAGCTGAC	AATAATGTGC	AAGTTGGGGA	1020
TGGACCCCAN	CAAAGAGAAA	TTGTATTCCC	AAATCTACA	GACNATNCAA	GTTGGGGTGG	1080
GNCGACGAAA	TAAATTTTGC	GAAAATATCA	TTTCTGTCCC	ACTCCCTTAA	AACTTATTCT	1140
TTTGTTAGT	AAGTGCCTTA	ATAGCCTTGA	TCTAACTTAT	CAATCTTACC	TTTACGATAA	1200
AATGATTTAG	CAATATATCC	ANNITGGTACA	TTGAAAACG	TTGAAGCTAA	TTTTAATACG	1260
TAAGTTGTAA	TAAATATTTT	NAATNCAACT	GTACCAGGTA	AACTTCCGAT	AAAAGCGATA	1320
GCTACAAATA	AAGCTGTATC	CAATTATTGA	GCTTG			1355

(2) INFORMATION FOR SEQ ID NO:1070:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 688 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1070:

CCTTTCTGGN	CCANACATTA	TTTCTCGGGG	NATTTGAAAA	ATGAGGGATC	AGGTCAATTA	60
ATTATTGATG	CACCCACGCA	CAATCCNAAT	TGATGTTATT	AGTAAGTTAC	ATCAAAATAA	120
AGATATTCAA	TGGCATCAGA	TTAAATCTTC	TATCATTGAA	ACATTACAAC	CTTATTTATT	180
TGAAAAACA	GCTAGAAAAC	CAATGATTTT	ACCAGTCATT	ATGAAGGTAA	ACGAACAAAA	240
AGAATCAAAC	AATAAATAAT	CAAAAAGCTA	CTAACTTTGA	AGTGAAGTTT	TAATTAAACT	300
CACCACCCAT	TGTTAGTAGC	TTTTTCTTTA	TATATGATGA	GCTTGAGACA	TAAATCAATG	360
TTCAATGCTC	TACAAAGTTA	TATTGGCAGT	AGTTGACTGA	ACGAAAATGC	ACTTGTAACA	420
AGTTTTTTCA	ATTCTAGTCA	GGGGCCCCAA	CATAGTAGCT	GGCGGAAAGT	CAGCTTACAA	480
TAATGTGCAA	GTTGGAGTGG	GACGACGAAA	TAAATTTTGG	GAAAATATCA	TTTCTGTCCC	540
ACTCCCATAT	TCCCGATAGA	AAAACAGGAC	TTGAACTTGC	AGAAAAATAT	GGCATTGATG	600
GCGTCATGAT	TGGTAGCGGC	ATTTTCCATA	ATCCATTTCG	TTTTGAAANA	GAACCACGGC	660

AACACACAAG CAAGGAACTA TTAGATCT

688

(2) INFORMATION FOR SEQ ID NO:1071:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1722 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1071:

```

GGCACGAGCG GCACGAGCGT AAATAGCTGG AAAGATGTAG AACAGTATTT TTTAGATAAT      60
ATTGAGAAAT AAAATATATC ACTTGAAAAA TTTCATGTAG AAAAGATGAT GGATAGGCTA      120
TAAAGTAATT GTGACTGAGA TGAACCTTTA TGTCTTAGAC ACTACAACAC TATATTGGCA      180
GTAGTTGACT GCCGGGCCCC AACATAGAGA AATTGGATTC CCAATTTCTA CAGACAATGC      240
AAGTTGGCGG GGCCCCAACA TAGAGAAATT GGAACGCCAA TTTCTACAGA CAATGCAAGT      300
TGGGGTGGGC CCCAACATAA AGAAATACTT TTTCTTTAGA AATTAGTATT TCTTATGGGA      360
GTGGGACATA AATCAATGTT CTATGCTCTA CGAAGTTATA TTGGCAGTAG TTGACTGAAC      420
GAAAATGCGC TTGTAACAAG CTTTTTTCAA TTCTAGTCAA CCTTGCCGGC GGGGCCCCAA      480
CACAGAGAAA TTGGATTCCC AATTCTTACA GACAATGCAA GTTGGGGTGG GACGACGAAA      540
TAAATTTNGN GAAAATATCA TTTCTGTCCC ACTCCCTCCT ATTTTTAAGT ACACATTAGC      600
TTTGACTAAT GATAAAGAAT CGCTACATAA TCAATCATTA GTCGTTCTTT ATCATTTCGG      660
TCCCCTCTC AATAAATGTT AGTCTATCTC ATTATTATAA ATCGGATGAA TGTGTTAATC      720
TATNGCAGAT TACACGTCAA CCCGATTTTT TATAGAATTT GGGAAAGACG GATAAACCAC      780
TATGATTTNN NNTTCAACAT CAATCANTTT AGGGGGNATG CGGCAAAATT ATATGTCTNT      840
TTTTGGGACA GGGGANTAGG TTAAAGCTTA TAAAAACGAT ATAAGGTGCG TCGAATCTTA      900
TGATTACAAT CCAAACCCAA TATAATATCG GGTCAAGATC AANCCGGATG GNTTACAAAT      960
CANTGACAGG AAGTAACTTG AATAGCAATN TGGGATAACC TCAATATCAA TAGGTGTTTC      1020
TAATGAAATT TCGCCATCAA TATCAACTNT CATTGCTGGG ACCTGTTGTA AGTGAAATCT      1080
TTTTNCCAGG AATATGCTCC AATACCTTGA GTAATTTTAT CCAATTTCAT CTATCACGCT      1140
TTTAAAAATA TCATTTAAAA TACTGAAACT TTGTCCATTA AAAATGAAAG TGTTTCAAGTTC      1200
ACCCATCTTG AGGAGACAAA TCAGTCAATG GTANACGACT ACCACCAATG AATGGACCAT      1260
TTGCTGTTAG TATCATGGTC GTTTCGCCAG AATATGTCTT ATCATCTATT GATAATTGAT      1320
AATTAAATTG TGTGATTTT AGCAGTGTTT TGACAGTTGA TCCAATATAA CTCAATTTAC      1380
CAAATATATC TTTTGANCCA TCTTGACGT TTTTCAAGTT TTGAACAATG AGACCTAAGC      1440
CAACAAAGTT GAGTGCATAT TGATTATTTA TTTTAATTAC ATCGTATGTA CCAACTTGTTG      1500
CAGAAATCAT TTGTTCACTA GCTTGTTTAT GATTAGGTGC TATATTTAGC GTNTGTGTAA      1560
AATCATTAAT AGTACCGCCT GGTAAAATGC CAATAGGGAG TTGAAGGTCA TGTGACATAA      1620
CACCATNTAT AGTTTCGTAAC CGTGCCATCA ACGGCAAGGA ATAAATAATA TNTCTACATC      1680
TTGNGGATAG TTTTAGTGTG GTTCTCGGC AATATTTAAN AC      1722

```

(2) INFORMATION FOR SEQ ID NO:1072:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2437 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1072:

```

GTGTTACGGT AGGTTGTTGA TCCTAATTTT CCCTGNCAGT TGGTCCCAGT ACCCAGCCAT    60
TTCCCAACTT ACTAAAAAAG AAATCCAATT ANNCCGAAAG AAAATATTGA AGTCATTGAA    120
ATTAACCGAA GCGTTCCAGT GCACAGGTAG TTGCCTCCCC AACCAAGCTT TAAATATTTT    180
CAAATACGCA ATTAAATATA TGGGGTGGTG CATTAGCATC AGGTCATCCA TACGGTGCAA    240
GCGGTGCCCC ATTAGTGACT CGATTATTTT ATATGTTTGA CAAAGAGACT ATGATTGCAT    300
CTATGGGGAT AGGGGGAGGT CTAGGAAATG CAGCATTATT TACTCGATTG TAACCAGCGA    360
TTAAATGTGT CATTTTCTAA GGATAGTGTG GCTGCATATT ATCAGTGTTC TANCCAACCT    420
TATAGAAAAG AAGTCTCGTG CCCATTAATG TGTNCGTCAT TATGGCCACA ATTTGATTTA    480
TTTAAAAAAA TATCCAAATA GCGAGCTGAT TTTACCACAA ATCAGCAATT AATCAAATC    540
NCAAGATAGA AGTAGACACA ATATATGTAG GGCATTTAGA AGATATTGAA TGCCGACAGA    600
CTCGCAATAT CACACGTTAT ACAATGGCTT TAACATTAAC TAAAAATGAT CAACATGTCA    660
TANCGGTTAC ACAAACTTT ATTAAGGCGA TGAAGTAGAG ATGAAGTTTA ATGAGATATG    720
GATAAATGAA TATTTGGCGC TCGTAAATGA TGATAATCCA ATACATAATG AGATTGTGCC    780
AGGACAATTA GTGAGTCAA TGATGCTGAT GGCTATGTCA TTAGAGACAA ACCAGTGTCA    840
AATTAACACT GTTAAACCTA TTTTAATAAA TGAAAATATC GAATTCATTG AACAAACGGA    900
ACACGAAATT ATAGCAATTA ATGACGATGG AGAGATTAAA ATAAAAATTT CTTTGAGCAC    960
AAAAAATAAA CCGATATTAG CTGCATGAAC GCATATTAAT TAGGAGATGA AAGGACAGCT   1020
AATATCAGTT ATGTATTGTT ATTATTATTG GGAACAGAGA TGAATATAGG TTACGTTTCT   1080
TTCTTTGCAC GGGGATGCAT TAATCTAAAA TAATAATAAC AACTATATCA ATGTTTAATA   1140
AATTCTGGAT TATTGGAACG ATTAGTCAAT TTAACAACT TNCATATGAT CTATATCGTC   1200
TTGTNATAAA GAGAGCAATT TGAATATTTT AGTATCACTA AATGAATCGN CACATTTAAT   1260
TGAAACATGC TGAAACGTTT GGGTTATAAT TTCATAAACT GGTGCGCCTT CATGGTGATA   1320
CTGTGGAATA AATAATCATA ACCATATTTA CCTCCTTNGG CTACTCTATG GGTATATTAT   1380
AAATAACATT TTTATGTGTG ACATCAACCT TAAGTATCAA CTTTTTATCA GACATAGAAC   1440
GTANGATTTA CTAAGACTAT TTATGTATAA AAGTTCTAAA TAAATATATA TTTATAGAGT   1500
CGCCTGGCAG NCATTTGGGA AATATAACAT ATATGATTAG AGAGGCATCT ATCGCAAAAG   1560
AATGATAATG ATAGAGGTAT TGAGCATATA GATGAGTTTA AGTTCATCTT GAAAATAAAG   1620
GGTTATTTAG TCATAGATGT AGATGTATAG GAAATATTTG TATGTATTGN TCGATATGTA   1680
TGAAATTTTC AATAAAAGCT AATAACGCTT ATATGTAACT TTCAAATTTA AATTATATAC   1740
AGAGCATGAT GATTATAAAA AAATANCCAC ATCACATAAA TTGAGTTCAT ACCCAATTTA   1800

```

AGTGGTGTGG	CTAATAATGT	TGATTTATAG	ATGAACCGCC	TAATCGTTAA	ACCTCTGTTA	1860
CTTCAACATC	GATATGTTCA	ATACGGTTGT	ATGCACCGTG	ATCCACAGGA	CCAACAAAAT	1920
CATTCAATTT	CCAACCGTTT	TTAATAGCAG	AAGCGACGAA	AGCTTTTCGCT	CGTGCTAATC	1980
ACAGCTTCTT	TCGGTGACTT	ACCGTTAGCT	AAATATGCAG	GTGTTGCCGC	AGCAAATGTA	2040
CAACCAGCAC	CATGGTTATA	ACTTTGTTGG	AACATGTCTG	TTGTTAGTTG	ATAAAATGTG	2100
TGACCATCAT	AGTATAAGTC	ATACGATTTA	TCTTGATCTA	AAGCTNTGNC	ACCTTTAATG	2160
ATGACATGCT	GTGCGCCTTT	ATCAAAGATA	ATTGNTGCAG	CCTTTNACAT	ATCTTCAATT	2220
GAATTTAATT	TACCTAATCC	TGATAATTGA	CCCGCTTCAA	ATAAGTNTGG	TGTCACTACC	2280
GGTGGTTTAG	GTAGTAAATA	TTTAATCATC	GCCTCAGTAT	TTCCAGGATT	AAGCACTTCA	2340
TCTTCGGCCT	TTACAAANCCA	TGACAGGATC	TTACTACAAA	ATATTGTGCA	ATTAGATGCT	2400
CATATACTTC	TCCAGNACGG	GTGGATATCT	CCTCAAG			2437

(2) INFORMATION FOR SEQ ID NO:1073:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1759 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1073:

GGCCCCCTCCT	GAAGGTTGTN	CCNCCCCCAG	TATGGTGCAT	GGACGAAATG	CCTCAATTCTG	60
CTTGTTGCAG	ATTATCTCCT	CCACCACCAC	AAGTTTCGTC	TTTATCGTCC	TCCNATAGAA	120
GTAGGGTTTC	CTACTACTTG	NCCATTCATA	ATCTGTTGCA	TTTCATGTTT	GATNTGGTGA	180
AGATTTAGGA	GCCACAAATT	GCTTGCAAT	TATTGCCGAC	TTCTAATACA	CCAGATGCCG	240
CTAAATCTTT	CACACCAGGA	ACATCAACTT	TAGATTTGTC	GTTAACCTCA	ACACGTAGAC	300
GTGTGATACA	AGCGTCTAAA	TGTTTAATGT	TTGCTTTGCC	ACCCATAGCT	TCTAATACTG	360
CATATGGTAA	TTCACTTGCT	GAAGCAGTAA	CAGCTTGTTGA	TTGCTTATCT	TCACGACCTG	420
GTGTTTGTGA	TTTTAATTTT	ACAATTAAGA	ATCGGAATAC	GAAGTAGTAA	ATAACTGCGT	480
ATACAAGACC	TACAGGAATG	ACTAACCACC	ATTGTGTCTT	ATTAGGTAGT	ACGCCAAGTA	540
AAACGTAGTC	GATGAAACCA	CCTGAGAAAG	TATAACCTAA	GTGAACATCC	AATAAGTACA	600
ATGTTAAGAA	TGATAAACCA	TCAAGTACTG	CGTGAATAAA	GAATAATAAT	GGTGCTACGA	660
ATAAGAATGA	GAATTCATAA	GGTTCGTGTA	TACCAGNTAA	GANTGATGTT	AAAGCAGCAG	720
AACCCATTAA	ACCTGCTACT	ACTTTCCTAT	TTTCAGGGTT	AGCTGTGTGA	TAAATTGCTA	780
AAGCTGCTCC	AGGTAAACCG	AACATCATAA	CAGGGAATTC	ACCTTGCAATG	AATTTACCAG	840
CTGTCAAATG	TGCGCCTTCA	CGAATTTGTT	CGATAAAGAT	ACGTTGGTGC	ACCGTGAATA	900
ATTTCAACCAG	CTCGTGCAAA	CTGTGCATTG	CGTTATTTAA	TTCTGTTGCT	TTTGNAGNTT	960
CTTGATTTAC	ACCAGCTACT	GTAGTTGCAC	CATCAATGGC	ACGAGCGTTA	ACGCATCTTT	1020
TTGTGCATTG	TTAATTGATG	TTAAGTTATT	CAAGTTGTTT	TTGCTGTGTG	TCTTAGCTTG	1080
AGCTAAGTTT	TGCGCACCAT	TTAATGCATG	TTCTTTAGTT	GTCACCTGTG	ATGTTGCTTG	1140

CGTAATAGTA	TTTGCTTCCA	TCGTTGGGTT	CGATGTTTGA	TTAATGATTG	CTTTTGCTGC	1200
AGTAAC TGCG	CTGTGCTACT	CGTTACGATT	ATTTGGACTT	GCGTCAGTGT	AGTTT TGACC	1260
TGCTTTAATC	GTTGCTTCAT	TCGCAATACT	ATCTCTTAAG	CCTTTCATCG	CTGTATTCAA	1320
CGTTTGAGAA	CTATTTT TAA	CAGTTTGAAC	ACCATCTAAT	GTAGTTGCAC	TTTGAAC TTG	1380
TTCTTTT AAT	TTTGCTTTT	GTACATTATT	CAATTGTGCT	AAGCCGTCAA	TTGTATTGTT	1440
AGCATGCTCT	TTCGCTACAC	GTAAGTTGTT	ATCACCATT	AATGCTGTTT	TAGCCGCATT	1500
GACTTGTGAT	GCCGCACTAT	TTACGTCATT	GACTGTTAAT	GTCGCATTTG	GTGTACCATT	1560
AATGATATTT	TCAGCGTTAG	TCACTTT TGA	ATCATACGCT	TGACGTTTTT	CTTGATCAGC	1620
ATTGACATAA	TTACCGCTTG	CTTTTGT TCT	TTCTTTATCC	GCAATAGCTG	CNTTAAGTGC	1680
TGTCATCGCA	CCGTTCAATT	CAGTAGCTGT	ATGTTGAACG	TTATTTGNAT	CAGATACACG	1740
TTGTGCAGTG	GGAATTCCG					1759

(2) INFORMATION FOR SEQ ID NO:1074:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3822 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1074:

TGAANTATTT	TNCATAAGCT	TATTCCTCCT	TATATTNTCT	CCACTTCATT	GTTTNANGTG	60
NCTCCTGCAN	CATAGCATT	GAATCAAAAG	GAACCATTAG	NCTGCACAAC	AAGNTAATTT	120
CGATACGTCT	TNATCAAACG	TCAAGGGTGC	AAGCTTTAAT	CCTTCAGCCA	TCGTNAAATA	180
AGGNGCAAAG	CTATCCGTAA	GGTCTCCAAT	GGTCANACCC	AAATTTGAAC	CGCTAACCTT	240
GNCGCATAAA	ATAACATCTC	CAGCATTTTC	ACTCACAATG	TGCGCTCCGA	TCAAATTTCT	300
GGGTTTGGGC	GTTGNCTACA	AGTTAATAGA	CCCCTGTTGT	TTCGTGATTG	ACTAAGGCCC	360
GCGGTACAGC	GTCCAACGGA	AGGACCGATG	TTTTGACATC	GTAACCTTTT	TCTTTTGCCT	420
GTTGTTT CAGT	CAAGCCGACT	GTGGCGATCG	ATGGATTGGT	GAAGGTTACG	CCGGGAACAA	480
AGCGAAGATC	GATTTTGCCT	TTGCTAGAC	CCAACGCATT	ATTTGCCACA	ATCCCGCCTT	540
CATAAGCTGC	AACATAAACG	AATTGCGGAC	CGAGGGTCAC	ATCGCCCGCG	GCATATATTC	600
GGTTATT CGA	CGTTTGCAA	TATTCATTGG	TCAGCACTTC	GCCTTTTTTC	CCTGTTTTCA	660
CACCTGCTGA	TTCAAGGTTT	AAAGTCTCTG	TGTTCCGGCTT	TCTTCCTGTT	GCCACGAGGA	720
CTTGATCGGC	TTGATGACT	TGTTCTTGAC	CGTTCACTTC	AATATAAATG	CTTGTCGACT	780
TACCGTTTTG	CTCAACCTTT	TGATAAGTGA	CCCCAGTGAT	CAGGTTAAGT	CCTTGCTCAG	840
TTAAGGATTC	ATCGATGGCT	TCGGAATTTT	CAGGATCGTA	GGTTT TAAAC	AGACGCTCGC	900
TTCTTTGCAT	GAGAGTCACT	TCTGTTCCGA	GGTTGTGAAA	CATTTGACCT	AATCCGCTG	960
CGATATAGCC	AGAACCGATC	ACTGCCAATC	GTTGTGGAAC	CTCTTTTAAT	TCGAGTGCCG	1020
ATGTACTTGT	TAAATAATCA	ACCTCATTCA	TTCCCGGGAT	TTCCGGAACA	GCCGGAGAAG	1080
CCCCCGTTGC	GATTAAAAAG	CTTTTAGACG	TGATGTTGTG	TCCATTCACT	TGTATCGTCT	1140

TATCGTCGAT	AAACGAGGCC	TCGCCACGAA	TGAGATCAAA	TCCATATTCT	TCGATCAAGT	1200
CTATATATTT	TTCTTGACGC	ATTTGACTGA	CTAATCCATC	TTTTTGTTTCG	GTCAATTGGG	1260
CAAGGTCCGC	AGCACCGGTA	CTCGTTTGAA	GTCCGGTAAA	CGGATTGTTT	TGGGCGAGAC	1320
CGTTTATTTT	ACCGGCACGA	AGCATGGTTT	TTGACGGTAC	ACAACCGATG	TTAACGCAGG	1380
TCCCCCGAC	GGTTCCCCGT	TCTACCATGG	ACACTTTCGC	CCCGTTTCA	TTGGCCTTGA	1440
TAGCTGCAGA	AAACGCCGCA	CCGCCGGAAC	CAATAATCAG	AAGATCGTAA	TCGCCATCCC	1500
GATTGAAATC	TACACTGTTT	TCAGAGGGCT	GGCTTCTTTC	CTCTCCGGGT	TGATAGCCGG	1560
CTGCCGAAAT	ATTTTGCTTA	GCCTTTTCGA	TCTGATCATC	GNTGAGTTCA	AAAATGGCCG	1620
CACCAGCGTC	GGAAATCGGC	CGAAACATCT	TTAGCTCCGG	CTTGTTCCAA	TGCTTCGGTT	1680
ACATGTTCTT	CACAGCCTGT	GCATGTCATG	CCTTGAATGG	GTATTTTATA	TGAATTTTGA	1740
GTCATTTGAA	TCCCTCTTTC	TATTTAAAGT	TTGATAGACA	GTTCTGTACA	TTTATCTCAT	1800
ATTTATCTTG	TCTCATGTTT	CCGATCCACG	CTCTCTGGAG	GCGTACAGCA	ATCCGTTTTA	1860
TTTTTTGTTT	TTCCATTGCC	TTCAGGAGAA	TTGTATTTGT	TCCTCAACAA	CTTGCTGAGG	1920
ATCAGAGCAA	TCATAACAAT	GGCCAATGCT	GCAAAAATGC	CGGTCAACCA	CCAATTTCCCT	1980
GTCCGACCAG	CAAAGAGGGC	ACCAATACCT	GTGCTCCCTA	ATGCAACAAG	GAGAATCGGT	2040
CCTGCGCAAC	AAAGTAAGGA	ACCAATAAAG	GAACCAATAA	TATCCCGAAA	CAGGCCCAAA	2100
AACACCAGCG	GGTACCTTTC	GAGCGATTCT	CATCCATCAT	TCTCACCCT	CTTTCTAAAA	2160
AAAAATTTTA	TTCTTTGGGC	ACGAGGTACA	TACATGNCCT	ATAGCCTAAC	TTGAAATTTG	2220
TTCTGTTAGC	TTTTTTACAT	CTTTCATCTA	TTTTTTGTTA	CACCTGATCG	GTTGGATTTT	2280
AAAATGTACA	AATGCCACCA	GAACCGAAAT	ACCAAGTAATA	AGCCATGTAC	AAAACGGAGA	2340
GGAAATCAC	AACAGCTGCT	ATTTTTTGGA	TAGAACCCAT	ATAGTTGTGC	AGAAACTTCT	2400
GTACCAAGTG	GTCTGAAAT	CAANGAGACC	ATCGTGATCG	CTGNCACCAC	AACTCCCATA	2460
CCAAGGGAGT	AGATGATGAA	CTTGATGATC	ACGCCCGTTA	CGCTATTGTC	ATTGAGCGAT	2520
GCAGAGACCA	CCAACATAAN	GGCTGGCAAG	GTACAACCAA	GTGATGTCAC	GGCATAGGCT	2580
ATTCCGTAAA	AATAGATAGA	CCATTTCCCT	GGCTTGACTT	GAAAAGATCC	TATTTTANTC	2640
GGCAATGCT	TCCCGAATAG	CATGCCCAAC	CCCAATAAAG	CAATGAGTAT	ACCCATAACC	2700
AATGAAAGAA	TCGAAAAAAT	CCCTGTTAGT	GCGCTTCCCA	ATCCTCCTAT	CAATAAACCA	2760
GCCAATACAA	AAATCGTTAT	TTAACCCCGT	GGTCATCGCT	CCACCAAGCC	CTAATCCTTT	2820
AAAAATTGNA	TAGNGGAACG	AATGATCCTT	TGTTTCGCCT	CCAATTAAAT	AGGAGATATA	2880
AGAAGGAAGC	AAGGCGATAC	CACAAGGATT	AAAGGCCGCA	ACCATTCCAG	CGGTCAGAA	2940
GAAGAGAAAC	GAAAAACTCA	TAATTCCACT	CCTATTTGAG	TCAACGCTTC	TTTTAAATCA	3000
TCAAAGGACG	GTGGAACAGA	ACGATAGAAT	ACCTCATTTT	CAGAAATTGAC	CAGTACGATC	3060
TCTTCCAATT	GTTTGACGCC	ATAGGTATCC	GCAATTTCTT	TACCATTCTT	TAAAACATGG	3120
GGCCAATCCC	CGCCATAATC	CTGTTTAAAT	TTGCGAAGGC	TTTCTTTTGT	ATCTGTGTTA	3180
GGGTCTAAAC	TAACTGTGAT	CAATTGAACA	TCGTTCCGGT	TTAGTTGATG	CATTTCTTTA	3240
AAGATTTCCCT	CATTGTATAT	ACAAGATGGA	CACCAGGTTG	CCATAAAATA	AATGAGTGTG	3300
GGTTTCTCAT	TAGGTAGGCT	GACTGGATTT	CCTTGAATGT	CTTGAACCTT	TGATTCTATC	3360
GCTCGTGCCA	TCAGATTCTG	CTCCACAAGC	TGTTAAACCG	ATTAACAACA	CCGTCATTAT	3420
AGCGGTGAAG	GAAATGCGTT	TTTTCAATTCA	AATCTTCCCC	CATTTATTTA	TCAGGCCCTC	3480
CCATTAACGT	TTCAATAATA	GGACAGGTAT	ACATCGCCTT	TTCATCTGGA	CACTTTTCTT	3540
TTAATTCCTC	TAATAACCGT	TGGATTGCTA	ACAAACCCTG	CACTTTCCGC	TCGATTTCTT	3600
TGGTTTTTTG	GAACGGTAAA	GGCGTACATA	TCTTTACATC	TCTCCCCATC	TTGATCAACC	3660
ACACCAAACA	ACAGGTGGAT	TTCCTTTAGC	GAGAAATCCA	ATTCTTCAA	TCGGTTAATA	3720

AACCGTACCG ATCTGCTGTT TCCTCTGAAT ATATTCGATA CCCTGATTCTG TATTCTGGGA 3780
 GGCCCGNCTA TCAATCCTTT TCCGCTCGGT AATACGAACG GG 3822

(2) INFORMATION FOR SEQ ID NO:1075:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2314 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1075:

GGCACGAGAN TTTTANGCCG AGAAAACCTTG TTGGAGAGAT TAATTTTTTTT ATTTTTTTTAT 60
 TTTTACTTTT TATTTTCTAC AAATATTGTG GNAAATCTCT TTATGAGTAA ATAAAAGATA 120
 GAAGCATAAA GAATAAATGA AAATGTGAAA ATATAAGTTT ATATGAATGT TGTAGAAAAT 180
 CTTCAAAATT ATTAAGTTTA ATACGATCAT ATTAGCAGTT ATAAAGAATA TGAATAAGAT 240
 AATATTATTA AATTTCTTTT TGTATNTAAT ATGNAAAAAT ATTANTGGGA AAAAGTTCAA 300
 GAAAAATAAA TATTAGATAA GTTACTATAN AGAATAATGC AATATAGCCA ATGTTATAAA 360
 ACATATTATT TGAATACCAA TTATTGTTAT TAAAGAACTT ATATTAAAT ATCTGCTAAT 420
 GATTGGAAAC CTATTATGCT AAAAAATGGT ATTGAGAATA CTAATACGGA TATAGGTATG 480
 ATTATTATTC CGAGTAAGAA CGTTACAATT ATAAAGTTCA ATAAGTACTC TTTGTTTACT 540
 TTTTTCATAA TAATTTAATT CCTTTTATGT ATATAATATT TAATAATAAA AAATTTTAAC 600
 ATTTATAATT GGAGGATAAA AGTCATATGA AGAATTTAAA AAGTTTTTTT ATTAATAATA 660
 CTTTGGTACT AACATCTACT GCATTATTAT TTTCTAGTTT TGAACCTGTA GTTCATGCTG 720
 CAGAAAATAA GGAAGTTGTT AAAACAGTAG AAAATGATAA TGTAGAATTC AATGAATTGT 780
 TAGAAGGACA AGAATATATT TGGGAAGTTT TATCTAGAGA TGATGAAGGA TTTAAAATGT 840
 TTCTAGATGA GCAAAGAGCT TTTAATCCTA ATTTTGATAA TGATGTTTTA CTAGCAAAAC 900
 AAGAAGGTGC TTTAAATTCT TCAGTATTTG CTAATAATTC TATGACTTTA AACTCAAATA 960
 AGCCTACTCC TAGAGGTCCT ATCGGTGCAA CTTTAAAAGC TATTAAGGCT CTATCACCTT 1020
 CTTTGAGACA TGGTGGGAAC TGCTATATCT TGGATCATT AACCATTAAG TAGAAAACAT 1080
 GCTGTTCTTA GTAAAAAAT ATTCAAGGAA AGATGTCCTA ATGCAAATTG ATAGGTTAAG 1140
 ATAAAGTCTT ACGGAAATCA GCTGTTGAAA AAGCTTTGGG TAAAGCAGGT ATACCAAGAN 1200
 GGTGGATGCG AAAACTTTAA CTTATATTGG ATTTTLAGGT TATTTAGACA CTGAGCTGAC 1260
 TTGCCCTAAG ATTTTATAAA ATCTTAGGGC AAGTTTTTTT CTTTTTCTT ATCTNGATAA 1320
 AGTAGTATTT TCAATTGTG ATTGGGGTGA TGATTTTCTA GATACAGTTA AAATTAATAA 1380
 TCATAGATAA TGAGAGAACC TACAATTATC ATAAGTTTTC ACCTAAAAAG GATATATTAA 1440
 AGTTTACAA ATCTTTAATG CACCTTTTAG AGTGTTTTTA AATCTATTCT TTAATAGACT 1500
 ATAATATTCA CTATTTATTA CACCGTTTTT TCTTTAGATT AATGAATTTA GGTGATGATT 1560
 TTGAACTGCG TTTCTTCTTT TGTCTTGATA CTATAANAAN CGAAGTTATA TAACATAAGA 1620
 CGACTTATCG GAAGTAGATA TGCTTGATATA TTCACAGATG GTATAATAAT AGAGTCGCCCT 1680

ATCTCTCAGG	CGTCAAATTT	AGACGCAGAG	AGGAGGTGTT	ATTCATGCTA	GAAATTCTTG	1740
TTCACATCAC	GACCACAGTC	ATCAGTGGTT	GTATTGTTGC	GTTATTTACG	CATTGGCTAC	1800
GCAATCGCAA	CGATAAATAG	GCGACTATAG	TCACACCTAA	AAAATCCCCCT	CACTACGGCA	1860
ATAGTGAGGG	GATTGGTGTA	TTCACGCTAG	AATTCTTGTT	AATCATATTA	TAACACTGGT	1920
TAGTAGAGGA	ATGCAAAAAC	ATAAGAAACG	TAAGTGTAAC	TCTATAATTA	GAATTATTAA	1980
TTTCTCNTGA	TACTATAAAA	GATTCTGTTG	CAAAGTTGAA	TTTATAGTAT	AATTTTAACA	2040
AAAAGGAGTC	TTCTGTATGA	ACTATTTTCTAG	ATATAAACAA	TTTAACAAGG	ATGTTATCAC	2100
TGTAGCCGGT	GGCTACTATC	TAAGATATGC	ACTTNCCTGCT	CGATTTCTTT	GGTTTNGTGA	2160
ACGGNAAGG	CGTACATATC	TTTACATCTC	TCCCCATCTT	GATCAACCAC	ACCAAACAAC	2220
AGGTGGNTTT	CCTTTAGCGA	GAAATCCAAT	TCCTCATTC	GNTTAATAAA	CGNACCGATC	2280
TGTGTTCTCT	GAATATATCC	GATNCCNGA	CTCG			2314

(2) INFORMATION FOR SEQ ID NO:1076:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3191 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1076:

CCCCAAGTCT	CATATGAAGT	AGTTGGATTA	GTTCCGAAGT	ATGAGGATGG	GAATTTCTTG	60
ACATAGTAAA	GTGCCGGATG	ATAGTGCAAG	AGGTATCGTT	GCACAAAATA	TGACAACTGC	120
TGAGATTGAA	ACATTTGGTT	CAGATCCAGT	TATTATGCCA	ACGGGGTGCC	CCTGGTATTA	180
TTTTCGGTAA	AACAACAAAC	TCAATGATTA	ATACAGGATC	AGCGGCTTCC	ATTGTTTACC	240
AACAAGGCGC	TATTTATGCT	AATGCTGAGT	TCATTCAAAT	TCATCCTACT	GCAATCCCTG	300
GTGATGATAA	ACTCCGACTA	ATGAGTGATC	AGCACCNPTG	TTGAAGGTGG	ACGAATTTGG	360
ACATATAAAG	ATGGTAAGCC	TTGGTACTTC	TNAAGAAGAG	AAATATCCTG	ATTATGGTAA	420
CTTAGTACCT	CGTGATATCG	CAACCGCGTG	ANATTTTCGA	TGTATGTATT	AACCAACAAA	480
TTAGGNATAA	ATGNCGAAAA	CATGGNATAT	CTTGATTTGT	CACATAAAGA	TCCAACATGA	540
GTTAGATGTA	AAACTAGGTG	GTATCATTGA	AATTTATGAN	AAATTCACTG	GTGATGACCC	600
ACGCAAAGTA	CCAATGAAGA	TTTTCCCAGC	TGTTCACTAT	TCAATGGGTG	GTCTATATGT	660
AGATTATGAT	CAAATGACAA	ATATTAAAGG	GTTATTTGCA	GCTGGAGAAT	GTGACTTCTC	720
TCAACATGGT	GGTAACCGCT	TAGGTGCCAA	TTCATTGTTA	TCAGCGATTT	ATGGTGGTAC	780
AGTAGCAGGT	CCAAACGCGA	TTGATTAATA	TTTCAAATAT	TGATCCGATC	CATATACTGA	840
TATGGACNGA	AGTATTTTTC	AAAAACGTAA	AGCTGAAGAG	CAAGGAACGT	TTTGATAAAT	900
TATTAGCTAT	GCGCGGTACA	AGAAAATGCC	TATAAAATTAC	ACCGTGAAC	TGGTGAAATT	960
ATGACACCAA	ATGTAACGTG	TGTTCTGTGA	AATGAAAAAC	TGTTAGAAAC	AGATNAAAAG	1020
ATTGTTGAAT	TGATGAAACG	TTATGAAGAT	ATTGATATGG	AAGATACTCA	AACTTGGAGT	1080
AACCAAGCGG	TATTCCTTAC	CCGTCAACTA	TGGAACATGT	TAGTACTTGC	ACGTGTTATT	1140

ACGATTGGTG	CATATAACCG	TAACGAATCA	CGCGGTGCCC	ATTATAAACC	AGAATTCCTG	1200
ATAAGTATTT	TCGTCAGAAG	TACATAATAT	TTAAATCATT	TAATTTTGAG	AAGCATGGAA	1260
AATTTTGGAA	CAAATGGTTT	TACGTAAGAA	AATGGAAACA	TAAGATTTTA	GATGGTCATC	1320
AGCTTAATCA	AAATATATAT	GATCAGCGTC	ATTTAATGAC	AATCAATACT	GATGAAATTG	1380
AAAAAATGAT	TATAGAGACA	AAGAGGGCAG	AGTTGATTCA	TTGGATATCG	ATACTTCCAG	1440
TCATCATATT	CAATAAAGGC	TCTCGTTTAG	TAAAGTATAT	AAATATTTTC	TATGCAATGA	1500
TAGCTAATGT	TCCAATCATT	ATTGTGCAAC	GCTATAATCG	ACGAGATTAA	CGCAGGTACT	1560
ACGCATTTTA	AAACGAAGAG	GTGAACGTCA	TGACTAAACA	TATCATCCGN	TATTGGGTGG	1620
GNGGCTTAGG	TGGGATTTTCN	TGCAGCAATT	CGAATGGACA	AAAGTGGCTA	TTCCGNCTCA	1680
TTATATGAAC	AAAATACTCA	TATAGGAGGC	AAAGTGAATC	GNCATGAATC	AGATGGCTTT	1740
GGCTTTGATT	TAGGTCCATC	TATTTTAACG	ATGCCTTATA	TTTGTGAAAA	ATTATTCGAA	1800
TATAGCAAGA	AGCAAATGTC	AGACTACGTT	ACAATCAAGC	GTTTGNCACA	TCAATGGCGT	1860
AGCTTTTTTC	CAGATGGCAC	GACTATCGAT	TTGTATGAAG	GTATTAAAGA	AACAGGTCAG	1920
CATAATGCGA	TATTGTCGAA	ACAGGATATA	GAGGAACTGC	AAAATTATTT	GAATTATACA	1980
AGACGAATCG	ATCGTATTAC	TGAAAAAGGG	TATTTTAACT	ATGGTTTAGA	TACACTATCT	2040
CAAATTATTA	AATTTTCATGG	GCCATTAAAT	GCTCTTATTA	ATTATGATTA	TGTACATACT	2100
ATGCAACAGG	CCATAGACAA	GCGTATCTCG	AATCCATACT	TGCGACAAAT	GTTAGGCTAT	2160
TTTATCAAAT	ATGTAGGTTT	TTTCATCATC	GATGCGNCAG	CTGTATTATC	TATGTTATTC	2220
CATATGCAAC	AAGAGCAAGG	CCNTTGNTAT	GTAGAAGGTG	GAATCCATCA	TTTNGCCAAT	2280
GCCTTGGAAG	AGCTAGCGCG	TGAAGAAGGT	GTCACAATTC	ATACAGGTGC	ACGTGTGGAC	2340
AATATTAAAA	CATATCAAAG	ACGTGTGACG	GGTGTGAGAT	TAGATACAGG	TGAGTTTGTA	2400
AAGGCAGATT	ATATTATTTT	AAATATGGAA	GTCATACCTA	CTTATAAATA	TTTAATTCAC	2460
CTTGGATACT	CAACGATTAA	ACAAATTAGA	GAGGGAATTT	GAGCCGGCAA	GCTCAGGATA	2520
TGTGATGCAT	TTAGGTGTTG	CTTGCCAATA	CCCGCAATTA	GCACATCATA	ATTTCTTTTT	2580
TACGGAAAAT	GCTTATCTCA	ATTATCAACA	AGTTTTTCAT	GAAAAGGTAT	TGCCAGATGA	2640
TCCGACCATT	TATCTAGTAA	ATACGAATAA	AACTGATCAC	ACACAAGCGC	CAGTAGGGTT	2700
ATGAAAATAT	CAAAGTCTTA	CCACATATTC	CATATATTCA	AGATCAGCCT	TTTACCACTG	2760
AAGATTATGC	GAAGTTTAGG	GATAAAATTT	TGGATAAATT	AGAAAAAATG	GGACTTACTG	2820
ATTTAAGAAA	ACACATTATT	TATGAAGATG	TTTGGACACC	GGAGGATATT	GAAAAAATT	2880
ATCGNTCTAA	TCGTGGTGCA	ATATATGGTG	TTGTCCGAGA	TAAAAAGAAA	AACAAAGGAT	2940
TTACCTTTCC	TAAAGAAAGT	CAGTATTTTG	AAAACCTGTA	CTTTGTAGGT	GGATCAGNAA	3000
ATCCTGGTGG	TGGCATGCCA	ATGGTTACAT	TAAGTGGGCA	ACAANTCGCA	GACAAANTNA	3060
ACGCGCGAAG	AAGCGAANGA	ATAGGANGGT	GANATCTATT	GAAATCGGTN	NTCAGGACTA	3120
TTTAANAGAC	AATAGTGGNN	ACCCATCNTC	TTNTGGGGNC	TTGGGAGCAT	TTGGATNTTC	3180
NNCGGGGGNC	A					3191

(2) INFORMATION FOR SEQ ID NO:1077:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3815 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1077:

GGAGCATAAT	AAAGAGCGTA	TCTTAAACAT	TAATTTTAAG	TGTGATCCCA	AAGTAATTTT	60
CGTGATTTCAT	TGAAAATTGT	TCCGAAAGNA	CCGTGTGTCA	TCCAAGACAA	TATTTACCTT	120
AACAATATTG	ATTTGGGGTT	ACCTGGAACG	ATGTTATTAA	GTTTGGTTAG	CTGACAAAAA	180
TAGTCGTTAC	CGCCATCGCA	GGACCCAATG	CCGATTGTAA	TGGTTAGCAT	TATTAAATCA	240
ATGATGCATC	CAAAAATGG	AATATATAGA	TGCAAGTCAT	ATTGTGATTG	CGTTGTTAAT	300
CATCCTTGTG	ATAATCACAT	TGTTTATCTT	ATTATTCATT	GAATTAGTAG	AAGTGAGAAT	360
ACCATATATC	GATTTAATGA	ACGTTTCCGC	AACAAATATG	AAATCTTATT	TATCTTGGAA	420
AGTTAACCCCT	GCAGGCAGTA	TTACTTTAAT	GATGAGTATT	TCAGCATTTG	TTTTCTTGAA	480
AAGTGGCATT	CATTTTATTT	TATCTATGTT	TAATAAAAGC	ATATCAGATG	ACATGCCAAT	540
GCTGACATTT	GATAGTCCAG	TAGGTATTTT	AGTATATTTA	GTGATTCAAA	TGTTATTGGG	600
TTATTTTTTTA	TCGAGATTTT	TAATCAATAC	TAAACAAAAA	TCCAAAGATT	TCTTAAAGAG	660
TGGCAATTAT	TTTTCAGGAG	TTAAACCTGG	TAAGGATACA	GAACGTTATT	TAAATTATCA	720
AGCAAGACGC	GTATGTGGT	TTGGATCGGC	ATTAGTTACA	GTCATTATTG	GTATACCGCT	780
TTATTTTACA	TTGTTGTAC	CGCATTTATC	TACTGAAATT	TATTTCTCAG	TACAACTGAT	840
TGTATTAGTT	TACATCAGTA	TTAATATTGC	AGAAACAATT	CGTACATATT	TATATTTTGA	900
TAAATATAAG	CCATTTTTAA	ACCAATATTG	GTAAGGAGGT	AATTATGAAA	TACTTTTATC	960
CAGCTTGGTA	CGATGACCAA	CGATGGTGGC	AAGACACGAC	TGTGCCGTAT	TATCAACTAC	1020
AAAATAAGAC	GGAATTTGAC	GATATGATTA	GTTTAAATGGG	AATGCACCTT	GAAAATGACT	1080
TAGATTATCA	ACTGATTGTT	CTCAATCATG	CACCAAATTT	AAGAACATTT	TTACATCGAT	1140
ATGACTTATA	TGAAACAAAG	TATTCGTCTG	TGTTTGATGA	AATTCAAGGA	TTCAGTCACC	1200
ATGCCCCACA	AGCGATTAAT	TATCATCACT	TAAATGGGNC	GGATGATGTT	GGAGTNTGGG	1260
TACACGCCCCG	NATTTATTAA	AAATGTGTGA	CGAGTGAACA	GACCTATACA	NATATTTATT	1320
TNAGNCAAGA	AGGGTATTCA	NTTGGGTTTG	NAGANTGATT	NGAAAGAGAT	CAAGTNACAA	1380
CGGCCGTTATA	TTTTTGATGA	CAGAGGTTAT	TTATCAGCGA	TACGTTATTT	TGATGATCAG	1440
GGAGAGGCTT	CTTACCAACA	ATATTTAACG	GATTAATGGA	GATTGTGTAA	CTTCATGGAA	1500
GATTGGANAA	ATGGCAGGAG	TCACTGTATC	NANAAGGATA	TTCAACATCA	CTATCAACAA	1560
ACAGAATATA	ACAATATGGC	TCAACTAATT	GGAAGAAAAA	TTTCAAGCAA	TGATTGCACA	1620
ACAAATACAT	GAAGATGATC	ATGTGATTGT	GGCTTCAGAT	GCTAGGCACA	ATCGACAAAT	1680
AGCCAATCAT	ATCCAGCGA	AATGTGTTAAG	TTATTCATTT	TTTAAAAATA	GAAATGAANC	1740
TGTGTCAGAT	GAGGAATATC	AATCTATCGT	AAAGAATGCC	CATTTAATTG	TTGATAGTGT	1800
GCAACTAGAA	CGTGATTTAA	TTAGTCATCA	AGAGAAGTAT	CAGCGGGAGA	ATACAATGAT	1860
TCGAATCACA	CCATTTGAAA	CGAGACAATC	ACCTAATATA	AGTAGTCAAT	TGATGGAAAC	1920
ATTTATAGGT	GTATGGATAG	ATGGTATGAG	TGACGCTGAT	TTGCAACAAA	TGATGCAACG	1980
ACTTGTGGAT	TATATCGCAC	AGGAAGATTA	TTACCGTTTA	ATTTTATTAT	CGCGCCATCA	2040
AAATGACATA	CCGATGTGGC	TTCGTGAATG	TATTACGTCG	GTAAATGAGG	AATACCAAGC	2100
TAAACAGAAT	GCGGATGTTA	ATGTTTCAGC	ATTAATGACA	CCTGAAGATC	AAGATGACAT	2160
CATTGCTGTT	AAGACGATAC	ATGCTGAACA	TGATGTTGTA	GAAGCATTCG	GGACGTTGCG	2220
ACTTGTGATA	GATATGTCAA	AAGAACCTGA	TTTGTATTTA	CAAATTAGTG	CAATTAGCGC	2280

TGGGATTCCA	CAAATTAATG	GTCAACAAAC	AGATTACGTC	TCTGATTATG	ACAATGGCCG	2340
TATTATAAAT	ACAGCTGGAT	GAATTAGATG	ATGCGTTAAA	TTATTATTTA	TTTTATTTGA	2400
AAAATTGGAA	TTATGCGTAC	GCCTATTCTT	TAAAATTAAT	AGATGCATAT	GCTTCTAAGA	2460
ATATTATTAA	TCAGCTCGAT	GAGTTAATAG	AAGGTGAAAA	TGATGCCACG	TAAATTTAGA	2520
GTTTTGCAAA	TTGGAGGAGA	CGATTTAGAA	CCTATTTTTC	AACACAAAAA	AGGTGTGAGT	2580
TGGGATTACT	TCGATATTGG	ATTGTTTGAA	TTTGATAGTG	GTTATGTAGA	GGCTATTGAA	2640
GCGATTGTTG	AAGCAGAAGG	GCGCTTTGAT	TTTATCTATA	TTCAAGCACC	ATACTCGGAG	2700
ACATTAACGA	ATTTATTACA	AATGATAAGC	GAACCATACA	ATACGTATGT	TGATGAATCA	2760
TTTTGGTCAG	TTGAATATGA	ACAAGACGAA	AATTGTCCAA	AAATACGTTG	TTCAACCAAT	2820
TACATTACCG	GAATATTGGA	AGGAACGTAA	TAATNAATTA	GAGGCAGGNT	AGCTTCTCAA	2880
GGACAAGGAT	TGGAGATAAA	GTTTCCCCTA	AGTTAGCACT	TGTGCATCCG	AATTTTAAAG	2940
GAGATGTCGA	ATACCCAAGG	TAATTCAAGA	GCTCACGTTG	AGTGGAGAAT	TTGGAAAAGA	3000
ATTTAAACCT	ATCGCATCTT	GNCAAAATAA	TCTCGTTTAC	GATAAAGATA	AAGTCATTCA	3060
NATATGGCCA	GAATTTGATA	TTGATGGTGC	GGTCGAGTTG	CAATATACAT	TTAGATTGAT	3120
TCAGACTGGC	GCTGATGGTG	CATTAATTGA	ACAAATCATA	TTAACTGATG	ATATGTTAGA	3180
CAGTCCTTTA	GAGATACCTG	CGAAACCATT	TGATGCTTAT	ATAAGTGTA	CTGTTAAGGC	3240
GCGTGGGAAC	GGGACGGTAC	ATTTAGGACC	TAAACACACA	CGATGGTCCA	GANTAGANAN	3300
GGNTCAAATTT	TTACNTGGTG	GGAATCGTTT	CGAAGATANN	CNCCGNCNGG	AATTTAATTA	3360
TTAATCCNC	CCTGGTGATA	TGANACCCCC	ACTAAACGTA	AATTTTAGTG	GTTATCGANC	3420
ACCGGAAGGT	TTCGAAGGAT	ATTATATGAT	GANACGTATG	AATGCNCCGT	TTTTACTTAT	3480
CGCCGATCCT	CGTGTTGANG	GTGGTAGCTT	TTATATCGGT	TCATCTGAAT	ATGAACAACG	3540
TGATTATCAA	TGTTATTGAC	GAGACAATAT	TCATGCTGTA	AATCCAACAT	CAGGTGCAGC	3600
TGGTAAGTAT	CAATTCCTTAC	AATCAACTTG	GGATTTCAGTA	GCACCTGCTA	AATATNAAGG	3660
TGTATCACCA	GCAAATGCTC	CTGGAAGTGT	TCAAGATGCC	GCAGCAGTAA	AATTATATAA	3720
CACTGGTGGC	GCTGGACATT	GGGTACTGTC	ATAAGCCATT	TATGCATAGC	TAATCAATAG	3780
TTATATAAGT	AACTTTTAGA	TCGGAATATA	TCGGG			3815

(2) INFORMATION FOR SEQ ID NO:1078:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2848 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1078:

GGCNCGAGAC	GCTTAATTAT	GGAACNCCAA	GATGCNATTG	GACNCGGTTA	TAACATTGGN	60
ACAGGCACCT	TTACTAATTT	ATTAGAGGTT	TATCGTATTA	TTGGTGAATT	AAATATGGNA	120
AATCCAATCG	AGCNTTGAAT	TTAAAGGAAG	CACGAAAAGG	AGATATTAAC	CATTCTTATT	180
GNAGATATCT	CTAACTTAAA	GGCATTAGGA	TTTTGTGCTC	CTAAAAAATA	CAGTAGAAAC	240

AGGTTTAAAG	GATTACTTTA	ATTTTGAGGT	AGATAATATT	GAAGAAGTTA	CAGCTAAAGA	300
AGTGGAATG	TCGTGAAAAT	GACATTGAAG	CTGTCCATAA	TAATAAGGGT	TATGCCTATC	360
AAAGAAAATT	AGATGCACTC	GAAGAAGTGA	GAAAAGGCTA	TTACCCAATT	AAACGTGCGA	420
TTGACTTAGT	ATTAAGTATC	GTTTATTAT	TTTTAACATT	TCCGATTATG	TTCATATTCC	480
CCATTGCTAT	CGTCATAGAT	TCGCCAGGAA	ACCCTATTTA	TAGTCAGGTT	AGAGTTGGGA	540
AGATGGGTAA	ATTAATTAAA	ATATACAAAT	TACGTTTCGAT	GTGTAAAAAC	GCAGAGAAAA	600
ATGGTGCGCA	ATGGGCTGAT	AAAGATGATG	ATCGTATAAC	AAATGTCGGG	AAGTTTATTC	660
GTAAAAACAG	CATTGATGAA	TTACCACACC	TAATTAATGT	TGTTAAAGGG	GAAATGAGTT	720
TTATTGGACC	ACGCCCCGAA	CGTCCGGAAT	TTGTAGAATT	ATTTAGTTCA	GAAGTGATAG	780
GTTTCGAGCA	AAGATGTCTT	GTTACACCAG	GGTTAACAGG	ACTTGCGCAA	ATTCAAGGTG	840
GATATGACTT	AACACCGCAA	CACAACTGA	AATATGACAT	GAAATATATA	CATAAAGGTA	900
GTTTAATGAT	GGAATATAT	ATATCAATTA	GAACATTGAT	GGTTGTTATT	ACAGGGGAAG	960
GCTCAAGGTA	GTCTTAATTT	ACTTAATAAG	TTCAAATAAA	AGTTATATTT	TAAAGATTGT	1020
GACCAATNGT	TACAGNTAA	CGAGGANTCC	CTTGNGACNG	TATCAAATGG	CATTAAAGAA	1080
ATATGTTNCA	TCNTTTGATT	TGCNTGGCCA	ATAAATACTA	TTCATCTTGA	TGAGATAAGC	1140
CATGTTAAGA	AATTGAAAGT	ATAGCATTA	NGGGGTTTGT	AACAGTTGAA	AATTATATAT	1200
TGTATTACTA	AAGCAGACAA	TGGTGGTGCA	CAAAACACAT	CTCATTC AAC	TCGCCAACCA	1260
TTTTTGCGTA	CACCATGATG	TTTATGTCAT	TGTAGGCAAT	CATGGACCAA	TGATTGAACA	1320
NCTAGATGCA	AGAGTTAATG	TAATTATTCT	CGAACATTTA	GTAGGTCCAA	TTGACTTTAA	1380
ACAAGATATT	TTAGCTGTCA	AAGTGTTAGC	ACAGTTATTC	TCGAAAATTA	AGCCTGATGT	1440
TATCCATTTA	CATTCTTCCA	AAGCTGGAAC	GGTCGGACGA	ATTGCGAAGT	TCATTTTCGAA	1500
ATCGAAAGAC	ACACGTGTAG	TTTTTACTGC	GCATGGATGG	GCTTTTACAG	AGGGTGTTAA	1560
ACCAGCTAAA	AAATTTCTAT	ATCTAGTTAT	CGAAAAATTA	ATGTCATGTA	TTACAGATAG	1620
CATTATTTGT	GTTTCAGATT	TCGATAAACA	GTTAGCGTTA	AAATATCGAT	TTAATCGATT	1680
GAAATTAACC	ACAATACATA	ATGGTATTGC	AGATGTTCCC	GCTGTTAANC	AAACGCTAAA	1740
AAGCCAATCA	CATAACAATA	TTGGCGAAGT	AGTTGGANTG	TTGCCTAATA	AACAAGATTT	1800
ACAGATTAAT	GCCCCGACAA	AGCATCAATT	TGTTATGATT	GCAAGATTTG	CTTATCCAAA	1860
ATTGCCNCAA	AATCTAATCG	CGGCAATAGA	GATATTGAAA	TTACATAACA	GTAATCATGC	1920
GCATTTTACA	TTTATAGGCG	ATGGACCTAC	ATTAAATGAT	TGTCAGCCAC	CAAGTTGTAC	1980
AAGCTGGGTT	AAGAAAATGA	TGTCACATTT	TTGGGCAATG	TCATTAATGC	GAGTCATTTA	2040
TTATCACAAT	ACGATACGTT	TATTTTAATA	AGTAAGCATG	AAGGTTTGCC	AATTAGCATT	2100
ATAGAAGCTA	TGCCCTACAGG	TTTGCCTGTT	ATAGCCAGTC	ATGTTGGCGG	TATTTTCAGAA	2160
TTAGTAGCTG	ATAATGGTAT	ATGTATGATG	AACACCCAAC	CCGAAACTAT	TGCTAAAGTC	2220
CTGGAAAAAT	ATTTAATAGA	CAGTGATTAC	ATCAAAATGA	GTAATCAATC	TAGAAAACGT	2280
TATTTAGAAT	GTTTTACTGA	GGAGAAAATG	ATTAAAGAAG	TGGAAGACGT	TTATAATGGA	2340
AAATCAACAC	AATAGTAAAT	TACTAACATT	GTTACTTATC	GGTTTAGCGG	TTTTTATTCA	2400
GCAATCTTCG	GTTATTGCCG	GTGTGAATGT	TTCTATAGCT	GACTTTATCA	CATTACTAAT	2460
ATTAGTTTAT	TTACTGTTTT	TCGCTAACCA	TTTATTAAAG	GCAAATCATT	TTTTACAGTT	2520
TTTCATTATT	TTGTATACAT	ATCGTATGAT	TATTACGCTT	TGTTTGCTAT	TTTTTGATGA	2580
TTTGATATTT	ATTACGGTTA	AGGAAGTTCT	TGCATCTACA	GNTAAATATG	CATTTGTAGT	2640
CATTTATTTT	TATTTAGGGA	TGATCATCTT	TAAGTTAGGT	AATAGCAAAA	AAGTGATCGT	2700
TACCTCTTAT	ATTATAAGCA	GTGTGACTAT	AGGTCTATTT	TGTATTATAG	CTGGTTTGAA	2760
CAAGTCCCTT	TTACTAATGA	AATCGTTATA	TTTTGATGAA	ATACGTTCAA	AAGGATTAAG	2820

GAATGACCCCT AACTATTTTCG CTCGTGCC

2848

(2) INFORMATION FOR SEQ ID NO:1079:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1079:

```

GGCACGAGCG CACATCAACT GTTTAAAGAT AAATATACGA GAGAAATTAA TACTATGAAG      60
TATTACAATC TGTGGAAGTG AGGAGATAAT TATGAAGCGA TTATTCGATG TAGTGAGTTC      120
AATATATGGT TTAGTAGTTT TAAGTCCGAT TCTGTTAATT ACAGCATTAC TAATTAAAAT      180
GGAATCACCT GGACCAGCCA TTTTCAAACA AAAAAGACCG ACGATTAATA ATGAATTGTT      240
TAATATTTAT AAGTTTAGAT CAATGAAAAT AGACACACCT AATGTTGCAA CTGATTTAAT      300
GGATTCAACA TCGTATATAA CAAAGACAGG GAAGGTCATT CGTAAGACCT CTATTGATGA      360
ATTGCCACAA TTATTGAATG TTTTAAAAGG AGAAATGTCA ATTGTAGGTC CTAGACCAGC      420
GCTTTATAAT CAAGGATTAC GAATTAATCG AAAAACGTAC AAAAGCGAAC GTGCATACGA      480
ATAGACCAGG TGTGACAGGA CTAGCTCAGT GATG                                     514

```

(2) INFORMATION FOR SEQ ID NO:1080:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1080:

```

CCCCAAAGAA ATACANTTGT TGGTAGAAGA ACCCCCAACC CACAAGNTGG GGACCCCTTCA      60
TTTCCAACCN TATGGCGGAG GGTAAAGTA AATTCCTTGAA GCTTTGGTTG CCCNCAAATA      120
ATATGATATT TCCGAAATGG GCCGGAGCCG TATCCAACAA TTTAAAATCT GCCGGAGGTA      180
TTAAAGCATT ACTTAACCGC TCCGATTAAG ATGNNATTGA AGGAGAGATT AATATGGTAG      240
AATCAATGCT AACTTTTATG CTTGGGCCAT TAAGACAAAT CNCTGATTTT TATATGGAAC      300
ATTTACTCGT AAGTAATTCC ATCGTCATTG CAGGTTATTT TGCGACAGGT ATTTTTAAAA      360
AGAAAAAAGT TGTGAATTAA ATCANATTTG AGGTGATTTA CAAGTGAAAG CATTGAAATT      420

```

ATATGGCGTA	GAAGATTAC	GGTATGAGGA	TAATGAAAAG	CCAGTCATTG	AAAGTGCAG	480
TGACGTTATT	GTTAAAGTAC	GAGCGACTGG	CATATGTGGT	TCAGACACGT	CACGAAACAN	540
AAANATGGGG	CCATACATTA	AAGGTATGCC	ATTTGGTCAT	GAATTTTCAG	GTGTAGTAGA	600
TGCCATTGGA	AGTGATGTTA	CGCATGTTAA	TGTGGGCGAC	AAAGTGACAG	GTTGCCCAGC	660
AATACCTTGT	TATCAATGCG	AGTAGTGT	GAAAGGTGAA	TATGCACGAT	GTGAAAAAGT	720
TATTCGTCAT	TTGNCCTCAAT	ATGAACCTTG	GATCGTTCNG	CGGAATATGT	CAAATTCCCA	780
CCCCAAAATG	TTTTNAAGGG	TTCCAAGCCA	ATGTTGATTA	CCATTGAANC	AACCAATGGT	840
TTGAGCCATC	AGCCCCTTGT	TGCGCATGGG	TTTTATAAAT	CCGAATANAC	AACCTGGTAT	900
GACTGTTGCA	GTAATGGGGT	GTGGCAGTAT	AGGTTTGT	GCTATTCAAT	GGGCACGAAT	960
ATTTGGTGCT	GCACATATCA	TCGCTATAGA	TATAGATGCG	CATAAACTAG	ATATTGCAAC	1020
ATCATTGGGC	GCACATCAAA	CAATCAATTC	AAAAGAAGAA	AATCTTGAGA	AATTCATCGA	1080
AAATCATTAC	GCCAATCAAA	TCGATTTAGC	TATAGAATCA	TCAGGTGCTA	AAGTTACGAT	1140
TGGTCAAATA	TTGACGCTAC	CTAAAAAAGG	TGGCGAGGTG	GTATTACTCG	GAATACCATA	1200
TGATGATATT	GAGATTGATC	GCGTTCATTT	TGAAAAAATT	CTGCGTAACG	AGTTGACAGT	1260
ATGTGGCTCT	TGGAACGTGT	TGTCCAGTAA	TTTTCCGGGC	AAAGAGTGGA	CGGCAACCTT	1320
ACATTATATG	AAGACGAAAG	ATATTAATGT	AAAGCCTATT	ATTTCTCATT	TTTTACCGTT	1380
AAGAAAAAGG	CCCGGAGACA	TTTTGATAAA	TTAGTTAATA	AGAAAGACCG	ATTTGATAAA	1440
GTCATGTTTA	CGATTTATTA	GTATGCACCT	TTGAGGACGA	AAACGCTGGT	ATAGTTATAG	1500
CTATGAAAGT	GCGAATGCCG	TCTGGTCTAC	AGATACTATC	GAAATAATTC	ATCTTCGAAT	1560
ATACGTTGAT	AAATAGCCCG	TTTACTTGTC	TGAAATATGC	TTGTGAATCG	GTTGTTTTGC	1620
ATTTTGATATA	CTTAAATGA	GATGGCAATA	TTTGATAATT	TTTAAAGTGA	AAATCAAGTA	1680
CAGCCACTTA	ATAAGATAAA	TTTATTATAA	TATATGGTAA	AATGATGGCA	GTAATAATGA	1740
ATTTGAAAAA	GAGTAAACAT	TAATACCTTT	AACAATTTAA	TATCGTCAGA	GTTAATGATT	1800
AACTGCATGG	CAAAACAACT	TAGAATGGTC	AGTTACNNAA	ATACATTTTT	ATAAAAAATT	1860
ATCACACTAT	TGTGACAACT	ATCTTTGGAT	TAATAAAAGA	GGCAAGTGAG	CAATAGGTTA	1920
GGCTTATGTG	CGGGCATAGG	TCAGTAATGT	AGAAATGGAA	ATGATGTAAT	ACGTTAATTC	1980
GTTTGAACTCT	TTAAAAGTAT	TGGATAAATC	AGATAATCGC	CTGTTATACG	CATCAATCAA	2040
TGTTTTATAC	ATAAATATGT	CTGATATTTT	TAAGTCGTTA	TTTTTTGAATG	GAATAAATGG	2100
AATCTTACCC	CACGACCCCTG	TACTAAAATG	CGTTTTT			2137

(2) INFORMATION FOR SEQ ID NO:1081:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1528 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1081:

TCATTTTTTTT GATTGAGCCA AAAGGAGTCC CCCCTGTGAG CGGAATATTT AATTTATTTGA 60

GCTATTTAAT	ATTAAACGTA	CGCTTAACCC	CCCTANAGTG	ATATCGTTTC	TAGCGTTGTC	120
ATTATCATT	AGCGAAACAT	TTTAAAGACA	AATACACACT	GTACGATCAC	CAAACGTCAT	180
GTCGAACAAT	GTAACATTTG	GATTCGATAT	TTAAAATTGC	TTGTGATGAT	AAACTTTCTC	240
ATTTAGAAAA	CGCTTCCACG	TACATTCAAA	AAAATAACTT	TGTTAACCAT	ATTGTAACAT	300
TATTTTCATAT	ATTTTGGGGC	ATGAGAATGA	TTCTCACGCC	CAGTAATTTA	TTTATGCAAT	360
TGTTTCATGTA	GGTTCTTTTC	GACGTTTTC	GGAATACCTA	TATTTTAAA	ATCTTCAAGT	420
GTAGCTCGTG	CCTTCATTTT	CTTGATTGAA	CCGAATGAAC	GCAATAATAA	TGTTTTAACC	480
TTTGTTACCG	ATACCATCTA	TATCATCAAG	TATTGATTTT	AAGCCTGTCT	TTTGACGTGT	540
TTGTCTATGA	AATGTGATTG	CGAATCTGTG	AACCTCATCT	TGGATACGGA	TGCAACAAAT	600
AAAATGCCTG	CCTATTTTTT	TTCAGTGGAC	AATTTCTCTG	ACTAGCGCCA	TAATAATAAT	660
TCAGATGTTT	GGTGTATTATC	ATTTTCTCTG	AAACCTGCAA	CAGGGATATC	AAGACCTAAT	720
TCGTTTTGTA	GCACATCAAT	AACCCCGTTC	ATATGTCCTT	TACCACCATC	GACTATTATT	780
AAATCAGGTA	ATGGTAATCC	TTGTTTTAAA	ACGCGAGAAT	ATCGTCGTCT	TACTACTTCT	840
CTCATTGATT	TGTAATCATC	TGGACCTTTA	ACCGTTTGA	TTTTTACTTT	TCTATAATTT	900
TTCTTATCTG	GTTTACCGTC	GACAAATGTA	ACCATTGCTG	ACACTGGATC	CACACCTTGA	960
ATATTAGAAT	TATCGAATGC	TTCAATTCTA	ATTGGTGTTC	GAATTTCCAT	TTGTGTTCCA	1020
AGTTCTTCAA	TAGCTTTAAT	CGTTCTTGAC	TCATCACGTG	ATATTAATTC	AAATTTATTA	1080
TTTAAGGATA	CTTTAGCGTT	ATGTGCAGCT	AGGTCAACCA	TATCTTTTTT	GGGACCTCGC	1140
GCGGGTTGAA	CGATTTTAGT	GTCCACAACA	GATTGAATCA	TTTCTTTATC	CAAATTACGT	1200
GGTACATGAA	CTTCCTTAGG	TAAAATATGT	TGGTTTAAGC	TATAAAATTG	TCCAATAAAT	1260
GTATAAAATT	CTTCTTCTTC	TGTTTGGTGT	AATGGAATCA	TCGGNGTATC	TCGCTTTATC	1320
ATATTACCTT	GTCGGATTAA	AGAAAACTTG	GATACACATC	CATCCTTTAT	CAACACAATA	1380
ACCAAAGACA	TCACGAATCG	GNTTATCTGA	TGACATAATT	TNGGGTGGGT	GGGCAAGATT	1440
TGGATATTGT	TGGATTAAAT	CTCTATATTC	TTNAGCCGCN	CAAATCAAG	TGATTCACTT	1500
GGAGGNCACA	TNCGCTCTTC	TAANCTTT				1528

(2) INFORMATION FOR SEQ ID NO:1082:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2933 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1082:

AGGTTGATAC	ATATGTCTTG	TAAATACATG	TGTCATMGCT	TGACCAATTG	CAGCAATCTG	60
GACCCAGGAT	NGGTGCCTAC	CCAGTTATCT	CCAAATTTCA	CATTTCTGCG	TAATCTGGTG	120
CTACTTGAAA	TGACTTTTGT	ACCTTAATAG	CGGACTTCTG	TCATAAAATG	TGCATCCGGA	180
GTACGTGTTA	AAGGTACATT	AGAGCCCCAC	ATAATAATGT	ATGATGCGTT	ATACCAGTCA	240
CTTGATTTCAG	GCACATCTGT	TTGCTCTCCC	CAAATTTGTG	GAGAGGCAGG	TGGTAAATCT	300

GCATACCAGT	CATAAAACT	AAGCATTTC	CCACCAAGCA	AATTGATGAA	TCGAGCACCT	360
GCTGCATAAC	TAATCATTGA	CATCGCTGGA	ATAGGTGTAA	ATCCTGCGAT	TCGATCTGGA	420
CCATATTTT	TTATTGTATA	CAGTAATTGT	GCTGCGATTA	TCTCTGTAA	GTCTTTCCAA	480
TTTGAACGCA	CGTGCCCTCC	CATACCTCGG	GCTTGCTTAT	ATTGTTTGGC	TTTGCTTCA	540
TTTTCAACAA	TAGACGCCCA	TGCAGCAACG	CGATTACCAT	AGTTTTCTTC	TAATGCTTCA	600
GTCCATAAAT	CCCAGAGTTT	TCCACGAATA	TATGGATATT	TGATTGGAAG	CGGACTGTAT	660
TCATACCAAG	AGAATGACGC	ACCTCGTGGA	CATCCTCTCG	GTTCATATTC	AGGCATATCC	720
GGACCACAAC	TTGGATAGTC	AGTTTGTTGA	TTTTCCAGG	TAATCACACC	ATTTTTCACA	780
AATACTTTCC	AAGAACATGA	GCCTGTACAG	TTAACACCAT	GTGTGTTCT	TACTTCTTTA	840
TCGTGGCTCC	AACGTTCTCT	GTACATTTTT	TCCCATTCTC	TACTTTTACT	TTCTAGGATC	900
GACCAATTCC	CATTAAATTT	TCTGTTGGCT	TAAAGAATTC	AATCCAAATT	TTCCCATATT	960
TATATCCTCC	TACGTATAAA	AAATACGATG	TGTAGATGTC	GTGTTNTTAA	ATACTTTAAA	1020
ATGCCCAAGA	CTATTGCTTT	AATTAGATTG	TACATTTTTT	CACAAATATA	AAATATTAGG	1080
GAATCACCTA	ATTACTTAAG	GAATTTCCCT	ATCAATAACG	GGATTTCAAT	GAAATAATAC	1140
ACAATCATGT	ATGGTCGTGC	TTATTGCCAA	TCTAAATCGT	TCAAATTTGC	CACAACGACA	1200
AATAAGGCTT	CAACACGAAT	ATATTCTCTC	GGTTGAAACC	TTACTTATTC	ATTTATTTTT	1260
TATAAATTAG	TGACATAACA	CTGTATTAGC	ATCTGCACGA	TCGGTTGAAA	TATATGTTAC	1320
ATTTCTTGC	TGCTTAATAA	ATGCATCATA	GTAATCATAT	TGCCGACCGG	AATGATATGT	1380
CCCATTGAT	GTATCATTTG	GGTTTAGCAA	ACAGCCATAA	CCTTCGTCAT	ATAAATGTTT	1440
ACAGAGCATA	AGGGCGTCAT	GTCTAGAACC	ACTTACTACA	TAAAATTGCT	GAGTCGGATT	1500
AGAAGTTGTT	GAGACATTTT	CAGTATAACC	CACTACTTCG	CCTATAATAC	ATATACCTGG	1560
TTTCGCCTCA	ATTGCGTAAT	GCTCCAGTTT	CCCAACAATA	TTACTTAAAC	GCCCCTTAAC	1620
AACAACTCG	TTAAACACG	ATGCTTGAAA	GACAATCGCT	ATCGGATAAT	CAATATCTGT	1680
GTAAGTTGTT	ATCTGGGCGA	TAATTTTCCC	TAAACGTTTA	ACTCCCATAT	ATATCGCCAA	1740
CGTACCACCA	TTTACTAAAG	NGTTGACATC	TACGTCAATT	TCTTCTGAAT	CTNTNAAGTG	1800
ACCTGTAGAA	AATGTCNCAC	TCTTAGCAAC	AGCACGCNTC	GNTAATCCTG	TTTGCATCGT	1860
AGCAGCTGCA	GCACTCGCAA	GATGTCACAC	CAGGTACAAT	GTCANACGCA	ATAGTAAAAG	1920
TTGTTTAGTG	TGTCAACTTC	TTCTTGAAC	CGNCCAAATA	TTGCTGGGTC	GCCACCTTTA	1980
ACCTCACCA	ACCTTGTTAT	ATCGACGTGC	TGCTTCCACG	ATACATTCAT	TTATTTTTTC	2040
TTGCTGAATG	TGTTTTGCAT	ACGGCTTTTT	ACCAACATCG	ATAATTTTCA	TAGTCAAATT	2100
CGCATATTGT	AAAATTAACG	GATTCACTAA	TCGATCATAT	AGTATAACAT	CCGCTTCACG	2160
TATTAAACGC	TCAGCCTTTT	TAGTCAAATA	ATTCCGATTA	CCTGGTCCCG	CACCTATCAA	2220
GTAAACCTTG	CCATATTTAT	CTACAGACAT	ATATATACGT	TCCCCTCTGT	AACCTTCTACC	2280
TCATAAACAT	CTACACAACC	TTCATCAGGT	TCTTGTAACA	TCCCAGTATT	TAAATCAATC	2340
TTTTGATCAT	GAAGTGGACA	GAATACATAT	TCACCACTCA	CTGTTCCCTC	TGACAATGGT	2400
CCTTGTTTAT	GCGGACAAAT	ATTGTGGAAT	CGCGTGANTT	GTACCACTTT	CAGATAAAAA	2460
CCAATCCTAC	CTCTTTGCCCT	TTGNCAATAA	CCTTTTTTCC	AATTAGGGGT	GTTAATTCAT	2520
CTATAGTTGT	CACTTTAATT	TTTTCTTTTG	TTTCCATGTA	TTACACCTTC	TCCACTTCAA	2580
AAATTTTACG	TGCTTGCGCA	TTGCTAGNTA	TTGCTTCCCA	AGGTTTCACT	TCGACTGCTT	2640
TTTTAGCATC	CATAATGCGT	TCAAATAGTT	CATTTTGTCT	TTCTGGGTCA	AGTAAGACTT	2700
CTTTTACATT	TTCAAATCCA	AGTCTTCTTA	ACCATGGCGC	TGTTCTTTCA	GCATATATAC	2760
CTGTTTCGCG	ATATAGTGCA	TCAAAGCACC	ACATAATGTG	NTTACTTCAT	CTTCTGTTTC	2820
TACAGTTGTT	AAAAATTCAG	CTTTTTCGAC	TTCTGTACCA	CCATTACCAC	CGATATAGAT	2880

TTGGAATCCA TTTTCAACTG AGATAATACC AAAATCTTTA ACACCTGATT CAG

2933

(2) INFORMATION FOR SEQ ID NO:1083:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1083:

```

GGCACGAGCG TCATACCGTT ATGTGCNCGA ATGACAAACN TCTTATTGGC CCTGTTGATT      60
AAATCACATA GTGAACGATA AAAATTACCC CCAAGATNNN GAAATTGAAA CAAATGTTAA      120
TNANTTGANA CTTATCATAG GNATTAATGT TTTGACTTAT TGCCANANTT GATNACCAAN      180
TAAAATTAAG TTAAAGGAGG GACCGTTATG TTACATTATG TGATTCCAGT ATTAAGTCCT      240
ATTACTCGTA TTCTTAATTG GTTGGATTTT AATAAAGTTA ATTATCCGCT AATAAATTTT      300
TTATATAATA AAAGCTATAG TGTTTGTAAT ATTCCGATGC GGTTAAGCAG CCCCTGATAT      360
TAAACACTAT AGCTTTTTTG TTTTAAATTT TGTCCTTGTT TACGTAATAT ATCCTTTTACA      420
TGTTTAAATA AATCATCATT ATGATCTATA GTTGTMTTAT TTTTATATG TTTTGTCTC      480
GTTGAACTTT CGTCGACATC GTGACTACTA GATAGATTGG AATCATTTGA ATGATTGATA      540
AATTCGTTAC AATGTTTTAT CTTCCCATAT AAATCATTAG ATGTTTTGTC ATTCAATTTGT      600
TGAATTCCTC CTTCTAGTGT CTATATTATG CTAAGTTGTC TCTCCATTCA ACTAATGTTT      660
GGATATCTTC ACTAGAAATT TTACCTTCAT TTTCAGCTAC TTCAATTAAT TCATTGTAAT      720
CACTTAAAGT GTAAAAAGGT AGTTGAATAT TGCTAAATGT ATCATCTGCT TTTTTCAAAC      780
CGTAAGTAAA GATAGCTACA ACACCTAATA CTTCTGCACC TGCTTGTTTT AAGGCTTCAA      840
CTGCTGTGAC TGAAGATCCC CCTGTCGAAA TTAAATCTTC TATCACAAC ACTTTTTTAC      900
CTTCACTTTT AGCACCTTCG ATTTGATTTT GGTACCATG ACTCTTATTT GATGAACGAA      960
CATAATTCAT TGGTAATTTT AATTTTTTCAG CAATAAAAGC TGCATGTGGA ATACCAGCTG     1020
TTGCAGTACC AGAAATAACT TCTACTTCAG GAAAGTGTTT TTTAATTAAG TTAATTAAC     1080
CATCGCGGAT TGCGCCTCGA ACTAAAGGAT AACCTAACGT AACACGGGTA TCACAGTAAA     1140
TCGGTGATTT AATACCTGAA CTCCATGTAT ATAAATCATT TGGTGATAAT GTTACAGCTT     1200
CAATATCTAA TAATGATTTG GCAAATNCNT TTAGCCAATA TNCTAACNAA CTTTCTTTAA     1260
TTTTATGATA ACTTTGACTT GGATTGTCAC TTGGTGTAAT CGGTCTACCG ACTACAATAT     1320
GCGTCGGAAC CAAGCTGTCT TGGTTCCTCG GTGTCGTAAT ACGGGGTGGC CAACTTGGAG     1380
ATGCACCTTT AGGTCTAATA CCCGGTGGTT AC                                     1412

```

(2) INFORMATION FOR SEQ ID NO:1084:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1651 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1084:

```

AAGATGATTT AAANATCGGA CNGTCAATTA ATCGCTTGNA GACCCCAACC TCTTGATAGT    60
CTGAAGCCAT TACAAGAAAC ATATGATTCC ATTGCATGCG TAAGAACAAC CATTCCTGTA    120
CCTGCTGTAA CGCTNTTTGG CACACTCATC ACCAAATTGA GGTCATAAAT TCCAACGTCA    180
GTTGTAAAC CAAAATCAGC CANGCGATAT TTTACATTTG TTTCACATATC TGTGATACCT    240
GCAAATGGTG TTAATTCTGA ACCTGTACCT GATGTCGTAG GGATACAAAT GAACGTCGCA    300
TTTTCAGGCA TGCCTATTTT ATAAGTACGT TTACCGATGT CTAGGAACTT TTGTTTAGCA    360
CCGAAGAATG ATGTCTCAGG GTGTTCAAAG AACATCCACA TTGCTTTTGC AGCATCCATC    420
GCTGAACCAC CACCAAGTGC AATGATTGTA TCTGGTTGGA AATCAACCAT CATTTCCAGA    480
CCTTTATATA CTGTATTAGT TGATGGGTTT GGTTCGACTT CGCTAAATAT TTTAATTTGA    540
GGCTGTTCCG TTCTTTGTCT TAATACATTC TCAACTGTTT TTGTATAACC GAATTCCTACC    600
ATACCAGGGT CACAGACAAT CATCACTTTT TCAATCTTGT CCATTGTTGT TAGACTCATG    660
ATTGCATTTT CTTCAAAATA AATTTGAGCA GGCACCTTGA AAATTTGAGT ATTATTACGT    720
CGTTTAGCAA TCGTTTAAAT GTTTAATAAA TCTGTCGCAC TAACATTATG TGAAATTGAG    780
TTTCTACCGT ACGAACCACA ACCTAATGTT AAAGACGGAA TCAATTCGTT ATACATATCA    840
CCAATACCTC CAACCGCTGA TGGTGTATTT ACAAGTACAC GACAAGCTTT CATTCCTAGT    900
CCAAAATCTT TTTGTAATGT TTCATCTTCT GTATGGATAA CGGCTCGTGT GTCCTAATTC    960
CACAGCGAAC ATAATTGAGA ATAGCAACTA TAACGCATTT ATAAGCTTCA GAGAATTTGT   1020
ACCATTCCTG AATAATTTTT ATTTTAAGTA AATTACACAT TTTTAAACAC ATATAACCAG   1080
TAACTTGGTC ATTTTTTTAT TCACAAAAAA ACTCTCTTCA TCATGTCAAC AAAA ACTACA   1140
ACATGATTAT GAAGAGAGCT TTAATTTATA TCATCTGTAT AAGTACTTTA TACAATTTCA   1200
ATTATACCAG TGATTTTACA ACTTGTGGC ATCGTGGACA TAGATGCGTC AATTCATCAA   1260
CAGCACCAAG ATCCTCTGAA TAGTTCCAAC ATCTTTCACA TTTTTCACCA TCTGCATGTT   1320
CGATGACAAT ATCACCATGT TCATAAGCTG TTGCCTGATC ATCTAACTTA TCTACAACCT   1380
TAACTTGTGA CACGATAAAT AATTGATGTA ATGCATCAAA TGAAGTTAAG AATTCAGATG   1440
CATTAATTTT ATCGTTACTA GCAATCGNAA CTTTAGCTTC TAATGATTTA CCAATAACTT   1500
TNNCATTACG AGNAGTTTCT TAATGCACGG NTCACATCAT CACGGTNAAT TCAATAAATT   1560
GTNCGCCATT TATCCAATAA AGCTTGATCT ACTTCCTACA ACTTNAGGTA TGTTCTGGCT   1620
AAGTGAACAC TCNTCCTTTC TCTCAACTAT G                                     1651

```

(2) INFORMATION FOR SEQ ID NO:1085:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3386 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1085:

```

GCATCGGTTA AATGGCGTCA TTCCACTTAC GGGCATCTTN AGGCATTTTG CTTTCAAGT    60
GGCTAATTTA GCTTCACCGT TTAAGGCTAT TTATTAGCATC AGTCACTTGA GTTAATGCAC    120
GGAGTAATGT CATCTGGGTT AAGCGTTGGA TTGTGCGTTT GATTGATAAT ACCTTCCGCT    180
TGAGACACTG CATTTGTATA TGCTGTTTGC TTATCGACAT CAGCATCGTG GTAGTTCTCA    240
CTTGCTTTCA CAGTATCTTT ATTTGCAATA CCTTGTTTCA AGTTACCCAT TGCTGTATTC    300
ACATTTTGTG CATTTTGTGT TAGTTTGTCC AACCTGTAGC TAAAGCTTGT GCTTGATTGA    360
NTTGGTTTCG TAATGCATCA CGTTGTGGTG ATTTAAGTCA CGTNACGTAT CAAGATTTGC    420
TAAAGCATCT TGTTCGCTT GCGCTAATTT TTCATCACCG TTTAATGCAT CTTTCGCTTG    480
ATTCATAGTT GTAACGTGCT TTGTTACTGT ATCAGGCGCC AATACAGGTG TTGGTGTGCC    540
ATTTGCGATT TGTTCGCTT GGTTAGCTGC ATGTGTTATAA GCTTGTGTGT TGCTTTGATC    600
CGCTTGTTGA AAGTCAACTG ATTGTGGTAC TTGACTATTC GCTTGAATTT GTTGTGTCAA    660
CGTACCCATT GCATTATTTA ACGCATCAGC ATTTTGCTTA ATAGCATTAA CACCTGTAAC    720
AAGTTCGTGA TGCACACTT GGGTCTTTTA ATGCTGTTTT TTGTGGTTGA TTTAAGTTTG    780
GTAACGTATC AATGGCTGTA TTTGNATTGT CTTTAGCAAC TTGTAAGTTA TGGTTACCGT    840
TTAAATCACC CTTAGCTCGA GCCACTTGTT GTAACGCTTG AGCCACTTGT TGTGGACCCA    900
CGCTTGCAAT TGGGTGNACC ACTAATGATT TGGTCCAGCA TCGGCTACCG CATTTGAAAA    960
ATGCATTTTT GCTTATCAGT ATCAGCATTT GCCAAAGTTA CCATTTGCTT NAGGTGGTCT   1020
TAATCTGCAA TACCTTGTTT CAATTGTGTC ATTGCTTTGA NNFAAATCTT TGTGCTGTTT   1080
GCTTAATCGT GTTNACATTT GCAACAGTTT GCGCAGCATC GACTTGTTGT TTAAGGCAT   1140
CTTTGTGCGC TGGATTTAAA TCATTTGCAT TTGTAATAAC TTGTTTCGCT GCATCTTTTG   1200
CACGTTGTAA CATTGTCAAT ACCATTCAAT GCTTGTTTCG GCTTCGTTCA CACGTTGCAT   1260
CGCTTGTTTC CAACTTCAGT TTGAACTTGC ATTGCTGCCA TTGCTTTAG ATAAAATACC   1320
TTCTGCATGT GAAACCGCAT TAGTATAATC ATCTTTCTTA GCTNGATCTG CATCAGTAAA   1380
GTTAATGCTA TCTAATGTCT CAGTTTTATC TTGTAATGCA TTGTTTAAGT TAGTCATAGC   1440
ATTATTCAGA TTTTGAGCAT TTGCTTAAC ATTATTAAC TTTGCAATAT CTGGTGCTTG   1500
TTCAACTTGA GTTGTTAGCG CTTGTTTTTG AGCATCATTT AAATGATCTA GTGTACCAAG   1560
TGTTGTCTTA GCATCTTGTT TGGCATCAGC TAATTTGTGA TTACCGTTAA GTGCTTGATT   1620
TGTGTCAATC ACTTTAGTTA ATGCTTGTG AATTGTATTT GGATCCATTG TTGGATTTGT   1680
TGTTTGTGTT AACAAATCTT CTGCTTGNGT TACTGCATTA TCATATGCTG TTTGCTTGTC   1740
AGTATCAGCA TCGTGATAGN TCTCGCTACC TTTAATTTGT GCTTTATTCT CAATACCTTG   1800
TTTCAATTGT GTCATCGCGT CATTAAGCGT TGTTGCCGCT TGTGAATAG CATTGACGTT   1860
TGGTACAAGT GTTGCTTGCG TGATTTGTTT GCTGTATTCA TCACGTTGCG CTTGGTTTAA   1920
GTTTGGAAT TGATCAATAG CATGTTGAAC ATTTTGTTTC GCCGTTGCTA AGTTTGATAT   1980
ACCATTTAAA TCATTTTATG CTTGCGTAAC TNNATCTAAC GCTGCAGGAA TTTCGCTAGG   2040
TGTAACGACA ACATCAGGCG TACCACTAAT TAATGCTTCA GCTTTCGCTA CTGCTTGATT   2100
ATATGCATTT TTCTTGTCAG AATCTGCATT GACAAAGTTA CCATCAGCTT TTGTTTGTTC   2160
TTTATCTGCA ATGCCTTGTT TTAATTGTGT CATCGCATTG TNTAACTCTT GCGCCGTTTG   2220

```

TTTAACATTG	TTTACACCAG	CTACAGTAGT	TGCATTTTCGT	ACTTGTGTGT	TTAATGCATC	2280
TTTCTGTGCT	TGGTTAAGAT	CATTAGAGTT	ATTAATTAAT	GCTGTTGCTT	CGTCTTNTGC	2340
ATGTTGAACG	TTGGCATTAC	CATTTAATGC	TTGTTNTGCT	GCATTTACTT	GTTGGATTGC	2400
TTGNNCAACT	TCAGTTTGTG	TTGCATTACC	ACCATTAGCT	TGTGGAAATG	ATATTTNCAG	2460
CATTTGTAAC	TGCAGTGTTA	TATGCTTGT	GTTGNGCTTG	ATCTNNATCA	GNGAAGTTAC	2520
CTGNTGCTNG	CGTAGCATCT	ATATCACCTA	TCGCTTGTC	CAAGTTACCC	ATCGCAGTAT	2580
TTAAGTTTGT	CGCATTTTGC	TTAATTTGAT	TTGCTTCATC	ACCAGTATGC	GCGCCATTAA	2640
TTTGATTAGT	AACAGCTTGT	TTTTGCGCAT	TATTTAAGNT	GTCTAATGAA	CCTAAAGATT	2700
GCGTTGCTAG	TTGCTTCGCT	GCCTCTAAGT	TTTCATTACC	ATTTAAAGCA	TTTTTAGACG	2760
TGCTTACTTG	TCCAGCAGCT	TGATTGATAA	CAGTCGGATC	TAATGAAGGG	TTTGTAGTTT	2820
GATCAATAAT	ACCTTGTCGA	GTTGTGACAG	CATTATTGTA	CGCATCCTTT	TTATTTCGGAC	2880
TTGCATCAGT	ATAATTTTGG	TTTTGTTTTG	TTGTCGCATT	ATCTGCAATA	CTTTGACGTA	2940
ATTTGTCCAT	TGCTGCATCA	ACATTGTTTG	CTTTTTGTTC	ATTACCTTGT	GCTTCTGCAA	3000
CAGTAGTCGA	TTGTTGTACC	AATTGTTTTA	ATGCCTCTTT	TTGTGCATTT	GTTAAATGGC	3060
TTAAACCGTC	AATTGCTGTA	TTTGCGTGT	GTTTCGCTTT	TTCAAGGTTT	TGAGTACCAT	3120
TAAGCGCTGC	TTTTGTAGTA	TTCATTGAT	TCATAGCTGC	TTCAACTTGA	TCTTTAGGCA	3180
CGTTCGTACC	TGTAGATTTA	TTTAAATAT	TTTCAGCATT	ACGAACCGCT	TCATTGTATG	3240
CATTTTNCCT	CTCTGGATCT	TGCATCTTGC	AAAGTNNNGG	ACTGGCAAGT	GTAGTGTCTT	3300
TATCATTCAA	GCTATTTTTC	AAGTTANCCA	TCGCTGTTTC	AAAATCCTGA	GNGGGNTTGA	3360
TTGGTTGGNG	TTNACTTCAN	CTACAG				3386

(2) INFORMATION FOR SEQ ID NO:1086:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2334 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1086:

CCACCCANCT	GATTATAATG	TTTTAGCANG	AGCTAGACTT	GGTTGGTTAC	CATCATATCC	60
ACAATTTAAT	AAAAATAGTT	TGTTGTTTGC	AGAAGAAGCT	AAAGATGAAG	GCATTGAGTC	120
GAATGAGGCA	ATTTTAAAC	GAGCGATAAA	TGGAAGTTAA	GTCAAAACAA	ACGCAATTTG	180
CGATAGAAGA	TCCGGATTTG	AAAAAGAATC	ATCCGGAAAT	CACTGTTTAT	ATGGCGCTCA	240
AATCTAATCT	CAAGTTCGTC	AAAAGGTCAA	GAATACTTTA	TGAAGCATTT	ACTTGGCACA	300
AAATCAGGGT	TATTAGCTAC	ACCAAATGAA	GATGAAAAGC	CAGAAGAAAT	TACGTGGCGT	360
GAGGAAACAA	CAGGGAAAT	AGATTTAGTC	GTTTCTTTAG	ATTTTCAGAA	GACAGCAACA	420
CCTTTATATT	CTGACATTGT	TTTGCCAGCA	GCGACTTGGT	ATGAGAAGCA	TGATTTGTCA	480
TCTACAGATA	TGCATCCATA	TGTACATCCT	TTAATCCAG	CTATTGATCC	ATTATGGGAA	540
TCGCGTTCAG	ACTGGGATAT	TTATAAAACG	TTGGCAAAAG	CATTTTCAGA	AATGGCAAAA	600

GACTATTTAC	CTGGAACGTT	TAAAGATGTT	GTGACAAC TC	CACTTAGTCA	TGATACAAAG	660
CAAGAAATTT	CAACACCATA	CGGCGTAGTG	AAAGATTGGT	CGAAGGGTGA	AATTGAAGCG	720
GTACCTGGAC	GTACAATGCC	TAAC TTTGCA	ATTGTAGAAC	GCGACTACAC	TAAAATTTAC	780
GACAAATATG	TCACGCTTGG	TCCTGTACTT	GAAAAAGGGA	AAGTTGGAGC	ACATGGTGTA	840
AGTTTCGGTG	TCAGTGAACA	ATATGAAGAA	TTAAAAAGTA	TGTTAGGTAC	GTGGAGTGAT	900
ACAAATGATG	ATTCTGTGAG	AGCGAATCGT	CCGCGTATTG	ATACAGCACG	TAATGTAGCA	960
GATGCAATAC	TAAGTATTTT	ATCTGCTACG	AATGGTAAAT	TATCACAAAA	ATCATATGAA	1020
GATCTTGAAG	AACAAACTGG	AATGCCGTTA	AAAGATATTT	CTAGCGAACG	TGCTGCTGAG	1080
AAAATTCGTT	TTTAAATATA	ACTTCACAAC	CACGAGAAGT	AATACCGACA	GCAGTATTCC	1140
CAGGTTCAAA	TAAACAAGGT	CGACGATATT	CACCATTTAC	AACGAATATA	GAACGTCTAG	1200
TACCTTTTAG	AACATTAAAC	GGACGTCAAA	GTTATTATGT	GGATCACGAA	GTTTTCCAAC	1260
AATTTGGGGA	GAGCTTACCA	GTATATAAAC	CGACATTGCC	GCCAATGGTA	TTTGGGAATA	1320
GAGATAAGAA	AATTAANGGT	GGTACAGATG	CTTTGGTACT	GCGTTATTTA	ACGCCTCATG	1380
GANAAATGAA	TATACACTCA	ATGTATCAAG	ATAATAAGCA	TATGTTGACA	CTATTTAGAG	1440
GTGTCCACCG	GTTTGGATAT	CANATGAAGA	TGCTGNAAAA	CACGATATCC	AAGATAATGA	1500
TTGGCTAGAA	GTGTATANCC	GTAATGGTGT	TGTAACGGCA	AGAGCAGTTA	TTTCGCATCG	1560
TATGCCTAAA	GGTACAATGT	TTATGTATCA	TGCACAAGAT	AAACATATTC	AAACGCCTGG	1620
GTCAGAAATT	ACAGATACAC	GTGGTGGTTC	ACACAACGCG	CCGACTAGAA	TCCATTTGAA	1680
ACCAACACAA	CTAGTCGGAG	GATACGCACA	AATTAGTTAT	CACTTTAATT	ATTATGGACC	1740
AATTGGGAAC	CAAAGGGATT	TATATGTAGC	AGTTAGAAAAG	ATGAAGGAGG	TTAATTGGCT	1800
TGAAGATTAA	AGCGCAAGTT	GCGATGGTAT	TAAATTTAGA	TAAATGCATA	GGATGCCATA	1860
CGTGTAGTGT	GACATGTAAA	AACACTTGGA	CAAATCGTCC	AGGTGCTGAG	TAACATGTGG	1920
TTCAATAACG	TAGAAACGAA	GCCAGGTGTA	GGGTATCCGA	AACGTTGGGA	AGACCAAGAA	1980
CACTACAAAG	GTGGTTGGGT	ACTAAANTCG	TAAAGGGAAA	CTTGAATTAA	AATCTGGAAG	2040
TAGAATTTCA	CAAATTGCTT	TAGGTAAAAT	TTTTTATAAC	CCAGATATNC	CATTAATAAA	2100
AGATTATTAT	GANCCATGGA	NCTATAATTA	TGAACATTTA	ACAACTGCGA	AATCAGGGAA	2160
GCATTCGCCA	GTTGCTAGAG	CGTATTCAGA	AATTACAGGG	GATAACATTG	AAATTGAATG	2220
GGGACCTAAC	TGGGAAGATG	ACTTAGCAGG	TGGTCATGTT	ACAGGCCCAA	AAGATCCTAA	2280
CATACACAAA	ATAGAAGAAG	AGATTAAATT	CCAATTTGAC	GAAACTTTTA	TGAG	2334

(2) INFORMATION FOR SEQ ID NO:1087:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2698 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1087:

GGCACGAGAC TAATACCTGA AATTAATCCA CCACCACCAA TAGCGGCAAA TAAATAATCA 60

AAGTTAACGG	AATTGTCAGT	CTTTGATTGT	TCTAGCATTT	CTTTAGCAAG	CGTACCTTGT	120
CCAGAAATTG	TATGAACATT	ATTGAATGGA	TCTATAAAGT	TCATTTGATG	TTCACCTTGT	180
TAAGTTAAAG	CTTCAGCTAA	ACAGNGATCA	AATGTATCAC	CAGTGAGTAC	AACCTCAACG	240
TTACTATTTT	CAAAGAACCT	TACTTGATTT	ACCTTTTGTN	AAGGTGTAGT	GACTGGCATA	300
AAGATAACAG	CGTTTANATT	AAGTTTTTTA	GCTGTATAGG	CAACACCTTG	AGCATGATTA	360
CCTGCACCTG	CACATGTAAT	ACCTTTACTT	TTAGCTTCAT	CTGATAAAAC	AGAAATAGCG	420
TTGTAAGCAC	CTCTTAATTT	AAAAGAACGT	ACCCATTGTA	AATCTTCTCG	TTTTAAATAA	480
ACTTTACAAT	CATACTTTTG	AGATAAGTAA	TGGTCTAATT	GTAAAGGTGT	TTCTTTGACA	540
ATATCTTTAA	GTCTTAAAAA	TGCTTCATCG	ATATCTTNCG	TAGAAACTGN	TGTTTTGACT	600
GGCATAATAT	TCAACTCCCT	TAAAGTGATT	TNNCATATTN	NTCTATTAAT	GATTCATATT	660
GTAGGGTGAT	TGCAATTGTC	ATCTAAGCCA	TTTACCAAGT	TTATTTTTCC	AAAGTTTCAT	720
CAATTTCAAA	ATGGAAACGC	TTGTCTGGTG	ATGACACAGT	TTGATTTGGT	AAATCTATTT	780
CAATTTCCCT	ATATTGTGCA	AGATGTTTAC	GAGCACTTTT	TTCTAAANCG	ATAGGCAACA	840
TCGCATTTTT	AGTGCAATTG	ATATAAAATA	TGTCACGTAA	ACTTCCTGCA	ATAATAATAT	900
GNAAACCATA	GTCTTAAGA	GCCCAAGCAG	CATGTTTACG	ACTTGAACCA	CATCCAAAAT	960
TATCTCCAGT	AATTAATAA	GAAGCCCCTT	TATATTGTGG	TTTGTTAGGA	TTGAAATCAG	1020
GATTATCTGA	ACCATCAGGT	AAGTACCGCC	ATTATCAAAA	AGCAAATGGA	CCAAAGCCAC	1080
TTTTTGAAAT	ACGCTTTAAG	TGTACCTTAG	GAATGATTTG	GTCTGTATCG	ATATGTCTCG	1140
TGAAGAGAGG	GACTATTTTA	CCTTTATATG	TTGTAATAGG	TTGATTGCT	GCCATTTAAA	1200
CAACCACCTT	TCTTACGTCC	ACAAATTTAC	CATGAATAGC	TGCTGCTGCT	GCCATAGCAG	1260
GGGATACTAA	ATGTGTTCTT	GCACCTTTGC	CTTGTCGTCC	TTCAAAGTTT	CGATTACTTG	1320
TAGATGCACA	ATGTACGCCC	TCAGGTACTT	GGTCAGGATT	CATGCCTAAA	CACATTGAAC	1380
ATCCTGGTTC	ACGCCATTCA	AATCCTGCAT	TTTTAAAGAT	AGTATCTAGA	CCTAATTTTT	1440
CTGCTTCTTT	TTTTACTGTA	CGAGAACCTG	GTACGACAAT	AGCTGTAATA	TTTGGATGAA	1500
CTTTATTTCC	TTTAACAATA	TGACTAGCTT	CAATCAAATC	TGATAGTCTA	GCATTTGTAC	1560
ATGAACCGAG	AAAAACATAC	CCTAAGTCGA	TGTCTTCAGC	TTTTTGACCT	GGTCTAACC	1620
CCATATAATC	ATACGCACGT	TGATCGTTGA	TATCATTGAT	TTCAGGGAAT	GGTTCACCTG	1680
AATTAACACC	CATTTTCAGGA	TTAGTTCCCT	ATGTCACTTG	TGGTTCTAAT	GTTGAAACAT	1740
CAAGTTCAAT	TACACGATCA	AATATCGCGT	CGTGCCATCA	GAATATAGCT	CACGCCACTT	1800
ATCAACTGAT	TTAGCGAAGT	TATCGGCAAA	TGGTCTCCCT	TTAACATATT	CAAATGTTAT	1860
ATCATCAGGT	TGGATTATGC	CGTATTTGGC	ACCACCTTCG	ATAGCCATGT	TACAAATAGT	1920
CATTCGACCG	TCCATTGAAA	GGTTTTTAAT	TGTTTCGCCA	GTAAATTCCA	AAGCATAGCC	1980
TGTACCAAAA	TCAACACCAT	ACGTTTTAAT	TAAATGCAGA	ATAATGTCCT	TAGCATAGAC	2040
GCCTGTTGGT	AAGGTACCAT	TAATATCGAT	TTTTAAGTTT	TTGGGTTTTG	TTTGCCATAG	2100
CGTTTGAGTT	GCGAAAACAT	GTTCAACTTC	ACTTGTTCCT	ATTCCAAATG	CAATAGCACC	2160
AAATGCTCCA	TGTGTTGCTG	TGTGAGAGTC	ACCACAAACG	ATTGTTTTGC	CGGGCTGTGT	2220
AAGTCCTGTC	TCAGGTCCTA	CCATGTGAAC	AATACCTTGT	TCATCAGAGC	CCATATCAAA	2280
AATATGCACC	CCAAAATCTA	TGGCGTTTTT	TTGTAATGTT	GTGATTTGTT	TGTTTGCAAT	2340
TTCATCTTTA	ATATTGAAAA	TATCAATAGT	AGGAACATTG	TGATCGAGTG	TTGCAAAATG	2400
TAAATCTGGG	CGTCTTAATT	TTCTGTTTTG	AAGCCTAAGT	CCTTCAAATG	CTTGAGGAGA	2460
AGTAACTTCA	TGTATAAGGT	GTAAATCAAT	GTATAATAGT	TGCGGGTCGC	CCNATTTCCC	2520
GNATAACACA	TGTCTGTTCC	ACACCTTGTC	AAATAATGTT	TGACCCAGTT	ACATCTCCCC	2580
CTNAGTGATT	CAATTTTTGA	GATAGCATTT	CGAAAATATC	AGTAGTATTC	AATTTGCCCG	2640

CTAAATCTGC TGTCGTTTGC CCATGTTCAA TCATGTTATA AATATGTTGT TCTAATTC 2698

(2) INFORMATION FOR SEQ ID NO:1088:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1088:

GAATTCCTNCG CTACAATGTG GCATCGGCAG GCATTATCGT GTTTACTAGT TATCTTAATC	60
TTAATGAGTG GCGTTGCGAT TATTTTACGT GAACAAATNG NAGTAAAANA TTCTAATTTA	120
AACAATCAAT CTCATTTATC TATTANAAAG GGAGTTTAN ATATGGCGCA AACACTTGCA	180
CAANCTAAAC ANATATCTCA AAGTCATACG TNTGATGTCT CACAAAGTCA TCATAAACA	240
CCAGCTGATA CANAACTCAC AGTCCTGATA TGCCCTCATA AATATTAANA TTTTANTAGT	300
CAATAACAAG TTGAATATTA AAGTTAAACG CCCGTTAAAT AGCGTTAAAA AATTGAAAAT	360
GACAGGTATT TGGCAAAAAA TAAGAATTAA TTATTTATAT	400

(2) INFORMATION FOR SEQ ID NO:1089:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 644 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1089:

ATAATTTCAA TGTCCCCGTA TGTGTAGTGC GCTGGTTGCT TAACATTGTC TTGCGCTTCG	60
TTCAATATCT ACTTTTCTGT TACTGATTAC GTCATTATG CTTCACTCCA TTCTTGNAC	120
ATTTGGNTAT AAGTGACATC GANCCAGTAC GGATCACGTG NATGTTTTTG TGGCGTTCCC	180
AATCCATAAA AGCCATGGTC TTTAATCTTC TCTTTCTTTC CTGTTTATAT TCCGCTCTCA	240
CAATTTTCGTT GGTATCGGGT CCACAATCGC TTTTCTTCTG AGTTTCTCTC TCCCTTTTTC	300
TTCATCTTTT ATTTGACTCT TCATATATTC CAACTTCTTC TTTAGATTTT GAGTCCTTTC	360
TTCCACACAA TAATTCATCG CCGCGCATTT TATGTTTGTA TCTATATCTA AGAAGTTCTG	420
GAGATATATG ATATTTTCTT GAAACTTCTC TCAATGTCAT TAGTTTTCCT TTAATACGCA	480
CTCTTATAAC TTTTCTTCTA GCCATCATTC CACCTCTAAA TCTAAAACCT TGATATTTAT	540

AACGTTATAT TTTAATAGTT CACCTGGATT ATTAAATAAA TAGTCCGCCA AATTTTCTTT 600
 TTCTTTATCA ATCTGATTGT AATTAACACT TTCGACTTCT GTAG 644

(2) INFORMATION FOR SEQ ID NO:1090:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 650 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1090:

GGCCGATAAA TTACATGTTT GCCAAGTAGA TCTCGGAGAG AACGAACCTG TACAAATCGT 60
 ATGTGGTGCA CCCGCATACG TGTATGCGTG ACAATATGTC ATTGTTGCTA AAGTAGGTGG 120
 CAGATTGCCT GGTGGTATCA AAATTACGCG TGCCAANTCA CGCGGCGAAC GTTCAGAAGG 180
 TATGATTTGT NCGTTACAAG AAATTGGTAT TTCAAGTAAC TATATNCCGA CAGGTTGCGN 240
 NTCAGGCATT TATGTCCTTA GTGAATCCCA NGTNCCAGGA ACAGATGCCT TACAAGCTTN 300
 ATATTTAGAT GATCANGTAA TGGAATGTGA TTNAACGCCG ACTCGCGCAG ATGCTTTACG 360
 TATGATAGGN ACTGCTTATG AAGTCGCAGC ATTATATAAT ACAANATTGA CTACGCCAGA 420
 GACAACATCA AATGAGCTTG ANTTATCTGC AAATGATGAN TTGACTGTGA CAANTGANAA 480
 TGAAGATACC AGTACCATAT TATAGTGCAC GTGCTTGCTC ACAACGTGAA CATTTGNACC 540
 TTCGCCACTG TGGATGCACG CAGCCTTTAC TACACGCGGN TATACGTCCT ANTTAATAAT 600
 GTCGTCGACA TCTCAAATTN NTGTGTTTAT CAGACTACGG CCAACCCATT 650

(2) INFORMATION FOR SEQ ID NO:1091:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1562 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1091:

TTTATTCAGC ATTCGACCTA GTTGAACAAC GCAGTGGTCG TGATGCATTA GAAGTATTCG 60
 AAGAAGCAAT CAACAACATT ATGCCAGTAT TAGAAGTTAA AGCTCGTCGT GTAGGTGGTT 120
 CTAACATCA AGTACCAGTA GAAGTTCGNC CAGAGCGTCG CACTACTTTA GGTTTACGTT 180
 GGTTAGTTAA CTATGCACGT CTCGTGGTG AAAAAACGAT GGAAGATCGT TTAGCTAACG 240

AAATTTTAGA	TGCAGCAAAT	AATACAGGTG	GTGCCGTAA	GAAACGTGAG	GACACTCACA	300
AAATGGCTGA	AGCAAACAAA	GCATTGCTC	ACTACCGTTG	GTAAGATAAA	AGCTTTTACC	360
CTGAGTGTGT	TCTATATTAA	TGAATTTTCA	TTAAGCGTTC	ATGCTTAGGG	CATCGCCATA	420
TCTATCGTAT	TTATTCACTA	ATATAAACTG	GAAGGAGAAA	AAATACATGG	CTAGAGAATT	480
TTCAATTAGAA	AAAACCTCCG	AATATCGGTA	TCATGGGCTC	ACAATTGATG	CTGGTAAAAAC	540
GGACTACGAC	TGAACGTATT	CTTTATAACA	CTGGCCGTAT	CCACAAAATT	GGTGAACAA	600
CACGAAGGTG	CTCACAAATG	GACTGGATGG	AGCAAGAACN	AAGACCGTGG	TATTACTATC	660
ACAATCTGCT	GCAACAACAA	GCAGCTTGGG	AAGGTCACCG	TGTAAACATT	ATCGATACAC	720
CTGGACACGT	AGACTTCACT	GTAGAAGTTG	AACGTTCAAT	ACGTGTACTT	GACGGAGCAG	780
TTACAGTACT	TGATGCACAA	TCAGGTGTTG	AACCACAAAC	TGAAACAGNT	TGGCGTCAGG	840
CTACAACCTA	TGGTGTTCCT	CGTATCGTAT	TTGTAAACAA	AATGGACAAA	TTAGGTGCTA	900
ACTTCGAATA	CTCTGTAAGT	ACATTACATG	ATCGTTTACA	AGCTAACGCT	GCTCCAATCC	960
AATTACCAAT	TGGTGCGGAA	GACGAATTCG	AAGCAATCAT	TGACTTAGTT	GAAATGAAAT	1020
GTTTCAAATA	TACAAATGAT	TTAGGTACTG	AAATTGAAGA	AATTGAAATT	CCTGAAGACC	1080
ACTTAGACAC	GAGCTGAAGA	AGCTCGTGCT	AGCTTAATCG	AAGCAGTTGC	AGAAACTAGC	1140
GACGAATTAA	TGGAAAAATA	TCTTGGTGAC	GAAGAAATTT	CAGTTTCTGA	ATTAAAAGAA	1200
GCTATCCGCC	AAGCTACTAC	TAACGTAGAA	TTCTACCCAG	TACTTTGTGG	TACAGCTTTC	1260
AAAAACAAAG	GTGTTCAATT	AATGCTTGAC	GCTGTAATTG	ATTACTTACC	TTCAACCTA	1320
GACGTAAAC	CAATTATTGG	TCACCGTGCT	AGCAACCCTG	AAGAAGAAGT	AATCGCGAAA	1380
GCAGACGATT	CAGCTGAATT	CGCTGCATTA	GCGTTCAAAG	TTATGACTGA	CCCTTATGTT	1440
GGTAAATTAA	CATTCTTCCG	TGTGTATTCA	GGTACAATGA	CATCTGGTTC	ATACGTTAAG	1500
AACTCTACTA	AAGGTAAACG	TGAACGTGTA	GTCGTTTATT	AACAATGCAC	GCTAACTCAC	1560
GT						1562

(2) INFORMATION FOR SEQ ID NO:1092:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1810 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1092:

TTGTTGACTT	AGGTTGAACA	TTGGCCTGCC	GATTTTAACC	ACTTGAAGAT	GAAAATGCAA	60
GCATCTCTTC	CCACGTCATA	TTTGGACCCA	TCGAAAAATT	CGGGTTCTCC	GAATCATCGG	120
AACATAACCA	AAAGAAGCTA	AGCAACATGT	AGNCCGTTGT	CACTGAACNT	CTTGTTTTTC	180
CGATGACAGC	TTCTATTTAG	AGAATGTCAT	GATTATTTTA	TATTCACTTC	NATGTTATCA	240
ATATTAGTGC	CATCTATGAC	GTCTGCCATG	CGATTTTCTT	GTAATTTTTT	GTGTAANTCA	300
AACGTGTACT	TTCCACCGTT	TTTCATGTTA	ATAACAATTT	TACCTGAACC	AACTGTTACC	360
GTAAAGATTA	TGATTNTCAA	TAAGTTGTTT	TCTCAATTTA	AAATCAAGCT	CTNTCAAGGA	420

AATCTGCTTC	CTTAGTAATC	ATGTATTCTG	AAACGATCGC	GTGAAATCAT	ACCTTGATTA	480
TCTTTTTTAG	TAACGCTTAA	TTCTGCTNTG	TGATCAACTT	TTTTACTATT	AGTCTTCGTG	540
ATGCCACCGA	CAGAATATTT	TTTAATTGA	TATTTATTGT	CTTCTAAANC	GATAAATACA	600
TCGATATTAT	CGTAAGGTCC	ATCTTTATAT	TTTTTCTCAT	CTTTTCCTAA	CTAAAGCTAT	660
TTTATAGATG	AACCTATTTG	GAATAACATN	CATAAACCTA	ACCGTCGTCC	ATGGTTTGAG	720
CAAAAATCCA	AACTGCTTTT	CAAATNCAAA	ACTCGGTTTC	GTGTAATACG	CTCTTAAATC	780
TTCATATTTA	GGAGTCATAT	CTGTTTGTGC	TTGTTTTATG	GTTGGAGATT	GTGGTGTGTC	840
TGATTTAGTA	GATTGCATTG	GTTGTGGCGT	GTTGTTTGAT	GGAGGTGTTG	TCACTTTAGT	900
TTTCGGCGTT	GTGGATTCCG	TGCGCGTTTG	TGATTGNTCT	TGTTTAGGCG	CTGGCGTTGC	960
TGATATATTA	AGCGATTTCT	GCTCTTCTTG	TTTAGGTTGT	GATATTTTCT	CTATTTTGGA	1020
AGCTGAGGTT	TTTTCCNCAT	TAGTATTTGG	TGCCTTCTCG	AGTTTAGGCG	TGCGTTCTTG	1080
TCTTGTGTTA	GCTGCTTGIG	TTGTCGCTGA	ATTTCACCT	GCTGTTATGT	TTATCATTGC	1140
TAATCGCTCT	GCTTTAAGCG	TTGGTACTTT	GTCAACTTTA	GTTGATTGTA	TTTTTTCTGC	1200
TTTGACCGAT	TGCGTCGTTA	CTGTAATTGC	GCCTGTTGTT	AAAAGCCCTA	GTGCTAAACT	1260
GGTTTTAGCA	ATTGTTTTCA	TATTCATAAT	TGTATACTCC	AATCTATATT	ATATTCGATT	1320
GTCTTTTTAC	GTAATTTGAA	TCATACAACA	TCATTATAGA	TGGCGTTCTA	AGATAATCAC	1380
ATTAAACCCT	TTTAACAAT	TATTGAAGTA	TTATTAAGTA	ATTTAAGCAA	AAAATAATGA	1440
GTGATTATGA	GGTTAATATA	GCGTCTCTAT	GCTGCCTNTG	AAATGATTTT	TAAGCATTA	1500
AAAGAAGTTA	AGCAACGTGT	GAATCCGTCA	CTTAACCTCT	CTATTTCAAT	TTCAAATTAT	1560
TTTCGTCGNA	AGTATGTGTA	TTAAGCTTCT	CTAACTNNGA	TTTCAATTCT	ATCAATATCT	1620
GTGACATTGA	TAACATCGGA	CATACGGTCT	TCTTGGAAC	TTNNTTATCC	AANTCAAATG	1680
TATACTTNCC	ATAGTATTTT	TTTGTGGACG	GNAATTTNCC	CTGTACTCAN	TTCAACCGNN	1740
AAGGACCATA	CTTATCAATA	AGGTATTNTC	TTTANTTTAA	NATCAATCTC	TTTCAATGAC	1800
ATCGCTCCTT						1810

(2) INFORMATION FOR SEQ ID NO:1093:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1228 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1093:

GGCACGAGCG	TCCAATTCAT	CGAACGCCTG	ATATGATTAA	ACAACATGAG	TATTTAGAAG	60
ATATTACGAA	AAATATAGAA	TTAGGGCATT	ACCAACCAAC	AACGACACAA	GTTTTTGAAG	120
GTTTATCACC	TGAAAACCTA	TATCAAGCAC	ATCAATTGTT	GGAAAAACAA	TCAATGATTG	180
GGAAATTAGT	AATTAATATA	TAGATTAGTA	AGTAAAGTCG	CCTTATGCAG	AAAATACTGT	240
ATAGGGCGAC	TTATTTTTTG	TGCTAGCGA	CTATTGATTG	TAAACGGAAA	TATGGCAACT	300
TTACAGGTAT	CAATCAATA	ATGCACTAGA	AAGGCATTAC	TTAAATACAA	TAAAATACCT	360

TGTTGCTCAA	TGATAAATAA	TTTGAGTGTG	TTTTATATAT	CATTTTFAAA	AGATGAGGCA	420
TTATTAATTG	TGCTATATA	AAATTACAAA	TGATTAAAAAT	GTTGCAGTTA	TGGGTATTGA	480
ACTTACCATT	ACACAGAAAG	GGGTTGTAT	TTATGAAAAA	TAAATCAGTA	AGTCTAGTGT	540
TTTGGGTATC	TTTAGTGATA	TGTACGATAT	TTGTTGCTTT	TGGAGCAATA	TTTCCGAAAC	600
AATTAGAAAA	ACTCACGCAA	AACATTACTA	CATTTATTGC	GCTACATTTT	TCTTGGTATT	660
ATTTATTGCT	CGTTTTAGTT	ATTTTATTTG	TCTGTGTGTA	TATTTTATTT	TCGAGATACG	720
CAAACATTAC	ATTAGGTGAA	GAAGGCGAAG	ATCCTGAATT	CTCATTGCCG	TCTTGGTTTG	780
CTATGTTATT	TAGTGCTGGT	ATGGGAATAG	GACTTGTGTT	CTGGACAACG	GCAGAACCAA	840
TCAGTCATGC	CTTCAAATTA	ACGCCTATTC	ATAAAGCTGG	CACGCAATCT	GCAATTAAATG	900
ATGCAATGCA	GTTTTCATTT	TTCCATTGGG	GGATTCATGC	ATGGGCAGTC	TATGGTATTG	960
TCGCGCTTGT	GTTTGCATAT	TTTAGCTTTC	ATAAAGGATA	TCCTGGCTTA	GTCAGCGCTA	1020
CATTGACGCC	TTTATTAGGT	GAAAAGGCAA	TGCGTGGACC	TTTAGGTGGT	GCCATTGATG	1080
TATTGGCAGT	CATAGCTACA	GTAACAGGCG	TTGCTGCACA	TTAGGTTTCG	GGGGCAATTG	1140
CAAANTAAAC	GAGGGNTTAC	ATTTTTTTTA	TTTAAATGGT	ACCGAGTNAC	TTCANGGANG	1200
CAAGTANTCT	TGATTGGNCA	TCGNAACC				1228

(2) INFORMATION FOR SEQ ID NO:1094:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1094:

GTTAATCAAG	TATCGAAGCG	GAACAATCAT	ACTTTAATGT	TGAAGATTTA	TATNGCGAAC	60
AAGCGATGGT	CCTAGTGCCT	AATATTAATT	TAGCACTGCG	CGCACAATAT	TTGTTNGNAT	120
CTNATGTCGA	TTACTTTGTA	TATNNTGGTG	ATATTGTTTT	AACTGACCNC	ATTACAGGTC	180
GTNTGTTACC	GGNAACTAAG	TTGCAAGCTG	GACTTCACCA	NGCTATTGAA	GCGAAAGAAG	240
GTATGGAGGT	TTCAACAGAT	AAAAGTGTTA	TGCCAACCAA	TTACCCCTCC	AGAATTTATT	300
TAAACTTTTT	GAATCAATTT	TCAGGTATGA	CAAGCTACAG	GAAAATTAGG	CGAATCAGAG	360
TTCTTTGATT	TGTATTCANA	AATAGTCGTA	CAAGCACCCA	ACTGATAAAG	CGATTCAACG	420
TATCGATGAA	CCAGATAAAG	TGTTTCGTTT	AGTTGATGAG	AAAAACATCG	CGATGATTCA	480
TTGATATAGT	TGAACCTTCAT	GANNCGGGGC	CGACCGGTTT	TACCTCATAA	CCGAGNACTG	540
CTGAAGCGGC	TTGAATACTT	TCNGAAGTA	TTATTCCAAA	TGGATATTCC	TAATAATTTA	600
CTCATTGCGC	AAAATGTTCC	AAAAGAAGCG	CAGATGATAG	CTGAAGCAGG	CCAAATTGGT	660
TCCATGACTG	TTGCGACTAG	TATGGCAGGT	CGAGGCACAG	ATATTAAACT	TGGTGAAGGT	720
GTCGAAGCAT	TAGCTGGATT	AGCTGTTATT	ATTCAATGAAC	ATATGGAAAA	TAGCCGTGTA	780
GACAGGCAAT	TACGTGGTCG	TTCTGGTAGA	CAAGGGGATC	CGGGATCATC	TTGTATATAT	840
ATTTCACTAG	ATGATTATTT	AGNTAAGCGA	TGGAGCGATA	GTAATTTAGC	GGAAAATAAT	900

CAATTATATT	CANTAGATGC	ACAACGATTA	TCGCAAAGTA	ATTTGTTTAA	TCGNAAAGTT	960
AAGCAAATTG	TAGTTAAAGC	GCAGCGTATC	TCGGAAAGAA	CAAGGGGTTA	AAGCTCGGTG	1020
AAATGGCTTA	ATTGAATTTG	NNAAAAAGCA	TNAGTATTCA	GCGAAGATCT	TNGTATTTAC	1080
GANGGAACGC	AAATCCGAGT	TTTTAGAAAT	TAGATTGATG	CTGAGAATCC	NAGATTTTTTA	1140
ANGCGGTTAG	CTTAAAGATT	GTATTTGAAA	TNGTTTGGGG	NAATGANGGA	AANGGTGCTA	1200
ACAAAATCGC	GNGTTGGGCG	AGTATATTTT	ATCAAAAATT	TAAGTTNCCA	ATTTAATAAA	1260
GATGTGGCTT	GTGTTAATTT	TAAAGATAAG	CAAGCAGNAG	TGACATTTTTT	ATTAGAGCAA	1320
TTTGAAAAGC	AATTAGCTTT	GGANTCCGTA	AAAACATGCA	ANGNGCATAT	TATTATAATA	1380
TTNCCGGCCA	AAANGTCTTT	NGGGAAAGCA	ATTGATNCAA	GTTGGGGTTA	GGAACAAGTC	1440
GGCTTTTNAC	AACAANTTAA	NAGCAAGCGN	TAATCAAACG	ACAAAANTGG	CAACCT	1496

(2) INFORMATION FOR SEQ ID NO:1095:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2606 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1095:

CCCAAATCCT	TTGAAATAAA	ACTTAATTAA	GTTCAAGAAN	TCGNGGTGAT	TTTCCCCGGA	60
AGTTTGTGTTG	AATATTATTA	TGGATTGATT	TGATAGAGCT	TATGGACCCC	ACATTAATAT	120
TGAAGTCCTG	GGGCCAAGTT	CACNCCCCCG	TGGGTGGAAT	TTCTATTGTTG	ATCCCTAAAC	180
CCAAACTATG	GACGTCCCAA	ATTCTAAATA	TGAAAAAATG	GCTGAGCATC	GTTTGATGAA	240
TCATGATTTA	TATCCCGAAA	AAATAGATAA	TCGTTAAATG	TATCATTTTAA	TAAACACACC	300
AATAAGTTGA	TTTTCTTAAC	TTATTGGTGT	GTGTTTTTCA	TTAGCATAC	ATAATAGGTT	360
ACATTAAAAT	AACATTTTAT	ACCCAAAGTA	CACCAAAAGA	ATATTAGTAC	ACGAATTANA	420
CAACATTTTT	ATAGAAACCT	ATTGCACTTT	AACGTCAATA	AGTATATTTT	TATATTATCT	480
CTAATTAAAT	GTGCGCGCTT	AATAACAGAA	TATTCTCAAT	ATTTTTATTT	TTTGTGATT	540
TGTTGGAATA	TTTAGTTGAT	AAGGCACAAT	CAAATTTACT	TAAACTATTG	TATTAGGGGA	600
AGAAAGGATG	GGATGTATAC	ATGACACAAC	AAAACGCCCA	TGAAATCAA	ATTCAAGACA	660
TACCTCAAAC	AGGATTTTTTC	GGGCATCCTC	GAGGACTAGG	CGTACTCTTC	TTGTAGAGT	720
TCTGGGAAAG	GTTTAGTTAT	TATGGCATGC	GTGCCCTACT	CATTTTCTAC	ATGTACTTTG	780
CCGTAACAGA	TAATGGCCTT	GGAATTGATA	AAACAACAGC	TATGTCAATT	ATGTCAGTTT	840
ATGGTTCATT	AATCTATATG	ACATCCAATA	CCAGGCGGAA	TGGATTGCTG	ACAGAATTAC	900
AGGCACTAGA	AGCGCTACTT	TATTAGGTGC	AGTCTTTATT	ATTATCCGAC	ATATTTGTTT	960
AAGCTTACCA	TTTGCAATTAA	TCCGCTTATT	CACATCAATG	TTCTNCATCA	TTATTGGCTC	1020
AGGTTTAAATG	AAGCCAAACA	TTCCAAATAT	CGGTGGCCGT	TTATATCCTG	AAAATGATAG	1080
ACGTATGGAT	GCAGGTTGTG	TTATTTTCTA	TATGTCAGTT	AATATGGGTG	CATTATTATC	1140
ACCTATTATT	GTGCAACACT	GTGTTAATGT	TAAAACTTC	CACGGCGGAT	TCTTGATTGC	1200

```

AGCAGTTGGT ATGGCATTAG GTTTAGTATG GTATGTACTT NACANCCGCA AAAACTTAGG 1260
TAGCGGTGGT ATTGAAACCN ACTAACCCAT TGACNACCAG CTTGNAAAGA AAAAGTATGG 1320
TCTTTATTAT CGGAAGTGGT GTCCTTAGCA ANTGTATTAA TTATCGGTAT TGGGGCATT 1380
ACTAACTCAA TATCAANTAA CTTAGGTAGG AATACTGTTT TAGTATTAGG TATTGCATTA 1440
CCANTCATT ACTTCACTTT AATTATTAGA AGTANAGATG TCANNGATAC TGNACGTTCT 1500
CGTGTTAAAG CATTTATTCC ATTATTTATT CTTGGAATGG TGTTCGGGC TATTCAAGAA 1560
CAAGGGTCTA ATGTATTAAA CATATATGGA ANTGNACATT CAGATATGAA ATTAACTTA 1620
TTTGGTTGGA AAACANACTT TGGTGAAGCG ATCTTCCAAT CAATTAACCC ATTATTTATT 1680
TTATTATTAG CTCCAATTAT TTCACCTTTA TGGCAAAAGC NTGGAACATA ACAACCTAGC 1740
CTGCCAGTAA AATTTGCAAT TGGTACGTTT TTAGCAGGTG CGTCATACAT ACTAATTGGT 1800
ATTGTAGGTT ATGCATCAGG TTCATCAAAC TTCTCAGTTA ACTGGGTAT TTTATCGTAC 1860
ATTATTTGTG TTATCGGTGA GCTATGCTTA TCACCAACGG GTAATAGTGC TGCTGTTAAG 1920
TTAGCACCTA AAGCATTATA TGCCCAAATG ATGAGTATTT GGTACTTAAC TAACGCTTCT 1980
GCACAAGCAA TCAATGGTAC TTTAGTTAAG TTAATAGAAC CACTAGGTCA AACAAATTAC 2040
TTTATTTTCC TAGGTGTTGT TGCAATTATT GTTACAACAA TTTGTATTAG CATTCTCACC 2100
TTTAATCATC AAAGCGATGA AAGGTATACG TTAATATTGT TGGCCTAATT CAAAAACAG 2160
TAAGTCATTT AAATGGCTTA CTGTGTTTTT ATAGGTTTCT ATTAATTAAA TTCAAGATAT 2220
CAGTATAAAT AAAAGCTTAA TATGCTCGTT ATAGACAGCT ATAACATAT TTTCTCGTCC 2280
CACTCTATAG ACATCAATGT CAGTTATTAC CATTTTCTCT ATTTAAAAAC ATATTTTGG 2340
TATTAACAAT TAAAAGTGGG TATATATATT TAATGAACCA ATTTTATAGAA AGTAGGCTAA 2400
ACTATGGAAT ATAAATATAC ACATGGTGTC CTCTTTTACC ATGAACACAG TGGATTAAAA 2460
AATATTAATC AAGGTATTGG GGAAGTTACA ACAGCATTAA GTTCAATTG TAAGCATCTT 2520
TCTATTCAAT TGAGTGAAAA CGAAGGTGAC ATTATTAAAT ATTGCCAAGA AATCAAACT 2580
AAAAACTATC CAAAAGATGT AGATAG 2606

```

(2) INFORMATION FOR SEQ ID NO:1096:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1096:

```

GGCACGAGCG ATATTGTCA GGAAGTTAAA GTTCATGGAG ATAAGGCTTT GAAAATGTAT 60
AATCTAACAT TCGATCATAC GAAAACAGAT CATTTAGAAA TTAGTCATGA ACAAATTAAA 120
GCAGCATTTG ACACATTAGA TGAAAAACA AAACAAGCAT TACAACAAAG TTATGAAAGA 180
ATTAAAGCAT ATCAAGAAAG TATTAAGCAG ACGAATCAAC AGTTAGAAGA ATCAGTGGAG 240
TGTTATGAAA TATACCATCC ACTAGAAAGT GTGGGTATTT ATGTGCCCTG TGGCAAAGCA 300
AGTTATCCAT CAACGGTTCT AATGACAGCG ACTTTAGCAC AAGTAGCGGG TGTAAGAAAT 360

```

ATTGTTGTTG	TGACACCACC	TCAACCTAAC	GGAGTATCCC	AAGAGGGTAT	TAGCTGCATG	420
TTATATTACG	CAAGTTAATC	AAGTGTTC	AGTTGGTGGT	GCTCAAAGTA	TTGCTGCATT	480
GACTTATGGA	ACAGAAACGA	TACCTAAAGT	TGATAAGATT	GTAGGTCCAG	GTAACCAATT	540
TGGTNGCATA	TGCCCAAAAA	ATATTTATTT	GGACAGGTAG	GTATTGTTCC	ANATTGCAGG	600
ACCANCAGAA	ATAGCACTTG	ATTATTGACG	ACACCGCCAG	ATGTAGATGC	CANCGNCTNT	660
NATGTTTTTG	GGCAAGCNAG	AACATNATGA	ATTAGNACGT	CCATNTNTCA	TTGGTGAAGA	720
TGCGCAAGTC	CTNAAAGATT	TNGAATCACN	TATTGCTAAN	GCATTGCCTA	ATGTGGACAG	780
ANACGACATT	GTTTCTANAA	GTATCGCNAA	TCAACACNAC	CTNATCCANN	ATNGTAATTN	840
NGATNTGGGN	GAAGCATCNC	CANCTCATGA	ATACAATCGC	GCCTGAACAT	GCGTCGATTC	900
AAACAGTAAA	TCCTCAACCA	GGAATTCCTG	TTGAACGAAT	AATTTCTATC	TCGTTATCAT	960
CGTAAGCGTC	ATTATCAACT	TGTGTTTCTT	GCATTTCTTG	TAATTCGGCA	ACAAACACTT	1020
CTTGATCTCC	TCGATCACGG	CTCTTACGAT	TAATACGTGT	TTTATATTTT	CGAACTTGTC	1080
TTTCAAGTTT	ATTATTAATT	AAATCAATAC	CTGCGTATAA	ATCATCGTTT	CGCTCTTCAG	1140
CTCTTAACGT	AACATTTTTC	AATGGAATTG	TTACTTCAAT	TTTAGTAGCT	GAATNTGAAT	1200
AAGTTTTAAC	TTTAACATGC	GCCACTGCAT	NTGGTACGTC	ATTAAAATAA	CGTTCCAAC	1260
TACCAATTTN	CTCCTCAAAT	ATAGNTGCCA	ATAGCATCTT	GTGATAGGGG	AGGGNTATCT	1320
CCAATGAATT	TNCAAATCTA	TATCATANGG	GAATCTCTCC	CTTAAACCTC	TTTATTGGTA	1380
ACTCTTTATT	ATATTNNNAC	ATTNNNACGC	TATCGNGCAA	ACGCAAACAC	TTTGGATTCT	1440
CTGATATTNT	NNAGCATATT	AATTTACAAC	CCTGCACGAT	GATTG		1485

(2) INFORMATION FOR SEQ ID NO:1097:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1245 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1097:

TTTAATTTGC	TAAACCCAAT	TCACTAATTG	TGGAGTTGAA	TTGTAAAAAT	GTGTTTTGAA	60
ACAAGGTACT	CTTCTAAGCC	TTCTTTGCCT	AATTCTCTAC	CGATACCTGA	TTGTTTGTAT	120
CCACCCATGG	CGCTTGTGCA	AAATATGGAT	GGAAATCATT	AATCCACACC	GTCCCAAGTT	180
TCAACTTGTT	AGCAACGCGT	TGTGCTTTTC	CAATATCTTT	AGAAAATACA	GCACCTGCTA	240
AACCATATAT	AGAATCATTC	GCTAATTGAA	TCGCTTCTTG	TTCAAGTTTCA	AAGCCTTCTA	300
CAGTAACGAC	AGGTCCGAAA	ACCTCTTCTT	GTACAATACG	CATTGACGTA	TCACAATTTG	360
TAATGACTGT	TGGCTCGAAG	AATAGACCAT	CTTTTAAATC	GTCTCTATCT	GGACGTTTAC	420
CACCAACAGC	AATTGTTGCG	CCTTCTGCTT	TAGCTACATC	CATATAAGAT	TCGATCTTAT	480
TACGATGTTT	TGTTGAAATC	ACTGGTCCCA	TTTCAGTATC	AGCATCAAAA	CCATTACCTA	540
ATTTGATTTT	TTTCACGCGA	TCAATAAGTG	CTTGCTCAAA	TTTGTCTTTA	ATACTGTTTT	600
GTACTAATAT	TCTNGATCCT	GCTGAACANA	CTTGANCTGC	ATGNAAATAT	CCACCATTTA	660

ACGCTTGGTC TACTGCCAAT TCANAATCAG CATCATCAAA GATAATGTTG GGATTTTATC	720
CGCCAAGTTC CAAGACAATA TTCGTAAACA TTATTAGCAG CATTTTTTCAT AATATGGCTT	780
ACCAGTCTCA ATGCCACCTG TAAATGATAC AAGGTCAACC CTCTTTATGA CCTGACATTA	840
CGTCACCCAA CTTCAGAACC TGCACCAAGA ATAAGATTAA TTGTTCTTTT AGGGAAACCC	900
AACTTCTTCC ATTAATTCAA AAACACGTAT TGTGTTAAT GGTGTAATTT CACTTGGTTT	960
CATAACTAGT GAACAACCCG TAGCAAGCGC TGGCGCAATT TTCCATGATG CTTGTAATAA	1020
CGGATAATTC CAAGGTGTAA TTTGTGTAAC TACACCTACT GGTTCCTTAA CAATTTTGCT	1080
TTCTGTATCT GGAATTGGTG AATCAATCAT TTCGCCACCA TCTTTATCTG CTAATCCAGC	1140
AAAATACATA AACACATTAT GAATATCATC CATATCTGCA GATGATTCTT CTAACGTTTT	1200
TCCAGTATCT AATGTTTCTA ATCGTGCTAA CGCTTCGCTC GTGCC	1245

(2) INFORMATION FOR SEQ ID NO:1098:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1098:

GAATTCNAGG TACTGCAGNT GNANTCGCAA CACATGTNGC TGTCAGTNT ATTCAGTCTT	60
AATTGATGCC ACAGNTAAA TTCGCNTATA TTAGNTNATT GCAANCGGG TATAACAATG	120
TNGCTATGAT TGCAGACGGA GTGAATGATG CNCCAGCACT TGCTGCATCT NCTGTNGGAN	180
NAGCAAGGCT CGGNCTGGG ACGGATACTG NANCAGAAAC AGCTGATATT GNATGATTGN	240
GAGGTGNACG AAGCNCACCT CCCATTGCAG CANCCCTCNN TCGAAAACT TTCTANNTCA	300
TTNGAGCTAA CATCACATGN GGNATCNGN GCCTNGAATA ATTGTCCTCC TTATCANCNT	360
ATCCCCC	367

(2) INFORMATION FOR SEQ ID NO:1099:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2917 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1099:

GGCACAATTC	GGCACGAGCG	CTCCATCGCA	AGCATTCGTA	GATAAAATTTG	CGAAATATTA	60
TACGCCGATC	ATTATGGTTA	TTGCGGCGCT	CGTTGCAGTC	GTTCCACCTT	TATTCTTTGG	120
TGGAAGTTGG	GATACTTGGG	TTTATCAAGG	ATTAGCGGTA	CTTGTAAGTTG	GATGTCCGTG	180
TGCATTAGTT	ATTTCTACTC	CAATCTCGAT	TGTCCTCGCA	ATTGGAAAATG	CAGCTAAAAA	240
AGGTGTGTTG	ATTAAAGGCG	GTGTCTATCT	AGAAGAATTA	GGAGCCATTA	AGGCAATCGC	300
ATTTGATAAA	ACAGGAACAC	TGACAAAAGG	TGTACCAGTG	GTAACAGATT	TTGAAGTATT	360
AAATGACCAA	GTGGAAGAAA	AAGAGCTATT	CTCTATCATT	ACAGCTTTAG	AATATCGTTC	420
ACAACATCCA	CTTGCTTCAG	CAATAATGAA	AAAGGCAGAG	CAAGATAATA	TCCCTTATTC	480
TAATGTACAA	GTGGAAGAAT	TCACTTCGAT	TACTGGGCGA	GGTATAAAAG	GGATTGTAAA	540
CGGAACACT	TACTATATTG	GAAGCCCAAA	ACTTTTCAAG	GAATTAAATG	TTTCCGATTT	600
TAGCCTTGGG	TTTGAAAAACA	ATGTGAAAAT	CCTACAAAAC	CAAGGAAAAA	CAGCCATGAT	660
TATTGGAACG	GAAAAAACAA	TTCTCGGCGT	AATTGCCGTT	GCAGATGAGG	TTCGTGAAAC	720
AAGTAAAAAT	GTGATTCAAA	AACTTCATCA	GTTAGGTATC	AAGCAAACAA	TTATGCTGAC	780
AGGTGATAAT	CAAGGTACTG	CAAATGCAAT	CGGTACACAT	GTAGGCGTTT	CTGATATTCA	840
GTCTGAATTG	ATGCCACAGG	ATAAATTAGA	TTATATTAAA	AAAATGCAAT	CGGAGTATGA	900
TAATGTAGCT	ATGATTGGCG	ATGGCGTTAA	TGATGCTCCA	GCACTTGCTG	CATCTTCTTG	960
TTGGAATTGC	AATGGGCGGT	GGCTGGACGG	ATACTGCAAT	TGAACAGGTG	ATATTGCATT	1020
AATGGGAGAT	GATTTAAGTA	AGCTTCCATT	TGCAGTAAGA	CTCAGTCGAA	AAACTTTAAA	1080
TATCATTAATA	GCTAACATCA	CTTTTGCTAT	CGGAATTAAA	ATAATTGCCT	TACTATTAGT	1140
TATCCCGGGA	TGGTTAACCC	TTTGGATAGC	GATTCTTTCC	GATATGGGAG	CTACTATTTT	1200
GGTAGCATTA	AATAGTTTAC	GACTGATGAG	AGTGAAGGAT	AAATAGGTAG	AAAACAGAAT	1260
AGTAAGGTCA	CGCTGTGCGC	AATTCAAGGG	GGGCTTTTCA	ATTTGAAGAA	AAGTCCTACC	1320
CCTAAAATAT	AAAATATTGG	AGATGGAAAA	ATGATCGCAA	CGATACTTAC	AGCAGCTGCG	1380
GTATATGTAG	CAACAGGAAT	TGATATCTCG	TTATATTAAAT	TCTGGTTCTG	TTGCAAAGTA	1440
AAAATATAGC	TAACCACTAA	TTTATCATGT	CAGTGTTCGC	TTAACTTGCT	AGCATGATGC	1500
TAATTTCTGT	GCATGGCGAA	AATCCGTAGA	TCTGAAGAGA	CCTGCGGCTC	TTTTTTATATA	1560
GAGTGTAAT	ACATTCAATA	CCTTTTAAAG	TATTCTTTGC	TGTATTGATA	CTTTGATACC	1620
TTGTCTTTCT	TACTTTAATA	TGACGGTGAT	CTTGCTCAAT	GAGGTATTTC	AGATATTTTCG	1680
ATGTACAATG	ACAGTCAGGT	TTAAGTTTAA	AAGCTTTAAT	TACTTTAGCC	ATTGCTACCT	1740
TCGTTGAAGG	TGCCTGATCT	GTAATTACCT	TTTGAGGTTT	ACCAAATTGT	TTAATGAGAC	1800
GTTTGATAAA	CGCATATGCT	GAATGATTAT	CTCGTTGCTT	ACGCAACCAA	ATATCTAATG	1860
TATGTCCCTC	TGCATCAATG	GCACGATATA	AATAGCTCCA	TTTTCTTTTT	ATTTTGATGT	1920
ACGTCTCATC	AATATGCCAT	TTGTAATAAG	CTTTTTTATG	CTTTTTCTTC	CAAATTTGAT	1980
ACAAAATTGG	GGCATATTCT	TGAACCCAAC	GGTAGACCGG	TGAATGATGA	ACGTTTACAC	2040
CACGTTCCCC	TTAATATTTT	AGATATATCA	CGATAACTCA	ATGCATATCT	TAGATAGTAG	2100
CCAACGGCTA	CAGTGATAAC	ATCCTTGTTA	AATTGTTTTAT	ATCTGAAATA	GCTCATACAG	2160
AAGATTCCCT	TTTGNTAAAA	TTATACTATA	AATTCAACTT	TGNAACAGAA	CCAGAATTTT	2220
GATATAGATC	TTGTAGATAT	CCTTTTAGAA	AAGTCGAAAG	AGATTGGCAT	ACAGGTACAT	2280
CTTCAACATT	CCGTTGAATC	CATTGAAAAA	GAACAAGGAA	AGTTTCATGT	GTACGCTCGA	2340
AAAAAAGAGG	GCACGAGCGG	TTTGAAGCAG	ACATTGTTAT	TCATGGTGCT	GGACGGGTCC	2400
CTGCCTTAGA	TATGAATCTT	GAAAAAGGGA	ATATAGAAAG	GAAAAACAT	GGTGTCATG	2460
TTAATGAGTA	TTTGCAAAGT	GTAAGTAACC	CGAATGTCTA	TGCAGCTGGA	GATGCTGCAG	2520
CAACGGATGG	CTTGCCCTC	ACACCTGTAG	CCAGTGCAGA	TTCTCATGTC	GTAGCATCTA	2580

ATTTATTGAA	AGGGAACAGC	AAAAAAATTG	AATATCCCGT	GATTCCATCT	GCTGTATTTA	2640
CCGTACCTAA	AATGGCATCG	GTAGGTATGA	GCGAGGAGGA	AGCCAAAAAC	TCTGGCCGGA	2700
ATATTAAAGT	AAAGCAGAAA	AACATCTCCG	ACTGGTTTAC	GTATTAAACG	GACAAATGAG	2760
GACTTTGCTG	CGTTTAAAGT	CTGATTGACG	AAGGATCATG	ATCAATTTTG	GGGTGCTCAT	2820
TTGATTAGTA	ATGAAGCCGA	TGACTGATTA	TCAATTTGGA	CAGCATCCGT	TTGGGATTTT	2880
AACCAAAGAT	TGAACAATGA	TATTTGGCCT	TCCCACC			2917

(2) INFORMATION FOR SEQ ID NO:1100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1514 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1100:

ATGATGTAAA	CCCAGTTCN	ANCTTCATCA	TTCAGTTGAT	GCAATAATGT	CACNNAACT	60
CTACCACCAA	GATGCACCAA	TAGGTTGTCC	CTAAATGCAA	TAAGCGCCAC	CCTTTAACAA	120
TTCACCCTTT	TCAGGGAGGT	NATTTTAAAT	TCACCGATCC	AACAGCTAAT	GATTGTCCTN	180
CAAATGCTTC	AATTTAATTC	CAAATACATC	AATATCGCTT	AATTCTTTTT	TACTACGTTT	240
CCAAAGCCTT	TTCTACAGCG	CCAACTGGTG	CAATACCCAT	AATAGAAGGA	TCTACGCCAT	300
GACTTCCCAA	AGCCATCCAA	GCACTGCCAA	TGGTTCGATA	TTTAATTCTT	TAGCTTTGTC	360
TTCTGACATG	ACTAACATCA	TCGCAGCACC	ATCATTGATT	CCTGATGCAT	TACCTNCTGT	420
AACTGTCCCG	TCTTTTGTGA	AAGCTGGTCT	TAAGCGACTT	AATTTTTCGA	CTGATACATT	480
TTCACGGACA	CCTTCATCCT	TAGTGACTAA	GATTGGTTCA	CCTTTACGTT	GAGGAATCGA	540
TACTGGAACT	ATTTCACTAT	CAAATTCACC	ATTTTGCTGT	GCACGTACTG	CTTTATTGTT	600
GTGAGATTAC	CAGCAACATG	TATCTTTGTT	CTTCTCTTGA	AATACCATAT	TGCTCCTACT	660
AAATTTTCAG	CAGTAATACC	CATATGATAT	TGAGTAAATA	CATCTGTTAA	ACCATCATAT	720
ACCATGCTAT	CAACCATTGA	GTGATGTCCC	ATTTTAAAC	CGAAGCGACT	GTTGTTGNCA	780
AGCATTGGTG	NCTGAGACAT	ATTCTCCATA	CCGCCAGCGA	GCACGATGCT	CATGCCCACC	840
AGTCAGCNAT	AGATTGATAT	GCTAATTGAN	TCGACTTTAA	CCCAGAGCCC	ACATACTTTA	900
TTCACTGTAA	ATGCAGGTGC	TGTTTCTGGC	AAGCCACCTT	TCATAGCAGC	AATTTCGTGT	960
GGATTTTGTG	CTTGTCCTGC	TTGTAGTACG	TTACCGATGA	TAACCTCATC	AATCTCACTT	1020
GGATTCAAAC	CCGTCTCTTT	AATAATATGT	TCTATTAAAG	TCGCACCTAA	ATCATAGGCT	1080
GGCAGTCTTT	TAAACGCACC	TCCAAAAACG	CCAATAGGTG	TCCTGTATGC	TGCTGCTAAT	1140
ACGACTCTCG	TCATGTCATA	TTTCTCTCCT	TATGATATAT	ACAATTTTAT	TACTAATACG	1200
TCTAATGAAC	CAATACGCCA	CTAACATCCA	ATTTATGAAA	CCAATTGCTA	CGTATGTTAC	1260
ATTTTCATTC	TTGTTATGCA	TTTAACAAAT	CATATTATAC	AATGATGTAA	TTTGTTTGGG	1320
CAATCGGAAA	CGTAAACGGT	TTCACTTTAA	CATTTACAC	TCTTAAATAT	GCTCTATCAT	1380
CCTCATCTAT	AGTACAAAAT	TATGCTTTGA	TTTACCACAA	ATTATCATTA	ATCATTTTCG	1440

TCGTGCCTCT AATTAAATTC TTTCTATCAT TGGATCGNTA TCACAGGTGG NTTCACCACA 1500
 ATTCTCATCA ATTT 1514

(2) INFORMATION FOR SEQ ID NO:1101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1030 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1101:

CGGTATTTCA ATCAGCGCCT CGTTCGGAGT GCGCTCAAAC GGTGCGAAAT ATGAAGCAGA 60
 AACCAAACTA TATCCGAATC CTAAGACATC AATATATCGC TTTAGGTTGA AGACTTCAAA 120
 GCATTGTGCC AAGGACAATT AGATGCGCAC AGACGGGGGC ATTTTATTAG CGACCATGAT 180
 TATCATATCG CCTTAAATAT CGCCACAATT TTAGCGGGTG GTGATTTACC AAGAAATACA 240
 TTTATAAATC AACGTTACAT TCAATCGTTG GAGAAAATTG GCTTTATTGA CTTACTAAAA 300
 ATCTAAAAAA TCATATGGAA AGAATTGCAC ATATGTTAAA AACTGGTAAG CCATTACGTA 360
 ATTAAAAGAT AGTCATTAAG AGAGGATGAT AACCATGCAA GAAGCATACA TTGTAGCTTA 420
 TGGGGCGTTC AGCCGCAGCG AAAGCAAAGC AAGGCGCATT ATTCCACGAA AGACCTGATG 480
 ATGTCGCAGC CAAAGTATTA CAAGGCGTAT TGAAACGTAT TGACGGAAAA TTCAATAAGN 540
 ATATGATTGA AGATGTCATT GTTGGTACGG CTTTTCAGA AGGATTACAA GGACAAAACA 600
 TTGCACGAAC GATTGCATTG CGTGCGGGAT TATCTGACAC GGTACCGGGT CAAACAGTGA 660
 ATCGNTACTG CTCATCAGGA TTACAAACCA TCGCGATTGC AGCCAATCAA ATTATGGCTG 720
 GTCAAGGAGA TATACTTGTA GCTGGTGGCG TTGAATTGAT GAGTGCCGTA CCAATGGGTG 780
 NCAACGAGCC CACAAACAAT CCAACCTTAC AATATGATGA TATAGGTGCG TCATATCCTA 840
 TGGGTTTAAC TGCTGAAAAT GTAGCATCCC AATTGACGT ATCACGCTCG AAGATGCCAA 900
 GATGCTTATG CTGTCAGAAG TCATCAACGT GCCTATGACG CACAACGTGA TGGTCGGTTC 960
 AAAGATGAAA TTATTCCAAT ACGGGTAAAC TCAGTTGAAT ATACAAACGC AGGACCAAAA 1020
 GTCTCGTGCC 1030

(2) INFORMATION FOR SEQ ID NO:1102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1102:

GGACTACTAA	AACAAGTAAT	CAAATCATT	CAAGANGTAT	TAAGCNCCCT	ATGATCCAAA	60
GCCCAACTCG	NNAAAGAAAT	TGCGTTTCGC	NTCAATTTGG	CAGGAAGTAG	ATAGCACATT	120
ACAAAGGACA	ACCGGGAGAC	ACTTTGTNAT	TCCCAGCATT	CGTTTATAAG	CGGAGACGCA	180
CAAGTAGTTG	CAGAGGGCGA	NGAAAATCCC	TCCTGCACATT	TTAGANACGC	NAAAACGTGA	240
GGCTAAAATC	CGTAAAATTG	CTAAAGGTAC	ATCTATCACA	GATGAGGCTT	TATTAAGTGG	300
NTACGGAGAC	CCTCNAGGCG	ANCAAGTACG	TCAACACGGT	TTAGCACATG	CTAACACAGT	360
TGATAATGAT	GTATTAGAGG	CTTTAATGGG	AGCTAAACTT	ACTGTTAATG	CGGACATCAC	420
TAAGTTAAAC	GGCTTACAAT	CAGCAATCGA	CAAATTTAAC	GATGAAGACT	TAGAACCAAT	480
GGTTTTATTT	GTTAATCCAC	TTGATGCTGG	TAAGTTACGC	TCGGAGATGC	ATCAACTAAC	540
TTTACACGTG	CAACCGAATT	AGCGCATGAC	ATCATCGTTA	AAGGTGCGTG	TGGCGAAGCT	600
CTAGGTGCTA	TCATTGTACG	TACTAATAAG	TTAGAAGCTG	GCACAGCTAT	TTTAGCTAAA	660
AAAGGTGCAG	TTAAATTAAT	CTTGAAACGT	GATTTCTTCT	TAGAAGTAGC	GCGTGACGCA	720
TCAACAAAAA	CAACTGCATT	ATACAGTGAT	AAGCACTATG	TAGCATATTT	ATATGATGAA	780
TCTAAAGCAG	TGAAAATCAC	TAAAGGTTCT	GGAAGCTTAG	AAATGTAATA	GGAGGTAGTG	840
ACATATGTAT	AAAGTAATCG	AACGTTTTGA	AGATGCACAA	GACAATGGAC	ATGAATATCA	900
AGTGGGAGAC	ATTTACCCAC	GTGATGGGTT	AGAAGTATCA	GAAGAACGGT	TCACTGAATT	960
ATCTACAACA	AACAACCGCC	GTAACCTAAT	CGCTATCAAA	CTTGTTGAAG	ACGATACAAC	1020
AGAACAGTCT	GAGGCGAGCG	CTGACGAGCA	AAAAAGTTTA	TCTGATATGA	AAGTAGCAGA	1080
ATTAANAGAA	CTTGCTAAAA	AGCGTGAAAT	TAAAGGCTAT	AGCGATATGA	AAAAAGATGA	1140
GCTTATCAAA	GCTTTAGAGG	GTGTTAAGTT	ATGGACGCAA	AAGACGTCAA	AATGATTAAT	1200
GGACTTTCAC	TCAATGATCC	GCTCTACGAT	GAGCAGGTCC	GATNTCTATG	AAGATNTTTA	1260
GGGGGTGGAG	GAGGATTATT	GGNTCAGAGG	TTGATGACAA	GAGTGCCGCG	GGTGTTAGAG	1320
GTTATGTTGA	TGTTCAAGTG	GGCAACTGGC	AATTCTCAGG			1360

(2) INFORMATION FOR SEQ ID NO:1103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1000 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1103:

GGCACGAGCT	CAAGTAAAGT	GCTACCATTT	TTCTTACAGA	CATTTGCCGA	NATCTTAAAC	60
TAAGACATAN	CCCCTAAAAT	ACTCNCTANA	GNACCGNACA	ACCNCAACAC	AATTCCTGTC	120
ATGATCTTAG	GCTTTGTGCC	ACCTNCCCCA	GTTGNCAAAT	GCTTTGTCCA	TCCTTCTTGT	180
AATGACTGAA	ATCCTTCTTG	ATACATNCGA	AATGCAACAA	ATGGAAATCC	TTCATAAACT	240

```

GTTACGGGCA ATGATTGTGA AGTAGATGCA CTTCTTAAAG CAAATCCTTC AATAAAAATG 300
ACGGGTCGCA CTTTTATGAC CTCCAGTTGC ATAATAATCT TCTTTATTTG TTAATGTCAC 360
CGGTCCAAAT GCATGCTGGT TAGTCCGCAC CGTCGTCTAA GGTANAAAAT ACATTCATAC 420
CACCAGCTTG TCATTAAATT AAATATCGCT GAAAACCCCTT CGTAGAAACG CTTTGTATA 480
TGATAAGGCT GTACGCTTAA CAATCCTTTTC TCACCTTGTA ATTGATACTG ATTAATCAAC 540
GTTTCAACAG CATCTTTCCT TAAGAAAGTT ACATCAGCAT CTACAAAGGC AATACGATTC 600
GTACATGCAT GCGTCACACC TTGATAACAA GCATGTGATT TCCCCATACC ATTTGCCGTC 660
AGTATCATCA ACAACATCTA CTACAGTCGC ACCATATGAA CGTGCTACAC GTGCTGTTTC 720
ATCTGTCGAT CCGTCATTCA TAACAATGAC ATCTACTGGA ACTTGCTGTT GTATTATCGA 780
ATGTAGTAAA TGACCTATTC TTTTTCTTC ATTTCTAGCC GGAATAATAA TTGTTAATGC 840
TTTATGATTG AAGTTCAGCG TTTTCGTCTT TAGCTGATGT CTACGATTAA ATATCAATGC 900
ACCACACGCC ATAGACATGG TCACTATTAC TGTTAATATT CGTGATAACC ATTTTCATAGA 960
TATCACTTCC TATTCTTCGC TTCTCGCGCG AGCCCGNGCC 1000

```

(2) INFORMATION FOR SEQ ID NO:1104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 916 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1104:

```

AAATCCTGCG CCTTGCACTN CCTTNCCATA AAAANCCTCC CCGTCAGCAG CGGATAGCCC 60
CCGCCCCAATC AATACCCAGG AACCAGAGAC NGGGCTTGTC AAGCGATACT ANCAGCGATA 120
TATCCAGCTA GTATTGGAGC CATAAATTTA AAGGCTAAAC TACCCAATGT TTCAATGGA 180
TTTCCACAA TGAATCATCT GGGATGACTA ATCCTTTTGA TGTCGTTTCA CCGCCTAGAG 240
TCAGCGCGAT GNCGATAAGG AGTCCACCAA CTCCGATAAA AGGANCCATA AACGATACAC 300
CGTTCATTAA ATGTTGATAC ACCATTTGAA TACCACTTTT AGACTTACCA GCGATCTTTC 360
GAATGATAAT TTGTTTCAGA TTGATAAATA GGCGCATCTT GATTAATGAT ACGTTGAATT 420
AGACCTCTCG GATTATGAAG CCCTACGAGC GAACATTTTC ATTAATCAAC CGTTTACCAA 480
CAAATCGGGA TAGATCAACT TGTTTATCAG CTGCAATTAT GACACCGTCA GCTTCTTCGA 540
TGTCTTGCGT AGTTAAAACA TTTTCAGCAC CAACACCGCC CTGTGTCTCT ACTTTAATAT 600
CCACACCCAT TTCTTTTGCT ACCTGCTCAA GCTTTTCTTG AGCCATATAT GTATGTGCAA 660
TGCCATTTGG GCATGAGGTA ATAGCTACAA TTTTCATAAA ATCATCTCCT TTTCTATATT 720
GTAAGCGTAT TCTCGATACT AAAAAAGAA TAATTACCGT TACTAGTGGC AATTATTCTT 780
GTAAGTATTC AAATAACTGT TGCTTTAAAC TATGATCATC TAAACTACAT AAATGGTTCA 840
CTGAATCATC ATCCAAGTTA GCAATTAATT GCATCATTTG TTTTGTAATA GCTTTGTCTT 900
TATGCGAAAT CGCTAA 916

```

(2) INFORMATION FOR SEQ ID NO:1105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1047 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1105:

```

GGCACGAGCT ATATCCAATT GGGGTAAAGC GGGTAAAGAC CAAGAGAAGA ATTTAAGAAG      60
ACATTAGCAG AAATTGAAAG GACACCGGCA CGAGCTAGCG CAACAAGTTT AGCGATTGAA      120
GCATTTGGTG CAAAAGCAGG TCCTGATTTA GCAGATGCTA TTAAAGGCGG TCGCTTTAGT      180
TACCAAGAGT TCTTAAAAAC TATCGAAGAT TCGCAAGGAA CGGTCAATCA GACATTTAAA      240
GATTCTGAAA GTGGCTCCGA AAGATTTAAA GTAGCAATGA ATAACTTAA ATTAGTAGGT      300
GCTGATGTAT GGGCTTCTAT TGAAAGTGCG TTTGCTCCAG TCATGGAAGA ATTAATCAAA      360
AAGCTATCTG TAGCAGTTGA TTGGTTTTCA AGTTTAAGTG ATGGATTTAA AAGGTCGATT      420
GTTATATTCG GTGGTATTGC TGCTGCAATT GGCCTGTAG TTTTGGGAT TAGGTGCATT      480
CATAAGCACA ATTGGCAACG CAGTAACTGT TTTAGCTCCA TTATTAGCTA GTATTGTAAA      540
GGCTGGCGGA TTGATTAGTT TTTTATCAAC TAAAGTGCCT ATTTTAGGAA CAGTCTTCAC      600
AGCATTAAC TGGTCCAATTG GTATCGTGTT AGGTGTACTG GCTGGTTTAG CAGTCGCATT      660
TACAATAGCT TATAAGAAAT CTGAAACATT CAGAAATTGT GTTAATGGTG CAATTAACAG      720
TGTTAAACAA ACGTTTAGTA ATTTCAATCA ATTTATCCAA CCTTACATTG ATTCCGTTAA      780
AAACGCTCTT AAACAAGCGG TTTCAGCAAT CCGTGATTTC GCTAAAGATA TTTGGAGTCA      840
AATTAATGGA TTCTTTAATG AAAACGGAAT CTCTATTGCA CAAGCGCTTC AAAATATATG      900
CAATTTTATC AAAGCTATAT TTGAATTTAT CTTAAAATTT TGTAATTAAA CCAATCATGT      960
GTGCGATTGT GCAAGTGATG CAATTTATTT GGCCGGCGGC TAAAGCCTTG ATCGTCAAGT     1020
ACTTGGGAGA ATATAAAGA GTAATAC                                     1047

```

(2) INFORMATION FOR SEQ ID NO:1106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1060 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1106:

TGTAATACCA	GCATTCTGCC	TGAACATGGT	GGACCGCCTT	TATTAAATAA	GATAAATAAG	60
ANTGNANTTA	TTGAAATAAC	CTGCATATTG	CATAATTAAC	AATGGCGCTG	TGGCGTAAAT	120
GACATGCGGG	AATGTGATGT	TTCTAAACTT	TTGCCAACTA	GACGCACCAT	CCATATCTGC	180
TGCTTCGTAC	CAATCTGATG	AAATACTTTG	CAGTACTCCA	GTGAACAGTG	CAAAGACAAA	240
TGGGAATCCA	AGCCATACTT	GAATGCCGAT	TAATGCCACT	TTTGCCCAAA	ACGGATCACT	300
TAACCATGCT	GGTGCTACAC	CTAATAAAGG	TTGCAAAATA	TCATTATTTA	TCGCACCAAA	360
TTCATCATT	AATAACGCTA	CAAATATTAA	AATTGTCACA	AATGATGGTA	CAGCCCAAGG	420
TAGGATTAAC	ACAGTACGGA	TAAATTTCTT	ACCTTTGACG	ACAGGGTGAT	TTACAATAAT	480
TGCCAAAAAC	AGCCCTAATG	CAATTTGAAG	TGTCGTTGCA	ACAAGCGTCC	ATACTAATGT	540
CCAAGTAATA	ACACTGAAAA	ATGTTTTCGG	CCAAACGCCA	ATTGTGAATA	ACGTTTAAAA	600
GTTATCTAAA	CCAACCCATT	CTAATGTGTG	TCTCGGAGGC	GCGTTGTATA	AATTGTAGTT	660
TGTAAATGCT	ACTCCAAACA	TAAATATTAA	TGGAAATACA	ACTACAAATA	TCAATAAGAA	720
TGTACCTGGT	GAGATTAGTA	AGTATGGGAA	CGTCTTGTC	CATGTTGCCA	CCATACGCGC	780
CTGCCGATCC	TTTATTTCTT	CATTGCGATT	AAATCGTTCA	GCATTACGAT	ATGCATCTAA	840
AATATTAATG	ACATATAGCA	TGATGGCGAA	AGCAACGAGT	AAGATAGAAA	TAATACCTTG	900
TGCAAGTAAG	ACACGAGAAT	CGTCTAACTT	AGGTACTGTC	CCTAATGTGA	ACAATCCCCA	960
AAAACCAATA	TTTAAAAAGC	TATAAAATAC	AGAAATAAAA	CTGATGAAAA	AGATAAAAAA	1020
TATCGTACCT	TTAATGGGTC	TTTATTATTA	AAACTGTCCC			1060

(2) INFORMATION FOR SEQ ID NO:1107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1107:

TAAATAGTG	ATTCTGGTCG	CTCGTCCAAC	ACCTAATTGC	GCATCAATAT	CCCATTGCNC	60
CCGGATGGGG	TNCCTTCTTA	CCTCCTACCA	AGTTCCCTGA	AAAATACNTA	TTGAATCTCC	120
TTCTNCGTT	GTATCCACAC	TTGACGGTTG	TAATTTAAAT	AACCGTCTCA	TCTTTCCATT	180
TGCGGAATCT	TTGATNATTT	GTAATATTTT	CCACAATCCA	AAGTCAACTT	TATGGGGTAT	240
CCAATCCACG	CTTTAATATG	GTAATTCCTC	AGCAATCGCA	CCTTTTAAAT	CATTATTTTC	300
AATGACTTTA	TTCTGTTTAA	AATCAACAAG	CAATAACTTT	CCAGGATTCA	ATTGACCTTT	360
AAAAGCAACA	TTACTTTTCAG	GTACGTCCAC	AACACCCACT	TCAGATGAGA	AGACAATAAA	420
GTTATCTTTA	GTAATCGTAT	AACGACCTGG	ACGTAATCCA	TTTCTATCTG	TAAGCGCGCC	480
AAGTTTGTCA	CCGTTACAGA	NCGAAATCAT	TGTAGGACCA	TCCCACGGTT	CCATTAAATA	540
ACTATAAAAT	TCATAAAACG	CACGTACATT	TGCATCATTC	GCTTCATTGT	ATAACCAAGG	600
TTCAGGTATG	AGTAGCATTC	GCTGCCCTTT	CTGGCTCCAT	GGCTAACGAT	AAGAATCTA	660
GCGCATTATC	TACAATAGCA	GAGTCACTAC	CATCCTCATC	GACAAATTGA	AACACTTTAT	720

GTTGATCCTC	GCCAAATAAT	GTTTCGATTA	AATTTATGTN	GGCGTGCTCG	CATCCAGTTT	780
ACATTACCTT	TAATCGTGTT	AATCTCACCC	ATNATGCATT	AACAATACGG	TTAGGATGTG	840
CCCTTTTCCC	AACCTCGGAA	TGTATTCTGA	CTAAATCTCG	AATGCACTAA	CCCTAGCTTT	900
GATTGATATA	AATCATCCGA	TAAATCTGNA	TATAGTTTTT	TAATTTGGTC	TGATCGTAAC	960
CAACCTTTAT	AAACAATTGT	TTTGCCTGAT	AAGCTCGTAA	AANACAATTC	TAAATCGCAC	1020
TGAGTCGAAT	AGAACTCTAA	TTGTTTTCTC	GCTAAAAACA	AACGCTTTTC	AACATCTTCA	1080
ATGCCCCTAA	TATCAATAAA	CACTTGTTGA	ATGACTGGCA	TCGTATCTGC	TACATGTTTA	1140
GCAATGGCAT	CTTTATTAAC	TGGTACATTN	CGATAACCAA	GAATTGATAA	CCCTTCGCCT	1200
TCAAAATATT	TTTTAAAAAC	TGCTTCATGT	TCAGAACCTA	AAATGCGTTC	TTTGAAAAAA	1260
AATAACCCCA	CGGCATATTC	ACCTTCACCT	GGGATATCAA	AGTCCGTTAC	ATGTTGTTTG	1320
AAAAATGCAA	AAGGTATTTT	AGTCATAATA	CCTGCGCCAT	CACCAGTGAT	GCCATCTGCG	1380
CCGACCCCGC	CCCTGTGATC	TAAGCGTCGC	AACATTTCAA	GCGATTTATC	AATGATGTGC	1440
TGAGACCTTT	TATTATCCAT	ATTTCGCATA	AAACCAATAC	CACACGCATC	ATGTTCCCTCA	1500
CGATAGTCAT	ATAAGCCTTT	AATTAATTTT	TCAG			1534

(2) INFORMATION FOR SEQ ID NO:1108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1108:

AGTTCCTCCT	TTCGTTAATT	GATTTCCCCT	ANNAAATCCA	TAAACTTTGC	NCGGGACCCA	60
AAGCCANCCC	GCGACAAGCT	GCAACTTCGG	ATCCCTAATC	CCACCGTGAT	GGGTGGTAAA	120
ATTGCTTTGG	GATCGTTACT	GCTAGCGGCT	CTGTAATATT	ATTTAATTCT	ACAAANCGGT	180
TCACCAAAGA	CTTAAGATGG	TCAGGCGCAT	CATATAACAA	TACCATCGTA	AACATCGCTT	240
TTAATAGACG	AATAGTTCCC	GCTCTCTAAG	GCTTCTATTA	AAACTTTGAT	TTTACCTGCG	300
TTAAACGGTA	CTGCAATAGC	AGGCTCTCCA	AATGTAACAG	CATGTTCTCC	TATTAAAAATA	360
ATCTTACCTG	TCGATTCCCC	ATATCCTTTT	CTTGTCATGT	CAATATCACC	TTTTATATTT	420
ATCCTATACT	TGATTCATTA	TTTTTATTTA	TTAGTAAAAG	ACATCATATT	CTAAGTTGCA	480
TACGCATTCT	CGTTAAATTT	CATTGCAGTC	TTTATCTCAC	ATTATTCATA	TTATGTATAA	540
TCTTTATTTT	GAATTTATAT	TTGACTTAAC	TTGATTAGTA	TAAAACTAAC	TTTCGTTTAC	600
TTCAAAGTTT	AAATCTTATC	GAGTGATATT	TCAGATTCTT	TATCTTTTTA	TAAAATAGCC	660
CTACAATTTA	TAATTTTCCA	CCCTAACTAT	AATACTACAA	ATAATAATTG	GAATATATAG	720
ATTTACTACT	AAAGTATTAG	AACATTTCAA	TAGAAGGTCT	TTTCTTTCAT	AGTCATACGC	780
ATTATATATA	CCCTATTCTC	AATCTATTTA	ATACGTAAAA	CATGAAATTT	TCTTATTAAA	840
TTTATTATTT	CCATCATATC	ATTACTTTTA	ATTAAATGAT	GTTCAATTTA	AATATGAGGG	900
TCAATAACAT	ATTTATGCCT	TTTTATGGAT	ACTTTTCAAA	AATAACAGCC	CCAAACGATA	960

```

ACTTGAAAGG GGGCTGTGAA ATATTTAACT ATTGCATTG GGTCTATCAT TTNCTTGTTT 1020
CTATCAATCA TTTTATCAAA ATACGTATCG TATCTTTGGG CATTCTTCTT GAGTAATGGG 1080
CGTCATATTT TAATACAACC GCCAAGATCT TTGATTGGAT ATTAATAGGC AAAAACATTA 1140
CATCTTGGAC AGTAATCGTT TGGTTAAGCA ATGTCTCTAA TG 1182

```

(2) INFORMATION FOR SEQ ID NO:1109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1109:

```

CAGTTCATCA TGGATGCTTT GAGCGGTATC CAAGTGTGGA TTTATTACAC ATATTGTATA 60
AGACATGTCA CCATTATTTA TTATCACACA TCACTAAGTC ATGTATTGAA ATATTGTCAG 120
TACATTTATG TTTAAAGAAG TTCAAATCAT TGAACGAGGT AATATTAATC ATTTCAAGTA 180
TGAGCATTG CATCCGTATA CTGAACGTCT AATTAAATAT AGAACACAAT TAAAGAGGGA 240
TTACTATGAT TGAGTTAAAA CATGTGACTT TTGGTTATAA TAAAAAGCAG ATGGTGCTAC 300
AAGATATCAA TATTACTATA CCTGATGGAG AAAATGTTGG TATTTTAGGC GAAAGTGCCT 360
GTGGTAAAAG TACGCTCGCT TCATTGGTTC TTGGCTTGTT TAAACCTGTT AAAGGAGAAA 420
TTTACTTAAG TGATAATGCT GTGTTAACGA TTTTCCAACA CCCTTTAACT AGCTTTAACC 480
CTGATTGGAC GATTGAGACC TCATTAAAAG AAGCGTTATA TTATTACAGA GGCCTAACTG 540
ATAATACTGC TCAGGATCAA TTATTATTAC AACATTTATC TACTTTTGAG TTAAACGCGC 600
AATTATTGAC TAAATTACCA AGCGAAGTGA GTGGCGGACA ATNACAAAGA TTTAATGTCA 660
TGCGTTCGTT ATTAGCACAG CCTCGCGTTT TAATATGTGA TGAGATAACT TCAAATTTAG 720
ATGTTATAGC TGANCAAAAT GTAATCAATA TANTAAAAGC GCAAACGGTT NCGGAACCTA 780
AATCATTTTA TCGTTATTTT TCATGATTTA ATCCGTGTTA CAACGCTTAG TTAATAGAAT 840
TATCGTTCTT AAGGATGGCA TGATAGTCGA TGATTTTGCA ATAGAGGAAT TATTTAATGT 900
TGATAGACAC CCTTATACAA AAGAATTAGT GCAAACATTT TCATATTAGC TATTTAAGAA 960
TGCGATAATT CTAGACTTGT TATAAAATAT AGATGAATCA AGTATATTAA TCTAGACACT 1020
TATCGATTTT ATTTTCTTTA TTAAAAATA ATAATAAAAA GGAGTATCAT TAATGGGATT 1080
ACTTTGATAT TGCCAAGTAT TCGTTCATAA GAAAGAGGCT TTAATTATTA TCCAAAGTGA 1140
ATGCGTCATT AACTTAAAAT CATTTTCAGA AACGCAGCAG GAGGCTGAAG TAAAGGNCAG 1200
TGGCAACAAA GTATATCGTT GTTATATTGA TATGGAACAT CCTAGAAAAT CCAAATGTAA 1260
TTGTCCTCAT GCTGATGGAA GACGAGTGAT ATGTAAACAT ATGATTGCAT TACTCTTTAC 1320
AGCTAGTCCA GAAGCAGCAA ATAAACATAT AATGATGTTA AACGAAGTTG AAGAAGACTA 1380
TCAATTACGC AGAAATATGT GGATTG 1406

```

(2) INFORMATION FOR SEQ ID NO:1110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1167 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1110:

```

ATATGATATT AAAATGCAGG AACGTATTTA GTACGAACGT AAAATTAATG ATTTAAAATG      60
CTAGTATGTA TATGATTTTG ATAAATAAAT GCTTTTAAAC GTAAATCAAG TTTGATACAG      120
AAAGGACTAA ATCAAAACAT TTATTCGTTG TAATAACGTT TAAATAAATT TATTAAAAAG      180
TCATAATAGT GTTAAAATGT ATTGACGAAT AAAAAGTTAG TTAAACTGG GATTAGATAT      240
TCTATCCGTT AAATTAATTA TTATAAGGAG TTATCTTAAC ATGTTAAATC TTGAAAACAA      300
AACATATGTC ATCATGGGAA TCGCTAATAA GCGTAGTATT GCTTTTGGTG TCGCTAAAGT      360
TTTAAGATCA ATTAGGTGCT AAATTAGTAT TTACTTACCG TAAAGAACGT AGCCGTAAAG      420
AGCTTGAAAA ATTATTAGAA CAATTAAATC AACCAGAAGC GCACTTATAT CAAATTGATG      480
TTCAAAGCGA TGAAGAGGTT ATTAATGGTT TTGAGCAAAT TGGTAAAGAT GTTGGCAATA      540
TTGATGGTGT ATATCATTCA ATCGCATTTG CTAATATGGA AGACTTACGC GGACGCTTTT      600
CTGAAACTTC ACGTGAAGGC TTCTTGTTAG CTCAAGACAT TAGTTCTTAC TCATTAACAA      660
TTGTGGCTCA TGAAGCTAAA AAATTAATGC CAGAAGGTGG TAGCATTGTT GCAACAACAT      720
ATTTAGGTGG CGAATTCGCA GTTCAAAATT ATAATGTGAT GGGTGTGCT AAAGCGAGCT      780
TAGAAGCAAA TGTTAAATAT TTAGCATTAG ACTTAGGTCC TGATAATATT CGCGTTAATG      840
CAATTTACAG TGGTCCAATC CGTACATTAA GTGCAAAGG TGTGGGTGGT TTCAATACAA      900
TTCTTAAAGA AATCGAAGAG CGTGACCTT TAAACGTAA CGTTGATCAA GTAGAAGTAG      960
GTAAAACAGC GGCTTACTTA TTAAGTGAAT TATCAAGTGG CGTTACAGGT GAAAATATTC     1020
ATGTAGATAG CGGATTCCAC GCAATTAATA NTATCATTCA ACAGCTTGGG TTCACCGTTT     1080
ATCATATATT GTGGAGCAAA AGCTTTNTGG GTTTTATTAA TAATCNGGCT GATGGAAAAT     1140
TATTGGATAT TTCAACCTGA CTTGATT                                     1167

```

(2) INFORMATION FOR SEQ ID NO:1111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1371 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1111:

GGTGGACAAT	CGGCTAAATC	ATTACGTGCT	CACAAATGGA	GATATTATCT	TCTCAGGTTG	60
CAGAGCATCG	CACAGCTCAA	AATTATGCTG	AAGTACAAGT	TAAGATTAAAG	ATAATCAATT	120
CTCNAAAGCT	CAGTGTGTGT	GTAAACCGAA	GTTATTGTAA	CCAAGAAGAT	TGTATCGAAG	180
TGGTGTAAGT	GAGTACTACA	TAAATAATGN	CCGTGCAAGA	NTNAAAGATA	TTGCCGATTT	240
ATTTTTAGAT	TCTGGATTGG	GAAAAGAAGC	GTATAGCATT	ATCTCNCAAG	GTAGAGTTGA	300
TGAAATACTA	AATGCTAAAC	CAATTGATAG	ACGTCACATT	ATTGNAGAAT	CGGCTGGTGT	360
ACTTANATAT	AAAAACGTA	AGGCTGAATC	ATTAAATAAA	CTTGACCANA	CAGAAGATAA	420
TTTNACGAGA	GTAGAAGACA	TTTTATATGA	TTTGGCACGA	GGTCGCGTAG	AACCTCTAAA	480
AGAGGAGGCA	GCTATAGCTA	AAGAATATAA	GACACTTTCA	CATCAAATGA	AACATAGTGA	540
CATTGTAGTT	ACAGTGCACG	ATATTGATCA	ATATACAAAT	GACAATAGAC	AATTAGATCA	600
ACGTTTAAAT	GATTTACAAG	GTCAACAAGC	AAATAAAGAA	GCTGACAAGC	AACGTTTAAAG	660
CCAACAAATT	CAACAATATA	AAGGTAAACG	ACATCAACTT	GATAACGATG	TTGAATCGCT	720
TAATTATCAA	TTAGTAAAAG	CTACGGAAGC	CTTTGAAAAA	TATACGGGAC	AATTAAATGT	780
TTTAGAAGAA	CGTNNAGAAA	AATCAATCTG	AAACAAATGC	ACGATATGAA	GAAGAACAAG	840
AAAATTTAAT	GGAGCTTTTA	GAAAATATAT	CAAATGAGAT	TTCTGAAGCT	CNAGATACTT	900
ATAAGTCTCT	GAAAAGTAAA	CACANAAGAA	CTCAATGCTG	TCATTTCGTGA	ACTTGAAGAA	960
CAATCTATAT	GTTTCAGACG	AAGCACATGA	TGNNAAATTG	GAAGAAATTN	AAAACGAATA	1020
CTATACATTA	ATGTCAGAGC	AATCAGATGT	TAACAATGAT	ATTCGTTTTT	TAAAGCATAC	1080
TATAGAAGAG	AATGAGGCTA	AAAAATCAAG	ACTAGATTCT	CGATTAGTTG	AAGTTTTTGA	1140
GCAATTGAAA	GATATTCAGG	GTCAAATAAA	AACGACCCAA	AAAGAATATC	AACAGACCAA	1200
CAAAGAACTT	TCTTCTGTAG	GGNAAGAAAT	TAAAAATAGA	GAAAGAGATC	TCTCTGACAC	1260
ACAAAAAGCA	CAATATGAAT	GCGNAGAGAA	TTTGTATCAA	GCATATCGAT	ATNCCGAAAA	1320
AATGAAAACA	CGTATTGATA	GTTTGGCAAC	GCAAGAGGAA	GAATACACTT	G	1371

(2) INFORMATION FOR SEQ ID NO:1112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1112:

GATGTGTGAN	TCTATTATNN	TTTNNAAGAT	AATTCATAGT	TATAATTTTN	ATTNCTGCTA	60
TCAGTCATAA	TCTTAAATAA	TTTGTGGAAA	NTTGAACAAG	TGTNCGNAAG	TAATTAATAA	120
CAGATCGTTG	AAGTGCAAGT	AATACCTTTA	TTTCTAATCC	CANAAAATAA	TAGCCACTCT	180
AANAAGTAAT	ATACTCTTAG	AATGGCTGTN	AGTTTAAAAT	TGTCGATTCA	AAGATAATAT	240
TCTACTTCAA	CATGACATAT	TAGTTAAGTA	GTCTATAGTT	TCCTTGGAAT	ATTATTTTAA	300
CTTTTTAGCG	TTATATAAAT	CAGCTAAAGG	CTTTAATTCA	TCATAAAATG	CTTGGAANTC	360

ATCTAAATCC	ATTTGTTGAC	CCGCATCACT	AAGTGCAACA	GATGGATCTG	GATGCACCTC	420
AGCCATAACT	CCATCAGCAC	CAACTGCTAA	TGCTGCTTTC	GCAGTTGGTA	ACATGATATC	480
TTTACGACCT	GTAATATGCG	TAACATCTAC	CATGACTGGT	AAGTGTGTAC	CTTGTMTTAA	540
AATTGGTACT	GCTGAAATAT	CTAAAGTGTT	ACGTGTCGCC	TTTTCATAAG	TTCGGATTCC	600
ACGTTACACAT	AAAATAATGT	TGTGATTACC	TTGTGAAGCA	ATGTATTTCAG	CTGCATAAAC	660
AAACTCTTCG	ATTGGAGCAG	ATAAACCACG	TTTTAATAGA	ATAGGCTTTT	TCGGTACGGC	720
CAGCTTCTTT	TAATAACTCG	AAGTTTTGNA	TATTTACGTG	CACCAATTTG	GGAATACGTC	780
TTTAAATACT	CATCAGCCAC	TTCCAAAAAT	CAATTTGGGA	TTTACGGAT	TTCGNTTGAC	840
AAACAATNTA	AATCAATATT	TATCTTTAAT	CTGTTTAAGT	ATTTTAAGTC	CTTCAACACC	900
TAGGCCTTGG	AAATCATATG	GTGATGTACG	TGGTTTAAAT	GCACCGCCAC	GAATAAATTT	960
TTCACCTTTA	GCATGTGAGT	TTTTAGCAAC	AGCTTCAACT	TGTTCAAATG	ATTCAACTGA	1020
ACATGGCCCA	AATACAAATG	ATTTATTGCC	GTCTCCAATA	ATGCCCCCAT	TATCAAATGT	1080
TACAATCGTA	TCTTCAGGTT	TCAACTTACG	TGATACGTAT	AAGTGTTTTC	ATTTTCAGATT	1140
TTGTAAATCT	GTAGAGCTTT	AAAATTC				1167

(2) INFORMATION FOR SEQ ID NO:1113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1237 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1113:

CTAGCATATA	TCTANTTTGT	CAGNTGGGGG	GATATCAATG	ATGTATTTAA	CCCAGTCTAT	60
TTTAATCNAT	TGTAAGATTA	CCCGAGATTA	TNAGAAGCAT	TTGTTGACNA	GGTATGATAT	120
TAACAGTTGC	AGGTCTTATA	TTTCAAACCA	GTTTTAAATA	ATGCATTGGC	AGATANCTTT	180
ACATTNGGAT	TGNCAAGCGG	TGCTACATTT	GGNTCAGGAT	TAGCATTATT	TTTAGGTTTA	240
ACAACGTTAT	GGATTCTGT	ATTTTCAATA	ACATTTAGTT	TGATAACATT	AATAACTGTA	300
TTAGTCATTA	CGTCGGTATT	GAGCCAAGGC	TATCCAGTTA	GAATCTTAAT	ATTAAGTGGT	360
TTAATGATTG	GTGCATTATT	CAATTCACCT	CTATATTTTT	TGATTTTATT	AAAACCTCGC	420
AAATTAAATA	CAATTGCCAA	TTATTTGTTT	GGTGGCTTTG	GTGATGCAGA	ATACTCAAAT	480
GTATCCATAA	TAGCAATCAC	ATTTATCATT	GCACTGTTTG	GTATATTTAT	CATTCTTAAA	540
TCNACTAAAG	TTATTGCAAT	TAGGAGAACT	NAAAAGTCAG	TCACTAGGCT	TAAATGTTCA	600
ATTGATTACA	TATATCGCGT	TATGTATAGC	TTCCNTGATN	NCGGCGANAA	ATGTCCCCAA	660
TGTTGCCATC	ATTGGATTCA	TNGGTATGGG	TGATACCNCC	AACTCATAAG	NAAATGCCAG	720
TGGAAACCAA	TCATTAGGGA	AGACNATTGC	CTTTGAATAT	TGTAATTGGA	GGACCAAATA	780
ATGGTTATGG	CAAGATTTTA	ATTGGGTAAC	CCAATATACT	TGTCACCCAG	TACCAAATAC	840
CCGGCAAGCA	TTATTATTTG	CATTAAATTTG	GTATACCAGG	TTATTTTACA	TGCTAATATC	900
TCAGTCGAAA	CGGTTACACT	AGCACATGAC	ATTTGCTAAA	ATAAAAATAA	CTATAACAT	960

AAAGAGGGCA	TAAGCGATGG	ATTTGAATCA	AATTNAAGCA	GTTGTATTTG	ACTTAGAAGG	1020
TACGTTGTTG	GACAGAGTTA	AATCTCGAGA	GAAATTNATC	GAAGAGCAAT	ATGAACGANT	1080
NCATGACTAC	TTANTNCATG	TNCAACTGGC	AGATTTTAAA	AAAGCATTTA	TTGAGCTAGA	1140
TGACGATGAA	GATAATGATA	AACCTGATTT	AGATAAAGAA	ATCATTAAAC	GTTTCCATGT	1200
CAGATAGGTT	AACTTGAAA	GACTTATTTA	CTGATTG			1237

(2) INFORMATION FOR SEQ ID NO:1114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1114:

GGCACGAGAC	AATATATCTA	CCGTGAATAA	CTGTGCAAAT	AGTGAAGTTG	TAGCCGCCAT	60
ACGCATTTCA	TTTTCATCAG	TTCTGCCATA	AATCAATGCA	TAGTCGGCAA	TTTGAGCCAC	120
GTGCCGATTA	TTCCGGCACA	GCTGTACTAG	ATATAGTTAT	GATGGGAATA	CTGTAATGTG	180
TGGCCACCTG	TGCAATTGAC	TGCAATTCAC	TATGACTACC	TTGATTCTGC	ACAAAAATCA	240
TGCAATCTCT	ATCATCATGC	GTGCAAAATG	TTGACACAAG	TAAATGCGTT	TCATGTAATA	300
ACCTGACATT	TAAGCCAATA	CGAGATAACT	TTTGAAAAAG	ATCACCAATA	GTCAAACCTG	360
ATGCGCCAAA	TCCAAATAAA	AATATTGTCC	TGGCATTTTT	CAACACATCA	CAAAATTGCAT	420
CAATTTGCGC	ATCCATAATA	TTAGTAGCTA	CAAATCGCAT	CCGTATTCCG	TTGCTCTAGC	480
AATCATTTTA	TTTTTCAAAG	TTTCTACAGA	TTTCAATTTCA	ATCAATTCTA	AATGTGGATT	540
GGTTGCAATA	TCTTCGGGTA	AGTATCGAGA	TATCGCAATC	TTTAGCTCTT	GAAAACCTTG	600
ATGTGTCAAT	TTCCGACTAA	ATCTAACAAT	TGATGCTGTA	CTAACATTCTG	TAACATCTGC	660
CAAATCATT	ACCGTCATAT	CAATGATTTT	ATGTGGATT	TTTAAAATGT	AATCAGCGAT	720
TATCTTTTCT	GTCTTCGTAA	AATCACTCAA	CTGTTTATCA	ATGCGATATT	AAAATATTTG	780
TCATCATTA	TCACCCAACA	AATCTGTCTT	GTGCGATCGC	CTTTGTGCGT	CCAAATAAAT	840
ATGTACAAAC	GAATCCACCA	GCATATGCAG	CAAGTAATCC	TGCAATATAA	CCTAAATACA	900
TATTATCTGA	GATTAATGGT	AAGAGTGACA	CACCACTTGG	GCCTATTGCT	TTGGCACCAA	960
TATGTCCAAT	TCCACCTATT	ACAGCGCCAC	CAATACCACC	ACCAATACAA	GCAGTTAAGA	1020
AAGGTCGAAC	TAATGGGCAA	AGTCACACCA	TAGATTAATG	GTTCTCCGAT	ACCTAGGAAA	1080
CCAAGTGGCA	ATGCACCTTT	TAAAGTATTA	CGTAATGTTG	TGTTGCGTTT	ACATCTTACC	1140
CAAAGTGCTA	ATGCGGCACC	TACTTGTCCA	GCACCCAGCC	ATCGCTGCAA	TTGGCAATAA	1200
GTAAGTAGCA	CCAGATTGGT	TAATCAATTT	CTATATGAAT	TGGCGTNAAA	AATATGATGA	1260
AGGCCCTAAC	AATAACTTAA	CGGTAGGAAG	CTTGGTCCAA	ATGATAAATC	CACTTAAATT	1320
ACGNCACCCA	ATACTTAATA	ATCCCCGTTA	CTACTGAAAC	TTAANTTGTC	TTTGAAACAA	1380
A						1381

(2) INFORMATION FOR SEQ ID NO:1115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1115:

```

GGCACGAGAC CGCATAGACA TCTAAACCAT GTGTCTCTTC TTTGTATTTA TTTGCATCTT    60
TTCCCAATAA AAATACTTGG AACTTTTGAT TTTGTTGGTT AAAAACGCAA AACGTTAGAG    120
TCATAATAAC CTTGACTGTA GGCCACTAAG ATTTGTTAAA TCAAACTAG GTCCTGAATA    180
GTATTGATGT AACTGGTTTG TATCATATAA ACGGTACATT TTTTCATACT TTCCTTTTGC    240
ATTAACCGAT TGATTTTCTG TTAGCATTAC ACTTGTTGTT AATATGCCTA ATACAAATAT    300
CGTCTTTAGC TATCGCTGTA AATTTCATAT TCATATGCAT CCAATCTTAA TATATTGGAT    360
CGCTTTTATT ACGTACCTTT GAATAATCAC ATTTATTATA AAGGGCATTG AGACCGACTG    420
ACATTAACAC ACGTTNTATT TAACATTAAA TCATGGTTAA TGAA                      464

```

(2) INFORMATION FOR SEQ ID NO:1116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 770 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1116:

```

GGCACGAGCG TGAAGAAAAA GATGCTTTAT ACGTTGTTAT TTCTAAAACA CAAGTTTCAA    60
AAGCAAAGCG ATTAATTAAA CAAATCGATA AAGATGCATT CCTCGTAATT CATGATGTAA    120
GAGATGTCTA TGGTAATGGC TTTCTTGCGAG ATGAATAAAT AAATGGTATG AGCACACATA    180
CTTAAATAGA AGTCCACGGA CAAGTTTTTG AACTATGAAG ACTTATCTGT GGGCGTTTTT    240
TATTTTATAA AAGTAATATA CAAGACATGA CAAATCGAGC TATCCAATTT AAAAAGTAAT    300
GTTAGTCAAT AAGATTGAAA AATGTTATAA TGATGTTTAT GATAATCATT ATCAATTGGG    360
ATGCCTTTGA AAATTGATAA TTTAAAAATA GAAATTATTT TTTATAAACA GAAAGAATTT    420
TATTGAAAGT AGGGAAATTA TGAATCGTTT GCATGGACNA CNAGTTANAA TTGGTTACGG    480
GGATAACACG ATTATAAATA AATTAGATGT NGAANTNCCA NATGGCAAAG TGACGTCAAT    540
CATTGGTCCT AACGGCTGCG GGAAATCTAC TTTGCTAAAG GCATTGTCAC GTTTATTGGC    600

```

AGCTAANNAA	GGCGAAGTAT	TTTTAGATGG	GTGGAAAATA	TTCAATACAC	AATCTACGAA	660
AGAGATTGCA	AAAAAAATAG	NCATTTTACC	TCAATCACCT	GAAGTAGCAA	GATGGCTTAA	720
CTTGTGGGG	AATTAAGNNC	ATTGNCCGGC	NTCCACATCA	AAANGGTTGG		770

(2) INFORMATION FOR SEQ ID NO:1117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 995 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1117:

GGCAAGAGCG	AGATGATTCC	AGTTCGATTA	TCCATTGGCG	CTAAAAACAT	TTATTTACCG	60
TTCAATCTTC	GTAAACAAT	TTTGAATAC	AGTACGGATA	CAATATGGAG	ATGTAAAAAA	120
CTAATAACCT	TTTACAAAT	TGTTTATCAA	AATATTTTAA	GTTTTGCAA	GCTTTTTATT	180
GTGATTATTT	TCAACAAAT	ACTATAATGA	GGATAGTAAA	TAGAGAGGAG	TCCTTAAGTT	240
GACGAAACGA	CAAATGGGTA	TATTCATTTA	TGCTGGAATT	ATCGGTGGCT	TGTTATCTGG	300
AATTGTAAAA	TTAGGTTGGG	AGNTCATGTT	TCCCACCTCG	CACACCAGAA	CGTAATGCNA	360
CCGAACCCAC	CTCAAGAGTT	ATTGCAACAA	TTAGGATTTA	GTAGTGAGTT	TACACATCAA	420
ACATATACAT	TTTCAAATAT	GGAATTGCCT	TGGGTAAGCT	TTATTGTCCA	CTTTAGTTTT	480
TCTATCGTCA	TTGCAATTAT	TTACTGCATA	TTAGTTAAAA	AATACGCTTA	CTTAGCAATT	540
GGACAAGGTG	CTGTTTTTGG	TATTGCTATT	TGGGTATTAT	TCCACCTTAT	CATTATGCCA	600
ATCATGCATA	CTGTACCTGC	TGTGTGGGAT	CAACCATACC	AAGAGCATCT	GTCAGAATTC	660
TTTGGCCATA	TCGTCTGGAT	GATGACAATT	GAATTAGTGC	GACAACATTT	TGTCTATCGC	720
TATAAATTAA	ATTAATACAC	TGACTAACAT	TAACGTGAGT	TTTAAATCAT	CGTTTGAGTA	780
TGATGATTGA	TGCTCACGTT	ATTTTATTAA	CTGACATGAT	ATGATTCCAG	CCAACTTACG	840
TGAGCATTAA	AGTCTCAAAT	GCGTCGTAAC	AAGATATTAT	TTTTGGCAAT	TTCAATATTG	900
CTCAGTATAT	TTTCACCTTA	TCACTTACAT	TAATCTCGTC	ATGATTTTGA	ATGATGCCAT	960
CGTGTATTCA	CCTTTCATTT	TTCCCAATAA	AAATA			995

(2) INFORMATION FOR SEQ ID NO:1118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 682 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1118:

CGTTAAACA	CCAAAGCAAC	TCTATCTAAT	TAAATTAAT	TTTATCATCA	TTATATATTG	60
AGTACCAGTG	TATTTAATAT	AACATAGTGA	GACTTTGTTT	TTATNTTATT	AATATCATNT	120
NACGTTTGTG	CTATAAATTA	TTTCTAGAGA	CACACANAAN	CCGATGCATA	CGCATCGGCT	180
TATTTGTAAA	TACAGTATTT	ATTTATCTAA	TCCCATTTTA	TCTTGAACCA	CATCAGCTAT	240
TTGTTGTGCA	AATCTTTCAG	CATCTTCATC	AGTTGCTGCT	TCAACCATGA	CACGAACTAA	300
TGGTTCTGTT	CCAGAAGGTC	TTACTAAAAT	TCGACCTTCT	CCATTTCATTT	CTACTTCTAC	360
TTTAGTCATA	ACTTCTTTAA	CGTCAACATT	TTCTTCAACA	CGATATTTAT	CTGTTACGCG	420
TACGTTAATT	AATGATTGTG	GATATTTTTT	CATTTGTCCA	GCTAATTCAC	TTAGTGATTT	480
ACCAGTCATT	TTTATTACAG	AAGCTAATTG	AATACCAGTT	AATAAACCAT	CACCAGTTGT	540
ATTGTAATCC	ATCATAACGA	TATGCCAGA	TTGTCTCCA	CCTAAGTTAT	AATTACCGCG	600
AGCATNTCGT	GCTATGCTAC	ATATCTGTCG	GCANCTTTAG	TTTTATTAGA	TTTAATTCCC	660
TCTTGGTCAA	GCGCTTNGGT	AA				682

(2) INFORMATION FOR SEQ ID NO:1119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1119:

TGTATAGGCC	TATTTGTATA	NAAAGTAATA	TGATGTTTAG	TGGCTATGTA	AGTGAAGCAA	60
TGTATAAATA	ATGATGAGTG	GTTTGTTACT	AATGATAATG	GCTATGTAAA	AGAGCAGTAT	120
TTATATTTNG	CGGGACGTCA	ACAGGATATG	TTAATTATTG	GTGGGCGAAA	TATATATCCA	180
GCACATGTTG	TNCGCCTTTT	AACGCAATCT	TCGAGCATTG	ATGAAGCAAT	TATCATCGGT	240
ATTCCACATG	AGCGTTTTGG	TCANATAGGC	GTATTGCTTT	ATTCTGGTGA	TGTGACACTT	300
ACACATAAAA	ATGNGAAACA	ATTTTTNAAA	AAGAAAGTGA	AACGCCATGA	AATTCCATTC	360
GATGATTCAT	CATGTAGAAA	AGATGTATTA	CNCTGCAAGT	GGTAAAATTG	CTAGAGAAAA	420
AATGATGTCG	ATGTATTTGA	GAGGTGAATT	ATAATATGAA	TCAAGCAGTC	ATAGTTGCAG	480
CTAAACCGAA	CTGCATTTGG	GNAATATGGT	GGCACTTTAA	AACATTTAGA	GCCAGAACAA	540
TTGCTTAAAC	CTTTATTCCA	ACATTTTAAA	GAGAAGTATC	CAGAGGTAAT	ATCTAAAATA	600
GATGATGTAG	TTTtaggtAA	TGTTGTTGGG	ANTGGTGGCA	ATATTGCAAG	AAAAGCATTG	660
CTTGAAGCGG	GGCTTAAAGA	TTCAATACCT	GGCGTCACAA	TCGATCGGCA	ATGTGGGTCT	720
GGACTTNGAA	AGTGTTC AAT	ATGCATGTCG	CATGATCCAA	GCCGGAGCTG	GCAAGGTATA	780
TMTTGCAGGT	GGTGTTTGAN	AGTACAAGTC	GAGCACCTTG	GAAAATCAAA	CGACCGCANT	840
CTGTGTACGA	AACAGCATT A	CCNGAGTTTT	TATGAGCGTG	CATCATTTGC	ACCTGAAATG	900

AGCGACCCAT CACATGATTC AAGGTGCTGA AAATGTGGCC AAGATGTATG ATGTTTCAAG	960
AGAATTACAA GATGAATTTG CTTATCGAAG TCATCAACTG ACAGCGGAAA ATGTAAAGAA	1020
TGGAAATATT TCTCAGGAAA TATTACCTAT AACCGTTAAA GGAGAAATAT TCAATACTGA	1080
TGAAAGTCTA AAATCACATA TTCCGAAAGA TAACTTTGGC CGATTTAAGC CCGTAATCAA	1140
AGGTGGGACC GTTACCGCTG CGAATAGTTG TATGAAAAAT GATGGTGCAG TTTTATTGCT	1200
TATTATGGAA AAAGATATGG CATACGAATT AGGTTTCGAG CATGGTTTAT TATTTAAAGA	1260
ATGGTGTTAC GGTAGGTGTT GATTCTAATT T	1291

(2) INFORMATION FOR SEQ ID NO:1120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1110 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1120:

GCGTGCATTA GATAGTATTT TACCATTTTT AGGAAAAGGG AATACTATTA TTGTAGAGTC	60
GACAATTGCG CCTAAAACGA TGGATGATTT TGCAAAACCA GTCATTGAAA ATTTAGGATT	120
TACAATAGGT GAAGATATTT GTTTAGTGCA TTGTCCAGAA CGTGTAAGTC CAGGAAAAAT	180
TTTAGAAGAA TTAGTTCATA ACAATCGTAT CATTTGGCGGT GTGACTAAAG CTTGTATTGA	240
AGCGGGTAAA TATGTCTATC GCACATTCGT TCAGGGAGAA ATGATTGAAA CAGATGCACG	300
TACTGCTGAA ATGAGTAAGC TAATGGAAAA CACATATAGA GACGTGAATA TTGCTTTAGC	360
TAATGAATTA ACAAAAANTT GCAATAACTT AAATATTAAT GTATTAAGAT GTGATTGAAA	420
TGNCAAACAN ACAATCCGCT CGTGCCAATA TCCATCAACC TGTCCAGGTG TAGGCGGTCA	480
TTGTTTAGCT GTTGATCCGT ACTTTATTAT TGCTAAAAGA CCCTGAAAAT GCAAAGTTAA	540
TTCAAAC TGG ACGTGAAATT AATAATTCAA TGCCGGCCTA TGTGTTGAT ACAACGAAGC	600
AAATCATCAA AGCGTTGAGC GGAATAAAG TCACAGTATT TGGTTTAACT TATAAAGGTG	660
ATGTTGATGA TATAAGAGAA TCGCCAGCAT TTGATATTTA TGAGCTATTA AATCNAGNAC	720
CAGACATAGN AGTATGTGCT TATGATCCAC ATGTTGNATT AGATTTTGTG GAACATGATA	780
TGTCACATGC TGTCAAAGAC GCATCGCTAG TATTGATTTT AAGTGACCAC TCAGNANTTA	840
AAAATTTATC GGACAGTCAT TTTGATAAAA TGAAGCATAA AGTGATTTTT GATACAANAA	900
ATGTTGTGAA ATCATCATTT GNAGATGTAT CGTATTATAA TTATGGCAAT ATANTTAATT	960
TTATCGACAA ATAAATGTG TCNAACTAGG GCATACATGA TTAAGGNAAG ATAAGCTCGT	1020
GCCATGTGTT TGNACNTCAG AGAGGATAAT GTTATGAAAA AAATTATGGT TATTTTCGGT	1080
ACGAGACCCG NAGCAAAAAA ATGGCACCAG	1110

(2) INFORMATION FOR SEQ ID NO:1121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 864 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1121:

```

GGGAGGAACA GATATTCAAT TGTAATGATA TAAATATCTC GGCACAATGA TGCTGGGATA    60
TTTTTTAACA AATAAGGCAA TAAAAGGTAT GGGAAATGCG TATCTAGCGC TAATGATAAC    120
TTAACATGCA AAGAAGATAC TATTTAAATA TTTCAATTTT AGAAATTTTA AAAATAAATT    180
CACTTTAAAA ATATTGCATT TATAGAGAAT AGAAATGTTA TATTAAGATA AATACATATT    240
TTTTTAGGAG GCAAAGTATG GGAAGTTGTA TTGAACATGT TACGAAACGT TTTGGCAAGA    300
TGACGGCAGT AAATGATATT TCATTAGAGT TAGAATCAGG CAAAATGTTA GGTTTTCTAG    360
GAAGAAATGG TGCAGGTAAC ACAACGACAT TTCGTATGAT TTTAGGCTTA AGTGAACCAA    420
CTGAAGGACA CATTACGTAT AACGGTAAAA AACTAGATAA AACAATGTAC AATCGTATTG    480
GTTATTTACC GGAAGAACGC GGTTTACATG CCGGAAATTG ACAGTTGAAG AAGAATTGAA    540
ATATTTGGCA ACTTTAAAGG GAATGTCAAA AACAGAAATA CAACAGCAAA TATCGTATTG    600
GCTTGAGCGT TTTGATATTA CTGAAAACCG CAAAANCGA ATTGATAGTC TATCAAAAGG    660
GAATCAACAA NAAATTCAGC TGTTAGCAAG TATGTTACAT AAACCAGAAT TACTAATATT    720
AGATGAGCCT TTCAGTGGTC TAGACCCAGT TAATGTTGAG TTATTAAGAG AAGCAGTTAA    780
AGACTTAAAT GATTGGGGCA GTACAATCGT TTATAGTTCT CACCGTATGG AGCATGTTGA    840
AGAATTATGT GATGATGTTT GTAG                                     864

```

(2) INFORMATION FOR SEQ ID NO:1122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1122:

```

AAACCCNCCT TGTCTCATTG AGTAAGAAAT CGTTAAAAGA TACATCCTTC CNAATTNNAA    60
AACCCCGNGC CTTTTGTATT GTTTGTCACA CGGATCTACG TTTANCAATG TTGTCATATC    120
CATGCTCCTC TTTGTNTAAT TTTAATAAAA ACGTCTTCCC TCCAATAAAA TAGCTANAGG    180
GCGTAAATAT ATGNNAATA CCNATTGATA AGTACCENAA CACTAAAGCT TTTGANTAAAT    240
TCCTGTACCA ATTTGAATAA AGACCTATA AAAATAATGG CTAGTATCAA TATTGATAAG    300
TTGNTCGCAT ATGTTTTAAA TAATGCAATT AATTCTAATA TGGCGTTCAC CTTCATCCAA    360

```

TATTTCCAAT	CGCTTTTCAG	TGTAATTCTT	ATCTGCAATT	TTTGGCATT	TGTCATCAAA	420
TTTTCTATTA	AACAGTGTA	ATTGGGTATT	GANNATAGCA	CTANCAAAAA	ATGGTAGTAA	480
AAAGAATAGC	ATGGCATTTC	CTTCAGCTTG	CCCTACCACA	AAAATTAGTA	ACACTACAAA	540
GGCAATAATT	GTCNGTATA	CGCTTAATAT	ACTTCCATTT	AAAACATAAC	GATTCGCAAG	600
CAATTCATAT	TGATCTGTTG	CATCGATATG	TACCTCTTCA	TCTACAAGTC	GCTTATACTT	660
CAATGCANGT	NTTTGATTCA	TCAAAACAAT	GGCTTCTACC	AATATGATGA	TCATAGTCGC	720
AACAATCGAT	ATTACAACGA	CATTGTTATA	AGTCGCAAAC	GTCAAGTTCT	CAATACCCAA	780
TCCATCAAAG	TTACNTAAAA	TTCCACCAAT	GATACCCCT	ACAAATCCAC	CCAGTAAAG	840
ATATCCGATA	TATNTTAGTA	TTTTCATGCT	TCACCCTCCT	CAATAATAAA	AACCGTTTCC	900
ACCGTTTCAT	TGAAAATGCG	AGCAATCTTT	ATTGCCGTTA	ATACTGATGG	CATAAAATTG	960
TTTCGCTCAA	TTAGCGAAAT	GGTTTGCTT	GAAACACCAG	CTAGTTTGCC	AAGCTGCGTT	1020
TGATTTAAGC	CATCTCGTGC	TCGTAACCT	TTCAATCGAT	TACGCACATC	GCATCAACTC	1080
CTTAGTCCTA	ATGTAAATGA	TATTTGTCTT	TGTGACAACT	ATATTGCTCA	AATCTACACA	1140
AAAAAATATG	ATTGTCCACC	TATGTATGAC	ATTGTNGAAA	CAACACCTCA	ACGCCTACAA	1200
GTCATAATTG	TTTACTTTTCG	GNTACACCTT	CCTGCATAAT	TAACAGCATT	CTAATTTTAG	1260
TATGATGCAC	GCATTTTCAC	TAAATCAAAC				1290

(2) INFORMATION FOR SEQ ID NO:1123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 809 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1123:

GCCCATCCAT	ATCTAATGTT	ATGTTAATAG	TCFTTTTAC	TTTTTTTCCA	TTTTTAATTT	60
CTGTATCTTT	TACCGACTNA	ATTGTGATTA	GNGGTACAGN	ATCGTATGTG	TTGTCTTTTC	120
TATTTAACTT	CCTTTTATAA	CCNACATGGC	TGTCATATTA	AGCATCTAAC	CTGGGCACAC	180
CANCACTAAT	GTTAACGCGT	TTTCTGGCA	TATCTTTGAT	GAATGGATCT	TGTAACCATG	240
TTAATAAATC	GTAGGTACTA	TTAAAACTAA	TCATATTATC	AAAGCGTGGT	CTTAGCAAAT	300
TTCTGNCAAG	CAGCATAAGG	TACCATTGCT	GGGTCAAGTA	GCAACAACCT	TTTCATTTGG	360
ATGTTTCGCT	CCTTGATATT	TTGCTCCTGC	ACCGCCTTCC	GAATTACCGC	CATCCGCCAC	420
AATGGTTTTG	TTTTTGTAAT	TATTTGGACT	AACACCATAT	TTTTTGTAAT	AGTTATACTT	480
ACTTAATTTA	TTAGCGTCAT	TTAGTTTGTC	TCTATATAAA	TCTGCAAATT	CGTCTGATTG	540
CTTAAGATAA	TCCGTTGACT	TATTACTATT	ATCCATTAAT	TTTCGATTTT	GTAAACCAAT	600
CATCTCCCGA	TATCTAAAGA	TTTTAATGGA	TTATTAGGGT	TTATTGCCTC	CATTAGATGT	660
TCCTTGATAA	ATCATGGTTT	GTTCAACAGT	TGGTTTTCCT	TTTTCATCCA	ACAATTCATA	720
AATTTTTTAA	TCTGAGGCAC	CTTTTTTATT	TTTATTTCCT	TTATCATTAT	ATTCATCAAC	780
CTGCTTAAAT	CTTTTTCCGT	TAACTGTAA				809

(2) INFORMATION FOR SEQ ID NO:1124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 569 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1124:

```

GGCACGAGCG ATCGAATTTT AATAAAATAT CATTGTTTAA CGGTCTTGGC GGACGCGTTT    60
GATGAATATC AGGAATCGCA TCTATTAAGC GTTTTGTATA GGTATGTTGT GGCGATTTAA    120
AAATACTTCA ACCGTGCCAC TTTCAACGAC ACTTCCATCT TTCATTACAA TCACATCGTC    180
GCAAAATTGA TACACAGCGC CTAAATCGTG AGTGATAAAA ATAATAGATG TTTCTGTGTA    240
CTCATAAAGG GACTTCATTA ACTGCAGTAA TTGATTTTGT GACTTGGCAT CTAATGCCGT    300
TGTTGGTTCA TCTGCGATTA AAATTGTGCG CTTTAAAATC AATGCCATTG CTATCATGAC    360
ACGTTGACGC ATACCACCAG AAAGTTCATG TGGATAAGCA TCAAATTGTC GAGTTGCATG    420
TTTTTATACC TACTTTTCTT AAAATGTTTT ATTGTCATCG ACTTTGCTTC AGATTTAGAT    480
ACACGTTTTA TGTTTGAAAT AGTACTTCCT GTAATTTGTT TGCCAATCGT TAATCCTTGG    540
ATTCAACGAA GAGAGTGGAT CTTGAAAAG                                     569

```

(2) INFORMATION FOR SEQ ID NO:1125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 993 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1125:

```

CTAGTTCTAC AGTGCCTAAG TTATATCACC TCCATCAAAA GTACGCGCTT ACATCATTGA    60
TACACAAGAC ATCATGACAT AGTTGTATAC TGTCTAATCT TCTACTATAC TAAGATAAAA    120
GGAGTGATCT TTTATGGAAG AAGTTTATGT TGCTGGTGCA ATACCAGAAG TAGGGTTAAA    180
ACTTTTACCA AAGAACAATT TTGNAGTTGN AATTGTATGA AGGTAAAGGA TTAAGTCGAT    240
AAAAGACCAC NTTANTTAAA GGTGTGTAAG AACCGCGACT GCCTTAATTA GTTTATTAAT    300
CTACAAACGT TGATAAAGAT GTTATCGATN CTGGTAAAAG ACNTAAAAAT CATTGCCAAC    360
TATGGCGCTG GNTTTAATAA TATTGATATC GAGTATNNCC GAGANAAAAG TATAGATGTT    420

```

ACAAACACAN	CTAAAGCATC	ANCAACGCG	NCTGCTGATT	TAACAATTGG	ATTAGTACTT	480
GCAGTAGCTC	GTCGTATTGT	TGAAGGGGAC	CAATTATCAC	GNACAACTGG	ATTTGACGGA	540
TGGGCACCTT	TATTTTTCAG	AGGTAGAGAA	GTATCTGGGA	AAACAATCGG	CATTATCCGT	600
TTAGGTGAAA	TTGGTAGTGC	AGTAGCTCGT	CGTGCAAGAG	CATTTGACAT	GGATGTGCTA	660
TACACTGGAC	CTAATCGCAA	AGAAGAAANA	GAACGAGAAA	TCGGTGCAAA	ATATGTTAGA	720
TTTAGATACA	CTATTAAAGA	ATGCAGATTT	TATCACTATC	AACGCTGCTT	ATAATCCCTA	780
AAATGCATCC	ATTTAATTGA	TACAGAACAA	TTTAAAATGA	TGAAATCTAC	GGCGTTATTT	840
AATCAATGCC	TCCTCCGTTG	GTCCCAATCC	GTGCACGAAA	CAAGCACTAG	TTGCAAGCCA	900
TTGAAAGATA	ATGAAATTGA	AGTGCTGCAC	TTGATGTTAT	ATGAATTTTG	AACCCAGATA	960
TTACCGATGA	ACTTTAAAAT	CACCTAATAA	TGT			993

(2) INFORMATION FOR SEQ ID NO:1126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1126:

TTCCTGAAAA	TACAATTAAT	GTTTATACGA	ATGTCATGCT	GTTCAAAGTC	TTGCAGCATA	60
TGCACCGAAA	GGCTTAATGA	TTCTCATACT	GGAGATGCGA	ATGACTATGT	TGGTAAAGGA	120
TTATCTGGTG	GTACGTCATT	GTCAAAGCAC	CTTTTGAAGA	ACGACAAAAT	GAAATTATTG	180
CTGGTAACGT	CTCATTCTAT	GGTGCACAG	GTGGTAAGGC	ATTTATTAAC	GGTAGTGCAG	240
GAGAAAGATT	CTGTATTAGA	AATAGTGGTG	TAGATGTTGT	CGTTGAAGGT	ATCGGTGACC	300
ATGGATTAGA	GTACATGACT	GGTGGACATG	TCATTAATTT	AAGGTGATGT	AGGTAAAGAA	360
CTTCGGTCAA	GGGTATGAGT	GGTGGTATTG	CTNACGTTAT	CCCGTCTGAT	GTAGAAGCTT	420
TTGTTGAAAA	TAACCAACTA	GATACGCTTT	CGTTTACAAA	GATTAAACAC	CAAGAAGAAA	480
AAGCATTTCAT	TAAGCAAATG	CTGGAAGAAC	ATGTGTCACA	CACGAATAGT	ACGAGAGCGA	540
TTCATGTGTT	AAAACATTTT	GATCGCATTG	AAGATGTCGT	CGTTAAAGTT	ATTCCTAAAG	600
ATTATCAATT	AATGATNCAA	AAAATTCATT	TGCACAAATC	ATTACATGAC	AATGAAGATG	660
AAGCGATGTT	AGCTGCATTT	TACGATGACA	GTAAAACAAT	CGACGCTAAA	CATAAACCAG	720
CCGTTGTGTA	TTAAGGAAAG	GGGGAGATAC	GATGGGTGAA	TTTAAAGGAT	TTATGAAGTA	780
TGACAAACAG	TACTTAGGTG	AATTATCANT	GGTAGACCGT	TTGAAGCATC	ATAAAGCATA	840
TCAACAACGA	TTTACTAAAG	AAGATGCCTC	TATCCAAGGT	GCGCTCGTGC	C	891

(2) INFORMATION FOR SEQ ID NO:1127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 691 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1127:

```

GTCCATCTGT TTTAATGCAT TGATATAGTT ATCAAGTTCC ACATATCTTT TGGGGATTTA      60
TAATCTGGTA ACATTTTATC CTTGCTGTGA TTGTGCTCGT CAAATAATGA ATTTTGTTTT      120
TCAATTAAAG TCGAAACATN ATAATCTGTG TTCACCCTGA ACGTATNTGA ATTTCGCACTC      180
AATAATGATT TATTGTATGT TTGGAACCAT TTTGTAATGT CTTTGTTTGC AGAAATTGAA      240
TTTACAAGCG TATCTGTAAA TAATTCCGGG AAGTCGTTAA TTGGATTTAA TAAGTAATTC      300
GAGAAATTAC TATTCACACC ATGTTACACG GTCATAATAG CGCCAACATT TTTTGTGCA      360
TTATGTAAAT TATCAATGAT GCTTGTTAAA TAAATTTGCA CTAAGTTTTT GTTAAAGTCG      420
TTAAGTACAT TACTTACAAC TTTTCTGTG TTTTAGCTA CTCTTCTTT TTGTCCTACA      480
GCTGTTTTAT ACTGTAGCGA TATTTTCGAT GGTGTTTTAG CGTCTAATTG CATTGCCAAT      540
TTTGGAAAAG TTTTCTTGGG ATAACAATCA TGAATNGGGC ATCCACCATT TNTCAANCCA      600
GACTCAGCAA CGTTTCTTGG TTAATGTTTC AAATTTATAG GNCTNCTCAA CTGGTTAACC      660
CTNNTAATAA ATTGCTTGA CCCAGCNCAA C                                     691

```

(2) INFORMATION FOR SEQ ID NO:1128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1028 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1128:

```

TCCAGCAATA TATTGCAATT ACCCTAAAAA CACGTTACTT TAATATTTAG TTAAACCAAA      60
TAAGCTGATG AATAGAATGG AAGATAATAC CTGAAACGGA AATAATCGTT TCTAATAATG      120
ACCATGTTAA GGAATGTTTC TTTTACAAGT TAAACCCCAA AATATTCTTT AAACAATCCA      180
AAATCCTGCG TCAATTTACA TGAGACAAAA TCACACTACC TGCACCTATC GCAAGTACAA      240
CTAATGCAAC ATTTACATCT GATGATTGTA ATAATGGTAA GACAATACCT GTAGTTGAAA      300
TCGCAGCTAC TGTAGCCGAA CCTAATGCGA TACGTAGCAC GAGCTGCAAC AANCCATGCT      360
AGTAAAATTG GAGACATCTC TGTACCTTCA AACATTTTAG CAATTGTATT TCCGACACCA      420
CCGTCAANTA ATACTTGTTT AAATGTACCG CCACCGCCNA TAATCAATAA CATCATTCGG      480
ATTGGATAAA TCGCATTTCG CACTGATTCC ATAATATGAT TCATCTTACG TTTTCTCATT      540
NATCCCATCG TAACGATTGC AAATAATACT GCTATTAGCA TGGCTGTCCC TGCTGTTCCCT      600

```

ATCATATAAA	TGATAGATTC	AAATAGATTT	GTAGGTTTGT	CGTGCCCAGT	TACAAGTTGC	660
GTTATCGTAG	ACACTAACAT	TAATATGACT	GGTAATGTTG	CAGTTAATAA	ACTCATACCA	720
AATCCTGGCA	TCTCTTGATC	CGTAAATTCT	TTTTGTGCAC	CTAACGCTGA	AATATCGCCT	780
TCTCGTGTAT	ACGCAGACGG	AATCATTTTT	TGTGCAACTT	TGTTAAATAT	AGGTCCTGCA	840
ATGAGTGTA	CTGGAATGGC	AATAATCATA	CCGTACAGTA	ATACATCTCC	AACATTTGCC	900
TTTAATTCCT	TTGCGATGAC	TACCGGTCCT	GGATGTGGTG	GTAAAAAGCC	ATGTGTCACA	960
GATAAAGCTG	TTACCATAGG	TAGTCCTAGT	TTTAACACTG	AAACATTTGC	GCGGCACGAG	1020
CTCGTGCC						1028

(2) INFORMATION FOR SEQ ID NO:1129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1129:

AGTATTTTTT	TGACCGAGAC	ATGCAAGCCC	TCCTGGTTGA	TTATCATTTA	CATATCGTAT	60
CATAACCAAT	CATAACAAT	AGTTTATTA	ACTTGTAGAC	ACAATGTTTG	CTAAAGTCAT	120
TTTTAAAAA	TATAGCCAAA	AAATTAGCTA	TATATTATAA	AAGCGTGATA	TAAATGTTTT	180
ATATAACAAA	GAAATAAAAA	TCATTTTTTA	CAATGGTTG	TAAGAAAAAG	ACATGCAGAT	240
GTTGTTAAAA	TTTTAATAAG	AATCAAGGAG	GCTATATTAT	ATGGCTAAAC	TAAATGTAGA	300
AGTATTTGCG	GACGGTGAC	ATATTGAAGA	AATGAAAGCA	GCTTATAAAA	ACAAACAAGT	360
GGATGGTTTT	ACAACAAATC	CTAGTTTAAT	GCCGAAAGCG	GCCGTAAGCA	GATTACAAAG	420
CTTTTGCTGA	AGAAGCTCGT	GAAAGAAATT	CCAGATGCTT	CAATTTTCATT	TGAAGTATTT	480
GCAGACGATT	TAGAACTAT	GGAAAAAGAA	GCAGCAATTT	TAAAACAATA	TGGCGAAAT	540
GTATTTGTTA	AAATTCCTAT	TGTAAATACA	AAAGGTGAAT	CAACGATTCC	TTTAATTAAA	600
AAACTTTTCAG	CTGACAATGT	GAGATTAAAC	GTNCGGCTG	TTTACACAAT	TGAACAAGGT	660
AAAGAAATAA	CTGAAGCAGT	AACTGAAGGT	GTGCCCACAA	TATGTTTCAG	TATTTGCAGG	720
ACGTATTGCA	GATACAGGCG	TAGATCCATT	ACCATTAAATG	AAAGAGGCTG	TAAAAGTTAC	780
GCATAGTAAA	GACGGCGTTA	AATTATTATG	GGCAAGTTGC	CGCTCGTGCC		830

(2) INFORMATION FOR SEQ ID NO:1130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 625 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1130:

CCGGANGNTG GAAGTTATCC AAGCTCCAAG TTCGGGTTGC NGGAATTNGG TAAATTCAAG	60
ACGTGGTAGT TGTCGAGAGN ACTATCACAT TTAACCGTTG ANNAAAGTTT GTTTAAGCAT	120
TGATTCCATC TTGANACCNA AATTACACTA TATTGTTGAA TTTCAGGAAT AAAGAANAAA	180
CTATTATGGA TCGTGCGAAA CCAATGGACG AGNCNATANN AAATGGTGAA GATTATGCGA	240
GTCTGATTGA NNAAGCTAAA GNNAAAGGTC TATCAGATAT TCCAAATACC AAAATCTTCA	300
AGTATAGATG AATTAAAGCA ACTTGCTAAT AGCCATATAT CTGATTTGGA AAATAAGCG	360
CAAGCATATT CAAGAACATT CGATGANCAA AAGCGATATA TGGATGAGAA ACATGAAGCC	420
TTCAAGCAGT CAGTGAATAG TGGTGGTTTA GTCACAAGTG GTTCTACTTC AAATGGCAA	480
AAAGCTAAGA TTAATAAGA TGATGGTAAG ATAATGCAGA TTACTGGATT TGATTTTAAT	540
AATCCAGAAC AAAGAATAGG TGATTCAACC CAATTTATTT ATGTTTCGCA AGCTATAAAT	600
TATCCAAGAG GTGTTAGTAC GTGCC	625

(2) INFORMATION FOR SEQ ID NO:1131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 572 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1131:

GGCACGAGCG ATTAATAGAA ACGCTAGGAA ACCAACGATT CTCCATTTAA ATACTTTTAA	60
AAAATTAATC ACTTGTTGTG TAGAGTCTTG TCCGTTTTGG TTATGATTGT TAGCCATGAT	120
ATACCTCCCT TACAACACTC GTGGACCAGA AGTTTTCTGA TCTCTCACAT TAACTTCTAA	180
CTTACGTACT GGCATTTCTG TGAAATATTC TACATTCTTT TTAATATCCG AACGAATTGC	240
TTCAGTTAAA GATTGAAC TT GAACATTATT TGGTACGAAA AAGTCAGTTT TAATGTCGAT	300
ATAAGATTTA TTTTTTTTGT TATATAGGTG CGCAACTACA TGTGGGTGTC TTACTTG CAT	360
CATATTTTGC AACCGTATCG AATGCCGTCT TTACAACAGC TTTACGAGAT ACGTAAACAT	420
GCACCATCAT CGAAGTCTTT GTATAATCCA GGTTTTCGAT GCGTAGGTTT GAAGATACTA	480
AATACTAATA TAAGACCTAT TAATATCAAT AGAGCAGCAA GTGAAATAAG TAATGGGTTG	540
GAACCACACA AATTGAAGGA AGTAGCTTTG AT	572

(2) INFORMATION FOR SEQ ID NO:1132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 693 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1132:

```

GGCACGAGCG GAATTATGAA AATAAGGAAG GTCAACGTGT ATATGTTACG GAAGTTATTG      60
CTGATAGTAT TCAATTTTGA GAACCGAAAA ACTCAAATGA CACTCAACAA GATTTTATACC      120
AACAACAAGT ACAACAAACA CGTGGACAAT CGCAATATTC AAATAACAAA CCAGTAAAAG      180
ATAATCCGTG TCGGAATGCA AATGGTCCGA TTGAAATAGA TGACAATGAT TTACCANTCT      240
AATTTANCCG GTTTGAAAGT GAGGTGTGTA TATGACTGGT TGGATAAGTA TTGATCGCTC      300
AATTCAAAAT CATTTGGCTAT TTAAAGAAAA GAGAACATTT TCAAAGTTTG AAGCATGGAT      360
ATATTTACTC ATGGAAGCGA ATCATTCAAA GGCAAAAGTG CCTATTGGAA ACCAAATTGT      420
AACCGTAGAA AGAGGACAAA GATTAACATC TATTTTGNCC TTGCTTTGAC CTTTTTAAC      480
GGTCACGATT TAAAGTGNAAC CCTTCCTTG ACTTACTCGA GAGTGATGGA ATGTTAGAAG      540
TCAAAACAAC ATCANAATAT ACCCTTATAA CCATTGTCAA TTATGACTTT TATCAAAGTG      600
AGCAGGGCAG GAACCAACAT CAAAACGACA TCAAACCAAC ATCAAAACAA CATCAGTCAA      660
ACATCAACCC AACATCAAAA CAACATCAAA CCG                                     693

```

(2) INFORMATION FOR SEQ ID NO:1133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 622 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1133:

```

ACTTGATCAA GTTGGATTAT TGAATTGAA ACNCCGTTGT ATCACCTTCT GGGCACGAGC      60
GTTGATGATT TAAGAAGATG CTGGTTCAAA TTGTTTATGC TGAAGACAGT ACCGTAAAGT      120
AAGAAGAAAG AAATCCAATT TACAACCGAT TGAAATTTTA CCATCAGATA TGGGCGGGGA      180
CTATGATGCG TTAGAAACAT TAATGGCGTC AAGACCTGAC ATTTTAAACC ATAATATTGA      240
AACTGTTTCGT CGCTTAACAC CGAGAGTTCG TGCGCGTGCG ACTTACGACA GAACATTAGA      300
GTTTTTACGT CGTTCANAAG AATTACAACC AGATATCCCA ACTAAATCAA GTATTATGGT      360
TGGATTAGGT GAAACTATAG AAGAAATTTA TGAANCATG GATGATTTAC GTGCGAATGA      420
TGATGATATT TTAACGATTG GTCAATATTT ACAACCTTCA CGTAAACATT TAAAGGTTCTN      480
AAAAATATTAC ACGCCTTTAG AGTTTGGTAA ATTAAGAAAA GTGGCAATGG ATAAAGGGTT      540

```

TAAACAGTGC CAACTGGACC TTAGTACTT AGTTCTTATC ATGCGATGAG CAAGTAAATG 600
AGCTGCTAAA GAAAAGCACG CC 622

(2) INFORMATION FOR SEQ ID NO:1134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 544 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1134:

GGCACGAGAC ATCAAGTTGG TTAAAGTCTA TTAAAGTTGA ATCAACATGT GGCATTTTGT 60
GATGAAGATT CACTAACGCA TTCTCTCATT TTGGTATTGG AGTGCCATTC GACAATTCAT 120
TCACACTTAT CTGTATTACA AAATTTAGCA ACCGTACTGG GCGATAACCA AACAGTCCAG 180
CAACTATTAA CTGCAAAAAA CGCACAAGAC ATTAAAAACA TTTTAAAGGA GCATGATTAA 240
TATGAAAATT TTAGTAGTAT GTGGCCACGG TTTAGGAAGT AGTTTTATGG TAGAAATGAA 300
CGCACAAAGAA GCACTTAGGC AACTTAATGC ACCATCTGAT ATCGAAGTTG AACATAGTGA 360
CATTATGACA GCAAGTCCAG AGATGGCTGA CTGTGTTTATT TGTGGTAGAG ATTTAGCTCG 420
AAAATGCCGA ACGCCTAAGG GATGTCTTAG TTNNTGATAA CATTTTAGAT AAAGCTGAAT 480
AACAACAAAA GCTCTCAGAA ANATNACAAC AACTTAACAT GATTTAAAGA NGGTCTACCG 540
TGCC 544

(2) INFORMATION FOR SEQ ID NO:1135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 657 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1135:

CAATTTAAAA TGGNATAAAG AGTCNNTCCC AAGGATTAAA ATAGGAATCC ATCCTTG GTT 60
GACTTTCNT TGTGTTGATT GTTTNACAC GATGCTGCGG NATACGTTTC ATTACCACTC 120
GTTCAAGCAA TTGCTAATGT AACCTTTTAT TTTCGTTCT AATCGGCAAT TACTATTTCA 180
ATGGCAGTGG TTGATTTATA TCAATACCTA AACTATAGG CATTACATAA TACACGACTA 240
AAATAATAAT TATTGCACTG ATTAAGTTTA CCCAGAATCC TACTGATGCC ATTTGTTTGA 300

TAGATATTTT	ACCTGAACCA	AAGATAATTG	CATTGGGTGG	TGTCCTACT	GGTAACATGT	360
ATGCACAGTT	AGCCGCCATA	GCTGCAGGTG	CCATAAGTAG	TAATGGATGC	ACTCCAACAG	420
CAACAGACAA	CGTTGCTAAA	ATCGGTAAAA	TCATCGTTGC	AGTTGCAGTA	TTAGATGTCA	480
CTTCAGTTAA	AAATAAGACA	AAGATTGTTA	TGACAATTAC	AATAAGAATC	GGACTAACAC	540
CATTTAATGA	TTTCAACTGT	TCGCCTAACC	ATTTTGCTAA	ACCACTTTCA	GAAATACCTT	600
TCGCTAATGC	TAAACGCGCA	CCAAATAAAA	TTAATACACC	CCAAGGGAGC	TCGTGCC	657

(2) INFORMATION FOR SEQ ID NO:1136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 570 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1136:

GGCAGGAGCG	CCAGAACTTT	ACCTTTTGCC	TTTTTCAAAT	CACACCAAGT	AACATATTCA	60
AAGCGTTGTT	GGTTTATAGT	TACCTTCAGT	TGTTAAAAGT	TGTGTTTGTT	TAACTTTAGA	120
AACTGATTTT	TTCGGTAAAA	TCATATCTTC	AATTTTACGT	AAAAGCAAAT	CAAATAAATA	180
CGTATCATCA	TGATGCCATA	ACGGCAATAT	CGCTAATGCT	TGATAGTCGC	CCGCTAATTC	240
TAAATAGATA	TGTGCATTCA	TAAACCAATT	GTGAATATCA	TGACCTGTAA	AACCTTCATA	300
TTTTATCAGC	AACCTCAACG	GATCATCAAC	TTTGAAGCA	TTTCAAAAAC	CCTTCTTCTC	360
CAAACATTCC	GATTAATTGC	GCTCTCTTTA	TCAAAAACA	CGGTACTATC	ATATGTTTTA	420
TAGAACTCGG	CAGCTGACTC	TAACTAGCC	ATAATCAAAT	ACGAAGGACT	AGATGTTTGG	480
AAGTAGCTTA	GATATTCTAT	AATAGTTTCT	CTATAAGGTG	CATTTTTATG	AATATAAAGT	540
ACCGAGCCCA	TCGTTAAAGC	TGGTAACGTT				570

(2) INFORMATION FOR SEQ ID NO:1137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 928 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1137:

TACATGTAAA	AGNANATGAA	TATATACATC	TTTAGTCTAG	TATTATACCT	ATAACTAGCA	60
------------	------------	------------	------------	------------	------------	----

TGTCCTTAAA	TGAATATGCT	ATCATGATAT	GGTAATTTTG	ATATTTAAAT	AAATTAAATT	120
GAGTAATGAN	AGTGGGTACA	TTATGTTTAT	CATTGAATTA	ATAAAAGGTA	TTATCTTAGG	180
GGTCGTCGAA	GGANTAACAG	AATTTGCACC	TGTTTCCTCT	ACTGGACATA	TGATTCTAGT	240
TGATGATATG	TGGTTAAAAT	CATCTGAATT	TTTAGGTTCT	CAATCAGCAT	TTACATTTAA	300
AATCGTCATC	CAATTAGGAT	CCGTCMTTGC	AGCAGCATGG	GCATTCCGAG	CGAAACGCTT	360
CTTAGAGATT	TTACATATTG	GTAAACACAA	ACATGTTGAA	GGAGAAAACG	ATCAACAAAG	420
ACGTTCAAAG	CCAAGACGTT	TAAATTTATT	ACATGTATTA	GTGGGTATGG	TGCCAGCAGG	480
TATTTTAGGC	TTACTATTTG	ATGATTTTCAT	CGAAGAACAT	TTATTTAGTG	TGCCAACTGT	540
TATGATTGGC	TTATTCGTAG	GTGCTATCTA	TATGATTATT	GCTGATAAGT	ATTCAAGTTAA	600
AGTTAAAAAC	CCACAAACAG	TGGATCAAAT	CAATTATTTT	CAAGCGTTTG	TAATTGGTAT	660
CTCTCAAGCA	GTAGCTATGT	GGCCTGGTTT	CAGCCGTTCA	GGCTCAACAA	TTTCAACTGG	720
GGTTATTAAT	GAAATTAAAT	CATAAAGCAG	CATCGGACTT	CACATTTATT	ATGGCTGTTC	780
CAATTATGTT	TAGCAGCTAG	TGGTTTTCTT	TATTAACAAC	TTATCAAGAT	ATTCCAGATT	840
GCTGATATAC	CTTTTATAT	TTTAGCTTTT	TAGCTGCATT	TACTGTTGGA	CTAATTGCAT	900
CAACATCCT	TGCATCTAAT	AACAAATC				928

(2) INFORMATION FOR SEQ ID NO:1138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 596 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1138:

GGCACGAGCT	CATTAACAAT	TAGTCTATAT	AACCCTTGCT	ATATTTTCAA	AAACAAAACC	60
CAATTACGTT	TTCATGTCAA	ATATCATCTT	GCATGAAATC	GTAAGTGGGT	CAATTGTATG	120
TTATTAGTTA	TTTTGTGTTA	CATCCTCATC	TATCGATTTG	GCAATTTGTT	TAATAGCTTT	180
ATGTGATTGT	CTAATTGGAT	AAATTGGAAA	ATCATGTACC	ATCTTAGGAT	AATCATAAAA	240
CTCAATGTAT	TGATGATGTT	GCAACATCAT	TTGTTTGAAT	AGCTTCATAT	CAGGATGTGT	300
CATTTACGTT	CCACCACCAA	ACATATAAAC	TGGTGGCAAT	CCTTCTATTG	TGCCATTAAT	360
TGGCGATATG	CGCTTATCTG	TTAATGGTAG	GCCATTCGCC	CATTTTTTCA	TAATCTCATT	420
GACACCAAAC	TGACTTAGAA	CCGCATCTTG	TTCGATTAA	GCGTCCGAAA	TATCTTTATT	480
AGATAGTGTT	GCATCTAAAA	TTGGTGAGAT	TAAAATACAA	TTTATTCCGG	TAATGGGCTG	540
TTGATTATCT	AAAAGAGATT	GTACAAAGGA	TAATGCCAGT	GCACACCTGA	ACANTC	596

(2) INFORMATION FOR SEQ ID NO:1139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1139:

```

GGCACGAGCG AGGGTTAATA TTATTAATTG CTATATGTTT GCTTTATCTA GCTTTTTATT    60
ATTTTTCACC AGATAAGGAA GAGAACTAG CTAAAAATA TATTCTATTC TTTTAAACAT    120
GGGCAGTTCC AGCGGCAATT AGTGGTATTT ATATTAAATA TATAACAAG GCTACGGTAG    180
AAAGATTTTT TAAATTAGTA TTTTTCATAT TTTCTATTTT ATTTATTTTT GTAATTTTAA    240
TACCAAAACT TACAGGTGAG ATACCTAGCT ATATCAATTT TGGACTTATG AACTATCAAA    300
ACGCTTCGTA CCTTTCAGCA TTTACTGCCG GATTAGGCAT TTATTTTCATT ATGAAAGGTT    360
CAGTGAAACA TAAGTGGATA TATGTTCTAT TTACAATAAT TGATATCCCT ATTGTGTTTA    420
TACCAGGAAG GCGTGGAAGT GCTATTTTAT TAATTCCTTA CGGCTTTATT TGCATTTATA    480
CTTATTACGT TTAAAAGAAG AATACCTATT GCAGTAA                                517

```

(2) INFORMATION FOR SEQ ID NO:1140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 571 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1140:

```

GGCACGAGCT GTTAAAGTAA ACTATACAAT TTAATTTCAA GGAAATTTCT CTTCAAACCA    60
TCTTGTTGCA AATTCATTTT CAAATAAGAA TACTAAATCG TCATATCTAT CTTTCACTAA    120
AATCGATCTT GATGTGTTCA TCTTATCTGT AATTTGGTCT TCATTTTCAA TCCAACGTGC    180
AATTTTACGG CCTACTGGCT CCATAACAAC ATCAACATTA TATTCGTTTT TCATTCTATG    240
TTCGAAAAC TCAAATTGTA ACTGACCAAC AGCACCTAAA ATAATTTGGT TTGTGTGTAA    300
TGTTTTATAG TATTGAATCG CACCTTCTTG TACTAATTGT TCAATACCTT TATGGAAATG    360
CTTCTGTTTC ATGACGTTTT TAGCAGAAAC TTTCATAAAA ATTTCTGGCG TAAATTGTGG    420
TAAATCTTGG AAACTGTANG TTTGTTTTCC ACCAACTAAA GTATCTCCAA TTTGATAATT    480
ACCAGTATCA TATAGTCCAA TGATATCGCC TGCTACAGCA TGATCACAGT TTCTTTATCG    540
TCTGCCATAA ATGACTTGAA CGTGTGATCT T                                571

```

(2) INFORMATION FOR SEQ ID NO:1141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1141:

GAATTCCATC	CATTCGTTAC	ATCAAGTAAT	CCAATTGCAG	GTAACGTTAC	TGTTGGTACA	60
GGTGTAGGTC	CTACATTCGT	TTCGAAGGTA	ATTGGTGTAT	GTAAAGCTTA	TACATCACGT	120
GTTGGTGATG	GTCCATTCCC	TACTGAATTA	TTCGATGAAG	AAAGAACTA	ACAACTGTAA	180
TCAATAATGC	AAATAAAAAAT	CCAGCGTGAT	AACCATGCAA	CATCGTATCA	ACTTTAATTT	240
GATTCATCAT	ATCAATTTTG	TTCATGCCAT	TATAGTCTGA	CATAGTTGGA	GAAAAGTTTT	300
TGGTTGCAAT	GAGATAAAAT	AGTAATTAAT	GCAGGTTGGT	CCCGATAGAA	CCAGCAATTG	360
GTGGTNCGT	GTTTNGGCAA	TAGGATGAAC				390

(2) INFORMATION FOR SEQ ID NO:1142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 736 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1142:

CTACACTTCA	CGTTGATAAG	CAGCTTCTAA	TAAATGGGTA	ACCATATTAT	GATAATATGT	60
TCTAGATAAA	ATTGAGCCAA	TAACCCAACG	CTTAAATCTT	GGATTATCAC	TTGTGTTAAA	120
TAAATAATTG	GCCATCAACA	TTTCATTCAT	TGTAGAAGGG	GCTTCAACAA	AAGTACATTG	180
ATGCTTCTGA	TTCAAGATAT	GGTTGATGTT	TTTGAGCTAA	TGTAAAATGA	CCTGCATGAC	240
CTAATTCATG	TGCTAAGACA	AATGCTTCAG	CCATTTTACC	AGTCCAAGAA	ATAAACACAT	300
ATGAATGTGT	AAAGTATGGA	CTTGNACAAA	ATGCGCCTGT	ATCTTTACCT	TTATTTCTGT	360
CAAAATCAAT	CCATCGCTGA	TCGTATGCTT	CACGTAACAT	GTTTGTATAG	TCATCACCTA	420
AAACAACCTA	ACGCACCCGA	AAAATATAAT	TTTTTTGAGT	CTTCAATTGA	AATCTCTGGG	480
TTCATAATCA	GGGTCTACAG	AAATCTTCAA	GTCTTCAAAA	CGCATGTTAT	CTAATCCGTG	540
AATACGTTGT	AAAAGTTTAG	CATATTTCTG	CATAACTGGT	GCCAAGTCAC	GCATAATCAT	600
ATCGATTTGA	CGGTCAAACA	TATCACGCGT	TACTTCTTGA	CTATGTAATA	AATAATCGAT	660
GACTGATTCA	AATCCACGTA	AATCAGCTTC	AATTTTTTCT	TGTTGTACTT	GCATATTAGA	720
TGTAGCCGCT	CGTGCC					736

(2) INFORMATION FOR SEQ ID NO:1143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1720 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1143:

```

AGNCAACTTA ATTGTGTTAA ATACAGTTTN GNATGCCAAA TGATGTGGTG GATGTTAATT      60
ATAACATATT AAGCCCACTC AATCGTTCCC CAATATTNTT CATTTNTAAT CTTCTGTTCT      120
TTATCTGNGA TTCTACACAC TGCACAATAG AAATCGTTAG TACTAGAGCC CTCACGTNTG      180
ATATTNGAAT CTANTCCACC ANGTAGCCAT CTTTGTTANT GACTTGGTCG AATTTNACCC      240
AATCANCTTT NGTGTATAGC CACGAATCTT CTTCAACGAC TGTACCGGTT AATCCNGNTG      300
TTTTTCTGAC TCTTATAGCT TTTTCTGGAT TAGGATAAAA TACACCTTTC CAATTCCATG      360
TTATTTAGTC AGCACTTGGA TTACTACTTG GCGCATCAAT TTGTCTGCCG ATAATAGCTT      420
CAGCAATCCG CTTGNGAAG CTATCTAAAT TATTTTNAAT GTAGTTTAAA TCTTTCTGTCG      480
ATGTGATAAA ACCTAATTCG ATTAAACGAT AATTAAGATT AAGGTCAGCG GACACGTTAG      540
CGTTCAATAA ATCCCCCTTA GGTGTCACAC CTCTTATTTT ACCTACTGTT TTATCTAATG      600
CGCTACTTAA TGCCTTGTC AATGTCATCAG CTGGGAAACG GTCGCTAATG ATTACATGCC      660
CGCCACTTGC TTGCGGACTA GCAGAATCTA AATGAAACTC TATGATTGCA TCCGGTTTAA      720
CTTCGTTTTT AATCCAGTAC ATGCCATAGT CTTTATAGTT TCCAACACGT TGACCGCACA      780
AAGTATCTTG ATATAAGTCT TGATTCATCG AGTTGCCACC GTATAACAAT ACTGTGTTGC      840
CTACTGACTC AAGATACTTT TACTACTTAG GTATAATATT TTTACGGNTA AAATCTCTTT      900
CGTTTTCTCC ATTGCAACG GCACCTGGGT CGGTAGAGTA TGCACCAATA CCATGACCAG      960
CCACAAGCAT GATTTTTTTA CCTTGTGATA ACTTATCTTG TTTAACTGGC GTCAGTGGC      1020
TTCTTAGCTT ATTAGCGGTC GTTCTTTTTC CGTAGAATGG ACGGATAAAC CACATAGGGA      1080
AGTCGNAGCC GTGTGTACGT CTTGTAGTAA CTTCTGGTGG ACTCCAGTAA GCACCGCCTA      1140
GCCAGTTCTG CTCTAAAATA GTTATAGAAT CTAACGTAGC GCTTATTACA ATACCTACAT      1200
GACCATAACC ACCGNCATAA TTACGGTTAA AAATAACGAC GTCGNCCCGG CAATGCTTGA      1260
AACGACACAG TATTTTCGGT AAACGGTTGC TTCGTTAGTG AAATCATTCC ATGTAGGAAT      1320
GTCCGCAGCG CCCACACCTT TCAACCTATG ATTAAATAAG TAAAGCCAAT ATTGGTTGGC      1380
AGTATCGAAG CATTGACATC CAAATGCATT GTCTGGATTC CACGCCTTAC CCTCTAGGCT      1440
TTTAAGGTAG CTAATAGCTT GACTGTATGT TCTAACCGAC GGCATTGTTA TCATCTCCGC      1500
TCACTTTAGG TGCGCCACCA GTTGACTGAA TGCCAGCTTT TACTTCATAA ATTTTGTGTT      1560
GCCCCTTCTT AGATGCGTGA GTAAAGNTGG GNTATTCTTC CACCACGCCC AAATTGAAAC      1620
AATCCCAGTA ACGACTGTGC TTATAAACAC TTCGNNAAC TGGGATTTGG AGAAATATTG      1680
TTTNGGGTTT GGTAAAAAAC TTGATTGGAT CCAAAGCGA      1720

```


(2) INFORMATION FOR SEQ ID NO:1144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1005 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1144:

```

ATCATGTTAC AAATCCATTA GGTGTAGGAG GTATCAATGA TGCAACAACT ATCTCTGAAA      60
CATAGATTAA ACAATGGTGA TTCAGTTTAT GGCATTTTTA ATTCTATACC GGACCCATTG      120
ATGATCGAGG TTATCGCAGC AAGCGGGTAT GACTTTGTTG TGATTGATAC AGAACACGTG      180
GCGATTAATG ATGAGACACT AGCGCATTTA ATTCTGTCAG CTGAAGCAGC GCATATTATA      240
CCAATTGTAC GTGTCACTGC AGTGATAGAT AGAGATATCA TTAAAGTGTT AGATATGGGT      300
GCGAGAGGTA TTATTGTGCC ACACGTTAAA GATCGTGAGA CAGTTGGAGC ATATTGGTGA      360
AATTAAGTCG GTTATTACCC GCAAGGATTA AGAAGTTTGG ATGGTGGTCG CATGGCAAGA      420
TTTGGACGGT ACAACCATTA CTTGGATGCA ATGGAGATGG TTAATGAGCA TTATTATGGG      480
GGATTGCCAT GATAGAAGAT TGTGGAGGG GGTATTGGCC ATGGACGATA TAGCTCAAAG      540
TCGAAGGGGT TTNGACAATG ATAGCCGAAG GTGCCNGCAG ATTTATCGCA GTCACTTGGC      600
ATACCATGGC AAACGCTCGT GCCGAATTCG GCACGAGCGG CACGAGCGGC ACGAGCTCGT      660
GCCGCTCGTG CCGCGGAAAA ATATATCGCC ATTTAAGTGC ATCTCTAGCG ACGTCTAAAC      720
AGAAAGGGGA TGATGGCTAA TCGGTATAGC TCANCTGNT ATTGAACAAT TAAAAGCACA      780
ATCTCATCCA GTGTGNCATT ATATCTATGA TTTAGTCGGA CTGGAACATC ATGTGCAACA      840
TATTACATCG NCATTGGCGA GTAATTGTCA AATGTACTAT GCAATGAAAG CAAATAGTGA      900
ACGAACAATC CTAGATACAA TTAGNCAGTA TGTNGANGGA NTCGAAGTNG CATCTCAAGG      960
TGAAAATAGC AAAAGGTCTT GCTTTNANCC AGCAACNCAT ATTAT                          1005

```

(2) INFORMATION FOR SEQ ID NO:1145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 808 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1145:

```

ACATTTTCAG CATCAGCAAT CGCTTGTTTA TAAACCTTTG GCTTATCTTG AATCTGCTTG      60

```

TGTGTAATCT	ATAGTTTGCT	CCAACGTTAG	CATGTTTCAT	AACTGCTTGT	TGTAATTGAT	120
CCATTGATTG	GTTCAATTGC	GTTGCTTGAT	CTACTAATTC	AGCGATTGGN	TGAAGTTTCG	180
TCGCTTGATC	AATATTTTGT	TTAGCAGTTG	CAATTTGATC	AGCATTTAAA	TGTGTTAATT	240
GGTCAATAGT	TTGTTTCGCT	TGTGTTTGTAG	CTTCAGCGAC	TCTCTCATT	CCATTTAACT	300
CATTCACTTT	TTTCTTGAAG	CTTAGTTAAT	GCTTGTTCCT	CAGCGTCTTT	ATTTCGCATTT	360
GAACCATTAG	TTGGATCTGT	AATGCNTTGT	GCAGCTCGTA	ACGCTTGATC	CTACTGCTTC	420
TTTTTTATCA	GTTGACGCTT	CAGTGTAATT	TGGTTGAGCC	TTATCTGTAT	TCACTTGATC	480
AACTTTATTT	TTCAATGTTT	CCATCGCGTG	ATCAAGTTCA	GTAGCAGTTT	GAACATGTTG	540
TGCAACCTCT	GTTCTTGTAG	GCGCTGCATT	TATAGCATCA	GTTAATGTTT	GTTGTTGTGC	600
ATGATTTAAG	TTTGGCAATG	CATTTACAGT	TGTTACTGCT	TGTTGTTGAT	CACGAGCAAG	660
TTTTTGATCA	CCATGTAGAT	TATCTTTTGG	AGNTGGTACT	TGCTTGTTGT	AATTGTTCTA	720
CTTGGTGATT	TGTCGAGTGT	TGGATTACCT	GTTTGGTTAA	TTAAATCTTT	TGGATTTNGG	780
GCTTGCTGCT	TGGGNAAGCA	TCTTTTGG				808

(2) INFORMATION FOR SEQ ID NO:1146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1146:

CTATTAAGGA	ATCCTTGNN	AATTCACATT	AGCAAGTTGG	ATTGTCCACC	TTATTAATTG	60
ATAAAGTATG	CAAATAATTT	CACAGTGT	CCAGCGGGGC	CAANTTATGA	TTGCAAGTAA	120
CCTATAGCAA	TCGTATTCTT	GTTCTTGCCA	ACGCTATTTA	AGTATCAGGT	TTAACCAACA	180
GGTGGGACAA	AAGGTTAGTT	TGAAATTAGG	GAGTGGGGCA	GAATTGATAA	AGAACCACTA	240
ATGACGATAA	AGATTAAAAAG	GGAGGACGTT	ATGATGACGG	ATTAAAGTTG	GAATCATTGG	300
GTGTGGTGGT	ATTGCGAATG	GCAAGCAACA	TGCCAAGTTT	ACNAAAAGTT	GAAAATGTTG	360
AAATGATCGC	ATTTTGTGAC	GTAGACATTT	CGAAAGCAGC	GAGTGGGGCA	GAAGCATACG	420
GAAC TGACAA	TGCAAAAGTT	TATGATGATT	ACAAAGCATT	GTTAAAAGAT	GACACGATTG	480
ATGTTATCCA	TGTTTGTACG	CCAAATGACT	CGCATTGTGA	AATTACTGTA	GCAGGGTTGC	540
ATGCCGGTAA	GCATGTGATG	TGTGAAAAAC	CAATGGCTAA	AACGACAGCA	GAAGCTCAAA	600
AAATGATAGA	TACAGCTAAA	TCAACAGGTA	AAAAATTAA	AATAGGTTAT	CAAAATCGCT	660
TCAGACCAGA	TAGTCAATTT	TTACATCAAG	CAGCGCAACG	TGGCGACTTA	GGAGACATTT	720
ACTTCGGAAA	GGCACATGCC	ATTCGTCGTC	GTGCAGTACC	GACATGGGGT	GTCTTTCTAA	780
ACGAAGAAGC	CCAAGGTGGA	GGACCTTTAA	TCGATATTGG	TACGCACGCA	TTAGATTTAA	840
CGTTATGGAT	GATGGATAAT	TATGAACCAG	AATCAGTGAT	GGGTTCAACA	TTCCATAAAT	900
TAAATAAGCA	GCATGATGCG	CCAAACGCTT	GGGGTTTCATG	GAATCCAGAT	GAATTAACAG	960
TTGAAGACTC	TGCGTTTGCC	TTTATTAAAT	GAAGAACGGA	GCGACGATCA	TTTTAGATCC	1020

GCTTGGGCGA	TTAATTCCTT	AGAAGTGGAT	GAGGCAAAAT	GTTCATTATT	AGGAACGAAA	1080
GCAGGTGCTG	ATATGAAAGA	TGTTCTACGT	ATTTCATGGT	AAGATATGGG	CACACTTTAT	1140
ACCAAACACG	TTGAATTNGA	AAACAAAGGC	GTCGACTTTT	ATGAAGGTAA	TGAAGTGGAT	1200
GAAGCTGAAG	AAGAANCAAA	AGCTTGGATT	GATGCAGTTG	TAAATGATAC	TGAACCAGTT	1260
GTGAAACCGG	AACAAGCAAT	GGTAGTTACA	AAAATTCTTG	AAGCGATTTA	TCAGTCTGCA	1320
AAATCAGGCA	AAGCAATTTA	CTTTGAATAA	CATCATACGG	TAAGGAGGCA	CATCATGACA	1380
AAATTAAAAG	TTGGTGTGAT	AGGTGTTGGT	GGCATTGCAC	AAGACCGTCA	TATTCCAGCA	1440
TTGCTGAAAC	TCAAAGACAC	AGTCTCATTA	GTTCAGTAC	AAGATATTAA	TACAGTGCAG	1500
ATGATTGATG	TTGCGAAGCG	CTTTAATATA	CCTCAGGCAG	TTGAGACACC	TAGCGAGCTG	1560
TTTAAACTTG	TTGATGCGGT	GGTCATTTGT	ACACCCAATA	AATTCATGCT	TGATCTTTCT	1620
ATAGAAGCAT	TGAACCATGG	TGTCCATGTC	TTATGCGAAA	AGCCAATGNC	AATGACGACG	1680
GAAGAGTGTG	ATCGCATGAT	TGAAGCGGCT	AATAAAAAATC	ACAAATTATT	AACTGTCGCT	1740
TATCATTATC	GTCACACAGA	TGTCGCTATG	ACTGCTAAAA	AAGCAATTGA	AGCAGGTGTG	1800
GTTGGTAAAC	CATTAGTAGC	ACCGTTGTCC	AANCGATGCG	TAGGCGTAAA	GNACCTGGGT	1860
GGGGCGTTTT	TACCCAATAA	AACCGTTGCA	AGGTGGCGGT	AGTTTAATCG	ATTATGGTTT	1920
CCCACTTGTT	AAGACTTATC	TTTGTGGCTA	TTAGGTAAAG	ATATGGTGCC	GCATGAAGTG	1980
CTAGGAAAAA	CATATAATCA	ATTGAGCAAA	CAACCGAATC	AAATTAATGA	TTGGGGAACA	2040
TTTGATCACA	CTAAATTTGA	TGTCGATGAT	CATGTTACTA	GTTATATGAC	ATTTGCCAAT	2100
CGAGCAAGCA	TGCAGTTTGA	ATGTTTCGTG	TCTGCAATA	TAAAGGAAGA	TAAGGTACAC	2160
GTTAGTTTAT	CAGGAGAAGA	TGGCGGTATC	AATTTATTTC	CATTTGAAAT	ATATGAGCCC	2220
CGCTTTGGAA	CTATTTTGA	AAGCAAAGCT	AATGTTGAGC	ATAACGAAGA	CATTGCTGGT	2280
GAGAGACAGG	CGCGTAACTT	TGTCAATGCG	TGTTTAGGTA	TAGAAGAGAT	TGTGGTGAAA	2340
CCGGAAGAAG	CACGCAATGT	AAATGCCCTT	ATAGAAGCGA	TTTATCGTAG	CGATCTTGAT	2400
AACAAGAGCA	TACAACTTTA	ATGATTATTA	TATATAATAC	AAAATTCTCA	ATATAAAAAG	2460
ANGGAGTGCT	TTTCAATGAA	AATAGGTGTA	TTTTCAGTAT	TATTTTACGA	TAAAAATTTT	2520
GAAGATATGT	TAGATTATGT	CGCAGAATCT	GGATTGGATA	TGATTGAAGT	TGGAACAGGT	2580
GGTAACCCAG	GAGATAAATT	TTGTAAGTTA	GATGAGTTGT	TAGAAAATGA	AGACAAGCGA	2640
CAAGCATTTA	TGAAGTCAAT	CACAGACAGA	GGCTTACAAA	TAAGTGGTTT	CAGTTGTCAT	2700
AACAATCCAA	TTTCTCCAGA	TCCGATAGAA	GCGAAAGAAG	CCGATGAAAC	GTTACGTAAA	2760
ACAATCCGTT	TAGCAAATCT	ATTAGACGTG	CCAGTTGTTA	ATACATTTTC	TGNCATTGCA	2820
GGGTCAGATG	ATACCGCTAA	AAAGCCTAAT	TGGCCTGTTA	CACCTTGGCC	AACAGCCTAC	2880
TCTGAAATTT	ATGATTATCA	GTGGAATGAA	AAGTTGATAC	CATATTGGCA	AGATTTAGCT	2940
GAGTTTCCNC	AAGAGCAAGA	TGTNNAAATT	GCCATNGAGT	TACATNCAGG	ATTTTITAGCT	3000
CANACACCAA	ATACGATGTT	NAAGTTACGT	GAGCCAACAA	ATGAATATAT	CGGTGCTAAC	3060
TTAGATCCTA	GTCATTTATG	GTGNCAAGGT	ATTGACCCAA	NTCCTGCGAN	TGCGATATTA	3120
GGCCCNANCA	AATNCAATTC	ATCACTTCCA	TGGAATTCCG	AAGAAACGTA	TGTTANTCNA	3180
GGGNATGTAA	ANATGTATGG	TCTAGCTGAT	NTCCAGCCAT	ATGGTNACGT	TGCGACANGN	3240
GCATGGACAT	TCCNTACAGN	TGGNTATGGA	CATAGTCCAT	ATGNATGGGC	AGATNTCATA	3300
AGTCAACTTA	NTATTAGATG	GAG				3323

(2) INFORMATION FOR SEQ ID NO:1147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1147:

```

GGTCTGCATA AAACCTTGGA AGTACTTAAG AAATCCCAAA GCCAATACAT GGATTACTTG      60
CACCCACCGT ATCGANACAA TGTTCGCGAA ACATAACGTA AAATATGGAG ACAATCCTTT      120
GATGCGTTGG TTTACTAATA ATGTTGCAGT AAAGGTTAAA CCCCAGTGGT AATAAAGGAA      180
TATATTANNN NANGATGNAA ATAGAAGAAA AACCCGATGG GTTCATGGCT TTTGTTACAG      240
CATTATATAG AGCAGACGAT ATAGTAGACA AAGACATGTC TAAAGCGCTT GATGCATTAA      300
TGAGTATAGA TTTCTAATAG AGGAGGTGAG ACATGAGTAT TCTAGAAAAG ATATTTAAAA      360
CTAGGAAAGA TATAACATAT ATGCTTGATT TAGATATGAT AGAAGATCTA TCACAACAAG      420
CGTATGTGAA ACGTTTAGCG ATTGATAGTT GTATTGAATT TGTTCGCGGA GCTGTCGCTC      480
AAAGTCATTT TAAAGTATTG GAAGGTAATA ACTGGCTCTG GGAATTCCTG CAGCCCGGGG      540
GATCCACTAG TTCTAGAGCG GCCGCCACCG CGGTGGAGCT CCAGCTTTTG TTCCCTTTAG      600
TGAGGGTTAA TTTCGAGCTT GCGTAATCA TGTCATAGC TGTTCCTGT GTGAAATTGT      660
TATCCGCTCA CAATTCCACA CAACATACGA GCCGGAAGCA TAAAGTGTA AGCCTGGGGG      720
TGCCTAATGA GTGAGCTAAC TCACAATAAT TCGGTTGGCG CTCACTGCCC GCTTTCCAGT      780
CNGGGAACC TGTGCTGCCC AGCTTGCAAT TAATGAATCC GGCCAACGCG CGGGGAGAGG      840
NGGGNTTGGN GTATTGGGCG CTCTTCCCGC TTCTCGCTC ACTTGACTCG CTGCGCTCGG      900
TCGTCCGGNT TGNGGNGAGC GGNATCAAG NTCAACTCAA AGGNGGGNAA TACGGGNTAT      960
CCACAGAATC AAGGGGGATA ACGCAGGAAA GAACATTGTT GAGCAAAAGG CCAGNAAAAG     1020
GCCAGAACCC NNAAAAGGCG CGNNNGCTG GNGNNNTTC CCCATAGGCT CCCNCCCCC     1080
CTGGACGANN ATCAAAAAAT CGNCGGTCA AATNNAGANG GNNGGGGGAA ANCCCGCNAG     1140
GATTATTNAG GNTCCAGGNG GNNTCCCCC G                                     1171

```

(2) INFORMATION FOR SEQ ID NO:1148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1148:

```

CTGCTTAAAT TCGAACGTGT CATTGACATT TTCAATAAGA AAAACAACGG AGCATGGAAT      60

```

TTCTGTCCGC	AAAACGCCCG	TTATTGGGAA	CATATCCCTA	AGAGTATTAC	AAAATTATCA	120
GATTTAAAAA	TCGTTGGTTT	AGATTTCTAT	ATCACTACTG	AAGAATCAAA	ACGATTTACT	180
GATTTTCCTA	AAGACTTTAA	AGGTATTGCA	GGTTGGATAT	TAGAAGTAAA	ATCGAATACA	240
CCAGGTAACA	CAACACAAGT	ATTAAGACGT	AATAACTTCC	CGTCTGCACA	TCAATTTNTA	300
GTTAGAAACT	TTGGCACGAG	ACTGGTGGCG	TTGGTAAATG	GGAGTTTATT	CGAAGGAAAG	360
GTGGTTGAAT	AATGATAGTA	GATAATTTTT	CAAAAGACGA	TAACTTAATC	GAGTTACAAA	420
CAACATCACA	ATATAATCCA	ATTATTGACA	CAAACATCAG	TTTCTATGAA	TCAGATAGAG	480
GAAGTGGTGT	TTTAAATTTT	GCAGTAACTA	AGAATAACAG	ACCGTTATCT	ATAAGTTCTG	540
AACATGTTAA	GACATCTATC	GTGTAAAAAC	CCGATGATTA	TAACGTAGAT	AGAGGCGCTT	600
ATATTACAGA	CGAATTAACG	ATAGTAGACG	CAATTAATGG	GCCTTTGCAG	TATGTGATAC	660
CGAATGAATT	TTTAAAACAT	TCAGGCAAGG	TGCATGCTCA	GGCATTCCTT	ACACAAAACG	720
GGAGTAATAA	TGTTGTTGTT	GAACGTCAAT	TTAGCTTCAA	TATTGAAAAT	GATTTAGTTA	780
GTGGGINTGA	TGGTATAACA	AAGCTTGTTT	ATATCAAATC	TATTCAAGAT	ACTATCGAAG	840
CTGTCGGTAA	AGACTTTAAC	CAATTAAAGC	AAAATATGGC	TGATACACAA	ACGTTAATAG	900
CAAAAGTGAA	TGATAGTGCG	ACAAAAGGCA	TTCAACAAAT	CGAAATCAAG	CAAAACGAAG	960
CTATACAAGC	TATTACTGCG	ACGCAAACTA	GTGCAACACA	AGCTGTTACA	GCTGAAGTCG	1020
GATAAANTAG	GTGGGAAAAA	GAGCAAGCGA	TTGGGGACCG	TTTAAACGAA	GTNGGACAAC	1080
AAATCAATGC	GCCTGGCCTT	GTNAAGGTAA	TNCAACAACA	AATTGGGAAA		1130

(2) INFORMATION FOR SEQ ID NO:1149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1149:

AACCCTAATT	GTTCCAGTTT	TGTNCCATTG	ATAATAATAA	ATTTNCGCCT	NTGAACANCT	60
TGATCAAAGT	TTTGTTCCCC	NGGTTGACCT	TCGTTGAAAT	ATTTCCAATT	TCCTTAAGTT	120
CCTCCGTAAT	CTTGAATCCC	CTGNCTNAAC	CCATCCATNG	NTTGGTTAAC	CGAATNCCCA	180
TTTGTGCCA	ATTGTTTGAC	CTCCAGTTNC	TAAAGTTCCA	CCTGTAACTT	GGTCTTTTAA	240
TCCTGTTTTT	TGAGGATCAT	TTAAGCTTGT	TAAATCATCA	ATTGCTTNCG	TCGCATTTGT	300
TTTAGCAACT	TGTAAATTAT	GATCTCCATT	TAACGCTTGA	AGTGTTGTTT	GAACTTTAGT	360
AATAGCTTGT	TCTACTTCTG	TTTGGTTCGC	ATTTTGACCA	GTTTGTGTTG	TAATCATTGC	420
TGCTGCTTCA	TTTACCGCTG	TATTATAAGC	AGTTTGTTTA	TCAGTATCAG	CATTGATGAA	480
GTTACCACGT	TGTTCAACGG	CTTGATGATC	TGCAATCGCA	TTAATTAAGT	TACCCATCGC	540
AGTATTTAAA	GATTCTGCTG	TTTGTTTGTG	ACCATTAACT	GCAGCAATAT	CAGATGATTG	600
CGTAATTTGT	GATTGTAAC	GTTGCTTTTG	CGCATTATTC	AAATGATCTA	ATTGATCAAG	660
TCTGTGTTTG	CTTGGTGGT	TTAGCTTGCT	TGCAAGGTTT	TCCATCACCA	TCTTAATTGC	720

AACTTTCCGG ATTTATTCAC TTGGNGTC

748

(2) INFORMATION FOR SEQ ID NO:1150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1232 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1150:

```

GGCACGAGCT CGTGCCGCTC GGCATTTTTT ATCTACATGT TTGCATTCTG GTTCATTTTT 60
AGTTCATTG CAGGATTATT TACGTTTACG GGTAGTGGTA GCTTAAACT AATTTTCAGTG 120
ATTTTAAATT TATTAGGTAT TGTTTTCGGT GTCATTTTAT TATTTAATCC ATTAATGGGT 180
ATCGTCTTTA TTTCGACGAT GATTGCTATG CATTGTATTC GTAGGTGTCA TTTATGTTGT 240
AGATGCACTT GCTTAAGTAA AATGAAGCGG TTCAAAGAA GGGTGTGACA TGAAGTTTGT 300
GTCATATCCT TTTGTGTGTG TTTATGAAGC ATAAAAAGG GGCGCTACCT ACAATAAGTA 360
AGATACGCCC ATATTTTTAT ATTTTACTAT TATTGTTTTT CAATACGATT AATAGTTACA 420
TTTAGTCCAA AATATTTTTC TAAAAATGT TTATAGTTAT CTTTAGTGAC ATCAAATTTT 480
TCTGAGCTAC CATTCCTTGT TAAAGTTAAA TGATTTTCAG ACATTGTAGC ACGGCCAAAT 540
GATTGTGGCA TTGTAATTAA TAAATGCTGT ACAAATATTG AATCTGGATG CGTTTGATTA 600
TATTCGATGT TGCTATTAAA ATCTTCTATT TGTTTAGGTT TGAATTCAGC TTCATATTTT 660
GTATGCCAAT GATCATTTTC GAATTTTGA ACATAGAAAA TATCCTTGTC TTCGTTGTTA 720
AAAATAGCGC GGAATGTACC ACTGATATCA GTAATTGGTT GTGTATGCTC AGATGAAGTA 780
ATAGGAATGG CATGTAGAGG TAAGTCTCCA AAGCCAACAT CAGTTACATA GAATACATCA 840
TTTATAGAAA CAACAAGTGA AGCATGTGAA CCGTTCAGAC TACGACCGCC ACCGGGTGTG 900
TGAATAGTAG CTGACATTAA TTCAGGATTA AATCCTTTTT GGTGTAAATA TGCTTTGGAA 960
AAATGTATTT AACTCATAAC AAAAAACCAC CACGTTTATC ATGAACAATT TNATTAAAAA 1020
GTGCATCGAT ATTTATAGAT ATCGGCTTAC TATTTTGGAC ATCAATATTT TCAAAAGGST 1080
ACAAGTTAAC ATAAACGTN GTTTGGATTA ATAATTTNAA TGCTTCAATA CTCGGNCGGA 1140
TTATTACGAG ATTGATCANT TGTNAATTAT TCTCTTACTT CCGCAATATT CAATAAGCAT 1200
TAGCGCCTCC TGGTATTAAA GATTATTATT AA 1232

```

(2) INFORMATION FOR SEQ ID NO:1151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1151:

```

GGCACGAGCG ACATTCATTA TGCCCAAATT TTTAAAATCT TTCTTTAACG AGCATCCGTT      60
TATCGATGTT TCTCTCCATG TCAAAAATGA AAATATTGAA AAAGATATTA ATAATCATAC      120
GTATGACATC GGGATTAGCA GAAATCAACC TAAACTAAGA GAAGTTCATT CTGAAAAAGT      180
ATGCGAAGGT AAAATTGTAT TGATTGCTCC CAATAAAGAG AATAATCATC TTCTAACTGA      240
GGCATCTTTA TTTGAAAAAT ACAAAATAAT AAGTGATAAC CATCCAGAAT ATTGGTCATC      300
ACTTAAAAAT AATATTTTAA ATATTTATGG AAAAGCACAA TTTCTATCTA TCAATGATGT      360
GCATACTTCA ATTAAATTAA TCGAAATGAA TCAAGGTATA TCATTCTGCTC CTATTTATAT      420
TAACAACAGA TAGTGATTAC AATATTTTCG TATTAAACAC GAAAATTTTA CAAGCGCCTA      480
TTTCATTTAC ATATATATAC AGCAAAAAGA AGGCCAGGAA TATGGCTTTT ATTAATCATT      540
TAA                                          543

```

(2) INFORMATION FOR SEQ ID NO:1152:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 613 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1152:

```

GGCACGAGCT CGAAACAATA AATTGTTCCA GTCCTTTTAA GCACCGATGT CTTATTTATA      60
ATATGTTTGT CTAATATCAT CTTTCTTTAT ACCAAACTGC TTATAGGATT TATCCATTAA      120
TTTGGCAATT TTATCTGCCC ATCGAATGTC ACTCGCATAT TGATGTTGCG CAGGATTTTC      180
TGGATTCCAT CGCATTTGAT ATAAATTCAG TTGATTGTTT TCAAAATATT CATTACGAAT      240
GAACTTTGCA CCACCAATAA TCGCCTTATC TGGTGATGTC CATTGTTTCCT TTTCAGCATA      300
ACTTTTCCCA CTACGAACAG CACTACTATC GAATGCTCCT ATACCAAAAA AGTTGTAATA      360
GCGTTTTTTC CCATCTTTAA TGCCTTTTGC TAATTCATGAT TTGCCGTTAC CTGTTTCTAC      420
TAATGCATGG CTAACAAGAT AAATGACNTT AACCTCATAT TTTTCTTGAG CTTCTAGAAA      480
AACTTTCCCT CGATTTTCTA AAATCCCCTT ACCTTTTAGC AATTGGGTAA CTTCAGATTC      540
CGACATTGGC ACTTTTTCTG TGATATCCAT ATACTTCAGT ATCATGTCTT ATGTGAAATA      600
GTCATGCTTT AGC                                          613

```

(2) INFORMATION FOR SEQ ID NO:1153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1153:

```

GGCACGAGAC ACAAGTTAAT ATTTGGTAAC TAACTTGTGT ACACGTGATA CGAAACTAAT      60
TTTTATTATT CATTTGATAC ATGTCTATTT AAATAATTTT GCATATACGT ATTCTGCCAT      120
ATCATTGAG GCAGTTAAGA TTAATGTAGT GTCATTTCCA CTCACCGTAC CTAATATCTC      180
TTCTATATTT AGCTGATCGA TAAAATAGTT TATGCCTTGG GCGAAACCAG GTGAGGTTTT      240
AACGATAATG TATGAACCAT TGATGATTGA ACTTAGAACT TCATGTTTAC AATAGTGTCN      300
AAACTTTTCT CTCATCTCCT GTTCCGTTTG AATATTAATA GCTTTATAAA TCCATGTTTC      360
ACAATCGATA GGGACCCCGA TATATATTAA GTTCTTTCAA GTCTTTAGC      409

```

(2) INFORMATION FOR SEQ ID NO:1154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1169 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1154:

```

AGAATTTTAC AAAGTTGCAC AAGCGCTATT AATCAATATC GGTACTTTAA CAGCACAAAA      60
TGAACAAGAT ATTATTGCGA TTGCTCAAAC GGCAAAATTGA GGCAGGCTTA CCCTATTTGT      120
ATTTTGACCC CTGTACCTGT TGGTGCTTCT ACATATCGAA AGCAATTTTG TAAATTATTA      180
TTGAAATCAG CGAAAGTATC AGTAATTAAA GGCAATGCAT CTGAAATATT AGCGTTGATT      240
GATGATACAG CAACTATGAA AGGTACAGAT AGTGATGCTA ATCTTGATGC GGTTCGAATA      300
GCGAAAAAGG CTTACGCAAT ATATAAAACT GCAATAGTAA TCACAGGTAA AGAGGACGTT      360
ATTGTTCAAG ATAATAAAGC CATCGTATTA GCTAATGGAT CTCCATTATT AGCACGAGTA      420
ACTGGAGCTG GTTGTATTATT AGGAGGCGTT ATTGCTGGAT TTTTATTTAG AGAAACAGAA      480
CCAGACATAG AAGCGTTAAT TGAAGCGGTA AGCGTATTTA ATATTGCTGC TGAGGTAGCT      540
GCTGAAAATG AAAATTGTGG TGGTCCTGGT AACGTTTTC AATTGTTGTC TTGATACGTT      600
ATATCATTTA AATGAAACAA CTTATCAACA ACGGATTCGT ATTCAAGAGG TGGAATAATA      660
TGTTTAACCA TTCGTATCTA AATGTGTATT TTATTTGTGG GACCTCCGAT GTTCCGAGTC      720
ATCGAACTAT TCATGAAGTA TTAGAAGCAG CATTAAAGGC AGGGATTACA CTTTCCAAT      780
TTCGAGAAAA GGGTGAATCA GCTTTAAAAG GAAACGATAA ACTTGTATTA GCTAAGAAT      840

```


TACAGCATCT	CTGTCATCAA	TATGATGTGC	CTTTTATCGT	TAATGATGAT	GTATCCTTGG	900
CAAAAGAAAT	TAACGCGGAT	GGTATACATG	TCGGTCAAGA	TGATGCGAAA	GTCAAAGAGA	960
TAGCACAATA	TTTCACTGAT	AAAATTATTG	GACTTAGTAT	TAGTGATTTA	GATGAGTATG	1020
CAAAATCTGA	TTTAACTCAT	GTTGATTATA	TAGGTGTTGG	ACCAATCTAT	CCTACGCCGT	1080
CGAAGCATGA	CGCGCATATA	CCAGTAGGTC	CAGAAATGAT	TGCAACGTTT	AAAGAAATGA	1140
ATCCGCAACT	ACCGATTGTA	GCTCGTGCC				1169

(2) INFORMATION FOR SEQ ID NO:1155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1155:

CCGCTTCGCA	CGAGCNAAGG	CTTTTATTGC	ANCCCTCGCA	TCTTCTTTAG	CTTACACTAA	60
ATCTTTGATG	TCTTGTAATG	CTTGTGCAAG	TTGTGCTTTG	GCTTGTTCAA	TTTCTTCTTT	120
AGTCATCGCA	TTGTTAATGT	CGTTATGACC	TTGTTGAAGT	ATTTGANTAA	TTCGATCTTT	180
AAGCGCTTGT	TTNTCCTTAT	CTGTTAGATT	TGGATTGTGA	TCGATTTCGN	CAATTAATGC	240
TTGAACCTGT	TTATCAACAT	CTTGTTTCGC	ATCTTCTTTA	GCTTACACTA	AATCTTTAAT	300
GTCTTGTAAT	GCTTGCGCAA	GTTGTGCTTT	AGCTTGTTCA	ATTCTTCTTT	TAGTCAGCGC	360
ATTGTTAATG	TCGTTATGAC	CTTGTGGAAG	TATTTGATTA	ATACGATCTT	TTAAGTGCTT	420
GTTTTTCCTT	ATCTGTTAGA	TTTGGAATTC	GATCAATTTT	GTCAATTAAT	GCTTGAACCT	480
GCTTATCAAC	GTCTTTATTG	GCATCAATTT	TNGCTTTNGG	TATTTCATTA	GCANGCACTN	540
GTTCAATCGC	GTGGTTGCCT	GCTGTTTGAA	CTTGAGATAC	AGCCTGATTA	CTTGTTGCTT	600
TATTAATGTT	GTTGATGATG	CTGGTTTGCC	AATCTTCTTT	GCTTTATTTT	TTCGGCAATA	660
AGCTTGCTTT	GATCCGTCGC	ATTGAAGCT	TCGATTTCCT	TTAGCTTATT	AGCTAAAGCT	720
TGATTAATTG	ATTGAATTGC	CTTGTCTTTA	GCATCTTGTA	GTGTTGATC	ACCATTAAAG	780
TTATGGATTG	CATCATTGAC	TGCTTGGATT	GCGCCATTGA	TATCATTAC	ATTTGTGTTA	840
TCACTATTTA	GCAATGTATT	TGCTAGACGT	TTGGCATCAT	CGAAGTTTGT	TTTAGCATTA	900
TCGTACGCGT	TTTGGTAATT	GACAGTTTGC	TCTGCATTTG	GAATTTCAAT	GTCAACTAAA	960
TGTTTCAATG	TTTCCATTGC	ATCATTTAAG	TCAATTTGAT	TATTAACAAT	ATCTGTTACA	1020
TCTGATACAG	TATCGGCATT	GTTAATTGCT	TTATGTGCAA	GATCTTGTTG	CTGTTGATTT	1080
AATCCATTTA	ACGAATTAAC	AAACGCATTT	GCTTTATCCT	TTGGCATTTG	CAAGGTTTGT	1140
GTCTCCATTT	AATGCATTTT	GAGCATCGAT	AATATTTTGT	TTCAATTGCT	CTGCTTCAGC	1200
TTTTGCAATT	GCATTACTTG	CACTTTATCT	AACTCATGTG	CTGCATTTCG	AATGCATATC	1260
ATAATTTGCT	TTCAATGTCA	TCTGCATGAT	GTATTTGTCT			1300

(2) INFORMATION FOR SEQ ID NO:1156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 529 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1156:

```

TTGGAGGATG GAACATATGT GGGGCGAATC CCCTGGGTGA AGATAATAAT CCATATGCCT    60
ATGTGATCAA GCACTTAGAA AAACATTGAA ATTATGTTTG ACATCACCAC AAGGAGTGAA    120
ACACCATAAG CTTAATTCTC CAGTTCTATA TGGGGTAAAT TTCCGTACAN ACTTGTATGT    180
TGTAAGTTAGC GTCTAACACT GCTGAATAAA TCGCAGGTCA ACTCATTGCA CGATATATCT    240
ATAGGCGTTG TGTGTGCCGT GTCCGCCATT TTTAACTAGC AGTCTATCAA TAAATTGTCC    300
GTTAGGCTTC AATCTAGATA ACATGTAATG ATTGCCTGGA CGCGCTTGNG TCATGTAAAT    360
AATTTTGTGTT CTAGGGTCTA CCCAACAATG ATTGCATTAC TCGGTTAGTA TATGGCGATA    420
AATCGGGGAG GAATTCCTGC AGCCCGGGGG ATCCACTAGT TCTAGAGCGN CCGCCACCGC    480
GGTGGAGCTC CAGCTNGTGT TCCCGGTAGT GNGATGGGTC GACGGNCAA    529

```

(2) INFORMATION FOR SEQ ID NO:1157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3110 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1157:

```

GATTCGAGCT CGGTACCGGG GATCCTCTAG AGTCGACCTG CAAGCTATAC CAAGCTAGAG    60
TACTGCGACG CAAACTAGTG CAACACCTAA GGCTGTTACA GCTTGGAAGT CGATAAAATA    120
GTTGAAAAAG AGCAAGCGAT TTTTGAACGT GTTAACGAAG TTGAACAACA AATCAATGGC    180
GCTGACCTTG TTAAAGGTAA TTCAACAACA AATTGGCAAA AGTCTAAACT TACAGATGAT    240
TACGGTAAAG CAATCGAATC GTCTGAGCAG TCCATAGATA GCGTTTAAAG CACAGTTAAC    300
ACATCTAGGA TTATTCATAT TACTAATGCA ACAGATGCGC CAGAAAAGAC GGATATAGGC    360
ACGTTAGAGA AGCCTGGACA AGATGGTGTG GATGACGGTT CTTGTTTCGA TGAATCAACT    420
TATACATCAA GCAAATCTGG TGTGTTAGTT GTTTATGTTG TTGATAATAA TACTGCTCGG    480
TGCAACATGG TACCCAGACG ATTCAAACGA TGAGTTCACA AAATACAAAN TCTTACGGCA    540
CATGGTACCC GTTTTATTAA AAAGAATGAT GGAAACTTAA CTAGCAATTT GGTGAGGA    600

```

ACGTCTTACA	ACGCTTTAAA	TCAAGCTAAG	CAGTATGTAG	ATGATAAATT	CGGAACAACG	660
AGCTGGCAAC	AACATAAGAT	GACAGAGCCG	AACGGTCAAT	CAATTCAAGT	TAACTTAAAT	720
AATGCGCAAG	GCGATTTGGG	ATATTTAACT	GCTGGTAATT	ACTATGCAAC	AAGAGTGCCG	780
GATTTACCAG	GTAGCGTTGA	AAGTTATGAG	GGTTATTTAT	CGGTATTTCG	TAAAGATGAT	840
ACAAACAAGC	TATTTAACTT	CACACCTTAT	AACCTCTAAA	AGATTTACAC	ACGATCAATC	900
ACAAACGGAA	GACTTGAGCA	ACAGTGGACA	GTTCCCTAAT	AACATAAGTC	AACGGTATTG	960
TTCGACGGTG	GAGCAAATGG	TGTAGGTACA	ACAATCAATC	TAAGTGAACC	GTACACAAAC	1020
TATTTCTATTT	TGTTGGTAAG	TGGAACCTTAT	CCAGGTGGCG	TTATTGAGGG	ATTCCGACTA	1080
ACCGCATTAC	CTAATGCAAT	TCAATTAACC	AAACCGAATG	TAGTTGACTC	AGACGGTANC	1140
GGTGGCGGTA	TTTATGAGTG	TTTACTATCA	AAAAACAAGT	GTACCCACTT	TAAGAATAGA	1200
CAACGATGTG	TATTTTCGATT	TAGGCAAAAC	ATCAGGTTCT	GGAACGAATG	CCAACAAAGT	1260
TACTATAACT	AAAATTATGG	GGTGGAAATA	ATGAAAATAA	CAGTAAACGA	TAAAAACGAA	1320
GTTATCGGAT	ACGTTAATAC	TGGCGGTTTA	CGCAATAGTT	TAGATGTAGA	TGATAACAAT	1380
GTGCCTATCA	AATTCAAAGA	AGAGTTTGAA	CCTAGAAAGT	TTGTTTTCAC	TAACGGCGAA	1440
ATTAAATATA	ACAGCAATTT	TGAAAAAGAA	GACGTACCGA	ATGCATCAAG	CCAACAAAGT	1500
GAATCAGATT	TGAGTGATGA	AGAACTTCGC	GGAATGGTTG	CGAGTATGCA	AATGCAGGTG	1560
GCACAAGTAA	ACGTATTAAC	AATGGAATTA	GCTCAACAAA	ACGCTATGTT	AACACAACAG	1620
TTGACTGAAC	TGAAAACTAA	CAAAAACAAGT	ACTGAGGGGG	ACGTTTAATG	ATGAAGATGA	1680
TTTATCCGAC	TTTTAAAGAC	ATCAAACTTT	TTTATGTTTG	GGGTTACTAT	AAAAACGAGC	1740
AAATTAAGTG	GTACGTAGAC	AAGGGTTTAA	TCGATAAAGA	AGAATACGCT	TTAATCACTG	1800
GAGAAAAATA	TCCAGAAACA	AAAGATGAAA	AGTCACAGGT	GTAATGCTTG	TGGCTTTTAA	1860
ATTTAACAAA	AAGTAGGTGG	CGTAATGTTT	GGTTTACCA	AACGACATGA	ACAAGATTGG	1920
CGTTTAACGC	GATTAGAAGA	AAATGATAAG	ACTATGTTTG	AAAAATTCGA	CAGAATAGAA	1980
GATAGTCTTA	GAGCGCAAGA	AAAGATTTAT	GACAAATTAG	ATAGAAATTT	TGGAAGAATT	2040
AAAGCGCGAC	AAGGTAGAAG	ATGAAAAGAA	TAAAGAAAAG	AATGCCAAGA	ATATTAGAGA	2100
CATAAAAATG	TGATTCTCG	GTTTGATAGG	GACTATCTTC	AGTACGATTG	TCATAGCTTT	2160
ACTAAGAACT	ATTTTGGTA	TTTAAAGGAG	GTGATTACCA	TGCTTAAAGG	GGATTTTAGG	2220
ATATAGCTNC	TGGGCGGTCC	TCCTGGTTGG	GGGTAAATGT	AAATAACAGT	TAAGAGTCAG	2280
TGCTCCGGCA	CTGGCTTTTT	ATTTTGATTG	AAATGAGGTG	CATACATGGG	ATTACCTAAT	2340
CCAAAGACTA	GAAAGCCTAC	AGCTAGTGAA	GTGGTGGAGT	GGGCAAAGTC	GAATATTGGT	2400
AAGAGGATTA	ATATAGATAA	TTATCGGGGC	AGTCAATGTT	GGGATACACC	TAACTTTATT	2460
TTTAAAAGAT	ATTGGGGTTT	TGTAACATGG	GGCAATGCTA	AGGATATGGC	TAATTACAGA	2520
TATCCTAAGG	GTTTCCGATT	CTATCGTTAT	TCATCTGGAT	TTGTTCCGGA	ACCCGGAGAC	2580
ATAGCAGTTT	GGCACCTTGG	CAACGGAATA	GGTTCGGACG	GACACACCGC	AATAGTAGTA	2640
GGACCATCTA	ATAAAAGTTA	TTTTTATAGC	GTTGACCAAA	ACTGGGTTAA	TTCTAATAGT	2700
TGGACAGGTT	CTCCAGGAAG	ATTAGTAAGA	CACCCTTATG	TAAGTGTTAC	AGGCTTTGTT	2760
AGGCCTCCGT	ACTCAAAAGA	TACTAGCAAA	CCTAGTAGTA	CTGATACAAG	TTCAGCATCA	2820
AAAAGCCAAT	GACTCAACAA	TTACTGGCGA	AGCGAAGAAA	CCGCAATTTA	AAGAAGTTAA	2880
AACAGTAAAA	TACACTGCTT	ACAGCAATGT	TTAGATAAAG	AAGAGCACTT	CATTGATCAT	2940
ATAGTTGTAA	TGGGTGATGA	ACGCTCAGAT	ATTCAAGGAT	TATATATAAA	AGAATCAATG	3000
CATATGCGTT	CTGTAGACGA	ACTTTATACG	CAAAGAAATA	AGTTTATAAG	CGATTATGAA	3060
ATACCGCATT	TATATGTCGA	TAGAGAGGCT	ACAGGAATTC	CGGAATTCGG		3110

(2) INFORMATION FOR SEQ ID NO:1158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1740 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1158:

```

GGTTAAACCG TACCCCAANA ATAAAGCNTG GTCAACCCNT CCAAATATAA ATTTGAAANC      60
CTTGCCCAGC TGTTTTATTA AGGGANCGAT CCAATTAACA CCCACATATT AATAATACAT      120
CAGCAAAGCC TTCAGGTTTT TGAATATAAC CTAAGTGCCC GCCTGGAATA TCTACAATAG      180
GTATGCCAGT TTCTTTGTTT ATATAAAAGT TAACATCTTG TGGGAAGGAG CCTCTAGAAT      240
CTGTCCCAT TTAGAGGTG ATTTTATCGC TGTATTTTGT GAAATCATCC AAAGTAATAT      300
CTGAATGCGT ATATTGTCTA ATTTCAAATT CTGACCAGAA CATCGTACGT TTGTACTGTT      360
CTATACGTCC TTCTTCAGTA TCAGCAGGTT GAGACATCAT TTTTGCATCA ATTGGTGCGA      420
TATTTAATGT TTCACCAAAT GTTTTCATAC CTTTTCCTAA GCCTTCTGTT AAAATTGAT      480
GCACAATGTC ATCATTTTTA TCTTTCCAAT AAGTACTGTC TGGTAAAAAT GTATTAATTG      540
GTGGTTCGTG AAATGCAATC TTTTAAACGA CTTCAGGGTA ATCTTTTAAC ACATGCATCG      600
CAACGATTGA ACCTGAACCT GAACCTAATA TATAGACAGG TTCATCACTT AATGACTTTG      660
CAAGTTCGGC AATGTCCTGT GCGTCGCGTT TGACACGATA ATCACTGTCA GGGTTTGAAG      720
CGGAATCAGG GAGTGGTTCA GTTAACTCGC TTCTCCATA ATCAGCCCGA TCCACGGCTA      780
CAACAGTAAA ATGGTCTTTT AACTGTTCTG CAAGAGGCAG AAAAATGTTT CCGGTNCCGT      840
TTGCACCAGG AATAAAGATG AGCACGGGTC CTTGTCCGAC TTGGTGGTAT CGTAATTTAG      900
CGCCTTGTA TTTCTAAAGT TCCATATTCA ATGACCTCCA TTTGTTAATT GTTAGATGAT      960
AAACCTAATA ATTTAGCACC ATTTGTATAA CTTATTTTCT CTTTTCCTTC ATCTGTTAAA     1020
CCCAGTTCAT CTAAAAATAC ACCTAATTTT TCAGGCTCAA TATATGGATA ATCAGCAGCA     1080
TAAAGAATTC TATCAATACC TACTTCTTTC TTGACTAAAT CAAACTGTGG CTTCGTTAAC     1140
ATGCCACTTG GTGTGATATA AAAACTATTT TTAAAGTAAT AGCTTACAGA GTGGTTCAAA     1200
TGTTTCAGCGA ATAAAGCTTC ATCCATACGT TCTAAGAAGA ATGGGATAAA CTCACCCCAA     1260
TGTCCAATAA TCATATTTAA CTTTGATAA CGATCAAAAA TGCCAGATAA TACTAGATGT     1320
ATTGCATGAA TTCCGACATC AATGTGCCAA CCATAACCAA AACAAGCAAA TGTTGCCGCA     1380
GTTACTTCAG GATAATTTCC TTTATAGTAT GATTGATAAA GTTCACTGTT AACTGGCGCG     1440
GGATGTAGAT AAATCGGTAT CGTGCTAAA TTTTCAGCTG TTTTGAAAAT AATGTCATAT     1500
TTGTCTTGAT CAAGAAAACC ATCTGTGCA CGTCCCATAA TGAGCGCACC TTTGGAATCC     1560
TAAATCATTG ATGCAACGNT CGAATTCTCG GGCTGCGGTT CANGCTCAAT GGTNGATAAA     1620
GTTGGCAAAG CCTACAAAGC GATTGGGATA TTGGCAATAT AGTTTCGCAA TTGNATCATT     1680
TGTTTGTGTT GCATGATTCA ATGGGTTTTT TGACCAACTN AAAATTGAGG AGGATCCCAA     1740

```

(2) INFORMATION FOR SEQ ID NO:1159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 646 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1159:

```

GGCACGAGCG GTGCCCATTA TAAACCAGAA TTCCCAGAGC GTAATGATGA AGAGTGGTTA    60
AAAACGACAA TGGCCTCATT CCAAGGCGCA TTTGAAAAAC CACAGTTTAC TTATGATGAC    120
GTCGATGTGA GTTTAATACC ACCTCGTAAA CGTGATTACA CAAGTAAGTC TAAAGGGGGT    180
AAAAAATAAT GACTGAACAA TCAGTGAAAA ACACTCCACA ACATGAAACA CAATCTAAAC    240
CGAAACAAAA AACAGTAAAA TTAATTATTA AACGACAAGA TACAAGTGAT TCTAAGCCTT    300
ATGAAGAAAC ATTTGAAATT CCATATCGTG AAAATTTAAA CGTCATTGCT TGTTTAATGG    360
AAATTAGACG TAACCCAGTT AATATTAAAG GTGAAAAAAC AACACCTGTT GTCTGGGATA    420
TTGAACTGCT TAGAAGAAGT ATGTGGAGCA TGTTCTATGG NTATCAATGG GCCGGGCAAA    480
GACAATCTTG GTCCTTGCGA TTGGTGAGTC CAAATTAGGA CAAACCTATT CGGTTTAGAG    540
CCAATGATAC TTCCCAGGT TNTCCCGTGA CTACAAAGTG ATCGTCCAGA TGTCGATAAC    600
TTAAACGTAT GAAAGCATGG TCCCAATGAT GGACGTATGA TTTAGG                    646

```

(2) INFORMATION FOR SEQ ID NO:1160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1160:

```

CTATTGCTTT TCAATAAATA AGATGATTTT GCGGATATTA ATAAAGAAAA ATGCATCATG    60
TAAAAAGTCG CGTACTAAAC GTTCGTCATC TGNTTCAATA AATGAATTAC TATTCACTTT    120
TTTATGTGCT TCTGGCATTG GCTTTAATGT CAGGTGTGAA GCTGCTTCAC TTAAATGCTC    180
ACGCTTTAAA ACGAAACACC ATCGCGGGAA ATCTTTNTAA GGGCAATAAC GTGGTAGGGC    240
CAAACCCATT NTTCAATGAA ATGGAGGCAT CAATATNTTT GGTGCATTGC GCATTCAAAA    300
GGGCAATAC CCGCGGATTA NTAAAGGCAT                    330

```

(2) INFORMATION FOR SEQ ID NO:1161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 956 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1161:

```

ACCAATCCGA TTNCGTNCGG TTGTCGCCAA TAAGACNCCG CCCAAAATAT TAATTTANNG      60
GGTNCCCAAT AAAGAATANC CGGACCACCT CCACCGAAAC CGAGTGTTCG CNCCTCAATA      120
CAATTGAAAA TGCAGCCCAA ATTCCGGATT GGNTAAAGCA GATACAGCAA CAAGATATGT      180
ATTTANAAGA TGAATTAAAA GACAAGTTTT TCTAGGGGGA AGTCTTAGGA CAATCTTATT      240
TAAAATACAC AACTTTCGCC TTATAAACCA AACTCCAAGT TTATGGTGCG TTAGGTGTTA      300
ATATGCCGTG NNAAATATAT ATCAATATGT TAATCGATGA AGAGGATGCG ATACCATTTA      360
ATGCACTTTA TGCAAGTGAT AAGGATGGTT TACCATTCAT TGAAAAGTGG ATTAAACAAT      420
ATGGTTCTGG AAGCTTGGAC CAAAGCAATT TTTAGCTGTA GCGATTGCTC CATTGATTCA      480
TATGCTTTAT TATCACGGTA TTGCCTTTGA ATCGCATGCA CCACAATATG ATGCTCAATT      540
CATGAAAATG GTTGCCCTAC ACGTATTGCC TTAAAAAGAT TTCCACGATG TTGTTCGTTT      600
TAAGCGTGAG CATTTAAGTG AAGCAGCTTC ACACCTGACA TTAAAGCCAA TGCCAGAAGC      660
ACATAAAAAA GTGAATAGTA ATTCATTTAT TGAAACAGAT GACGAACGTT TAGTACGCGA      720
CTTTTACAT GATGCATTTT TCTTTATTAA TATCGCCGAA ATCATCTTAT TTATTGAAAA      780
GCAATATGGT ATCGATGAGC AGCGACAATG GCAATGGGTT AAAGACATTA TCGAGGCGTA      840
TCAAGAAGCA TTTCCAGAGT TGAATAACTA TCAACATTTT GATTGTGTTG AACCTACGAT      900
TCAAGTTGAA AAGTTAACGA CACGTCGATT ATTAAGTGAC TCCGAGTTAA GANATC      956

```

(2) INFORMATION FOR SEQ ID NO:1162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 980 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1162:

```

TTTNCGCCCA CAAATCCCAN AGAAGACTTT GCCTTTAATT CCANCNACAT GGGNCATTAC      60

```

CTAAGACGAT	GTNGGTACCA	TGTCAGTCGT	ACTCCCACAT	GGTGTATTAT	TCCGTGGTGC	120
CGCAGANGGT	GTGATTCGTC	GCTATTTAAT	AGAAGANAAG	AGCTNCTTAG	AANCCGTGNT	180
TGGGTTACCA	NCCAATATTT	TCTATGGGNC	AAGTATTCCA	ACATGTATTT	TAGTATTTAA	240
AAAATGTCGC	CAACAAGACG	ACAACGTAAT	ATTTATCGAT	GCATCCAATG	ATTTTGNAAA	300
AGGAAAAAAT	CAAAACCATT	TAAGCGATGC	CCAAGTCGAA	CGTATTATAG	ACACATATAA	360
GCGTAAAGCA	ACGATTGATA	AATATAGCTA	CAGCGCGACA	TTACAAGAGA	TCGCCGATAA	420
CGATTACAAC	TTAAAGGCAT	ACCGAGCGAT	ATGTTGATAC	ATTCTGAAGAA	GAAGCACCAA	480
TTGATTTAGA	TCAAGTCCAA	CAAGATTTGA	AAAATATCGA	CAAAGAAATC	GCAGAAATTG	540
AACAAGAAAT	CAATGCATAC	CTGAAAGAAC	TTGGGGTGTT	GAAAGATGAG	TAATACACAA	600
ACGAAAAATG	TGCCAGAGTT	GAGATTCCCA	GGATTTGAGG	GCGAATGGGA	AGAGAAGAAG	660
TTAGGGAATC	TTACTACCAA	AATAGGTAGT	GGAAAGACTC	CCAAAGGTGG	AAGTGAAAAC	720
TATACAAACA	AAGGCATACC	ATTTTAAAGG	AGTCAAAATA	TTAGAAATGG	TAAATTAAAT	780
CTTAATGACT	TAGTTTATAT	TAGTAAAGAT	ATAGATTGGA	TGAGATTGAA	AAATAGTAGA	840
ACGTACTATG	GTGATGTTCC	TTTNNATAT	TACAGGAGCA	TCAATNGGTA	GGACAGGCCA	900
TTAATTCGAT	AGGTNGAAAC	GCATGTCTAA	TTTANTCAAC	ATGTTTGAT	TATTAGATTA	960
ANAAAGAGTA	TTATTATTAT					980

(2) INFORMATION FOR SEQ ID NO:1163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1664 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1163:

CCGTACATTA	ACAACCTGGA	TTAATTACAG	ATTACGTTTT	GTCTCATCTA	AAAATTGTTG	60
ATAATCTTTG	ATCAATTTCC	AAATCTGTAC	GTATGTATTA	TCTTAGTAGT	AGTTTAATAT	120
GCACTAAATA	CTTGCAATTG	ATATTTACCA	TATTTATTGT	CAAATCCAAT	TATCTTGTTG	180
TTTTCATAAA	ACGATTGCTT	TAAATAATCT	TCTAACACAT	CAAACATCGT	ATTATCACCG	240
ACATGGTGCC	CGTATAAAAT	AGTATTATGA	TTTAAATTCT	NCAATTCATT	TCTAAATCC	300
ATAAAAATAC	TACCTTTACG	TCGATGTTCT	CGCTCAAAAT	CTAAATTTAA	ATAATCGTGA	360
TTTGTCTTAC	CTTGTAAGTAC	TGGATAANTT	AATGATGTTT	CTGATAATTT	TATCCATCCA	420
ACAATGTCTT	TATTTATTTT	TTCAAGTGAT	TCAAATTGTG	GTCTCACATG	TTCTTGATGT	480
TTGNTCATCA	GCATNTGAAA	TTTNTGTTGT	AATTTCTCAT	AANTTGC GCG	TTCTTGCTTG	540
TCTTCAATAT	ATGTTTGAAC	AATTTTGTA	CCAAAAATGA	TAATAATTAC	AACCAATAAA	600
ATTTGTACAA	TAGTTAAAAA	TCGCTTCATT	CTCATAAAAA	CCCTCTTTAA	TAAACAANTT	660
TCTTCAGTCA	TCACTAAACC	AGTTGTGTA	CCGTTTGA	TTGATTTCG	TTGACTTTGA	720
CAAATTAAGT	AAATTAGCAT	TGGACCACCG	ACAATCATTA	AAATAGCATT	GGCTGGAATT	780

TCTAAAGGAG	GCTGTATCAC	TCGTCCTAAT	AAATCAGCCA	CTAACAATAG	CCATGCACCA	840
ATAACTGTAG	AAAACGGAAT	AAGTACTCTG	TAATTGCCCC	CAACTAGCTT	TCTAACCACA	900
TGTGGCACAA	TAATACCTAA	AAAGGCTAGT	TGTCCAACAA	TCGCAACAGT	TGCACTTGCT	960
AAAAATACTG	CTAATAAACC	TGTTAACCAT	CTGTAACGAT	CAATATTAAA	ACCGATACTT	1020
CGCGCTTGTA	TGTCGTCTAA	ATTTAGTAAA	TTCAATTTAG	GGGACAATAG	TAATGTTAAT	1080
ATTAATCCCA	ATAATGCTGA	TACTGCTAAT	ATGTATACGT	CGCTCCATAT	TTTCATTGTT	1140
AAGCCTTGAG	GAATTTTCAT	TAAAGGGTTT	TGAGTTAAAA	TTTCTAAAAC	ACCATTTAAT	1200
AATACGNATA	ACGCAACACC	TACTAATATC	ATACTTACAG	CATTGAATCT	AAATTTAGAA	1260
TGCAACAATA	TAATTATTAA	AAATGGTATT	AAACCTCCAA	TAAAACCTAA	TAATGGTAAG	1320
TAAAAGTACA	ATTGTGGAAT	AAACAACATA	CCAAGTGCTC	TCATTATAAG	TGCACCTGAG	1380
GAAACGCCAA	TGATATTCGC	CTCTGCCAAA	GGATTTTGTA	GTCCTGCTTG	TAATAATGCT	1440
CCAGAACTG	CTAACATTGC	GCCANCCATC	AATGCAANTA	ATAGACGTGC	CAATCCCCAA	1500
TCAATGATTG	AATCCACTGC	TTCATTGCTA	CCAGTTGTAA	ATTTTGTAAG	TAGGTCATTA	1560
AATGACAATT	TAATTGTACC	GGTTACAAAC	GAAATATAAG	CAGTTGCGAT	TAAAATGACT	1620
AACAAACATA	AAAATAGTAG	TTTCTTTTAA	TTTTTTATCA	TCAG		1664

(2) INFORMATION FOR SEQ ID NO:1164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1164:

TGAACCAGGA	AACTTGACAC	GAGACATCTA	ATCGACATGA	CTATGCGTTA	AAACCATTTG	60
GTAAATNCTG	TCTTAGATCA	TTTGAAAGAC	GGTGGTTATG	ATGTTATTNC	CATCGGTAAA	120
ATTAATGACA	TTTATGATGG	TGAAGGTGTA	ACAGAAGCGG	TTCGTNCGAA	GAGTAACATG	180
GACGGTATGG	ATCAATTGAT	GAAAATTGTT	AAGAAAGATT	TCACAGGTAT	TAGCTTCTTA	240
AACTTAGTAG	ACTTTGATGC	ATTATACGGT	CATCGTCGTG	AGAAACCAGG	TTATGCACAA	300
GCAATTAAAG	ATTTGATGTA	TNCGCTTGCC	AGAAGCTTGT	TTAGCAACTT	ANAAGGAAGA	360
CGATTTAGTA	ATTATTACAA	GCAGACCATG	GTAATGACCC	CGACAGCGCC	AGGGTNCGGG	420
ACCAATACGA	GAGAATATAT	CCCAGTAATT	ATTGTNAAGT	CCCGANATTT	AAAGGTGNGT	480
CAATGCACTT	AGANAGTGGA	TACTACATCC	AAGTTCTATC	GGTGCANCTA	TAGCAGATAA	540
TTTCAACGTA	ACATTACCAG	AGTTCGGTAA	AAGTTATTTA	AAGGAATTGN	NATAGAATAA	600
ATTTAGATAT	TATAAAAACA	GCAGTGTAGT	TAAGTATAAC	AATAGTTTTT	TCTACTGCTG	660
TTTTTATTAT	AATAGAGANA	CGTGTCGGTA	GGACCTCTTA	TTTAGGAGTA	TCCTGATTTA	720
ATGTTAAACA	ATACGTTTTC	GGATTGANCC	GGAAATTAAG	TCGACAATTG	CGACCATTAG	780
TCTCGTGCC						789

(2) INFORMATION FOR SEQ ID NO:1165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1165:

```

GGCACGAGAT ATATAAATAT GTATATACTT GTTTAATTTA TCTCTTTCTA TAAATAAAGA      60
CCTACCAGCA CTCGACTGAT AGGCCTTTTA ATATCTATAA TTATTTAATT TCTTTTGTTC      120
CGGCTAACTC TTTGTACCAA TAAGCACTTT TCTTAGGATA ACGTTCTTGA GTCTCAAAT      180
CGACATAGAA TAAACCATAT CGTTTTTCAT AACCATTGA CCAAGAGAAC ACATCCATTA      240
ATGACCAAAT AAAGTAACCT TTAACATTTG CACCATCTTT AATAGCATCT GCAATAACGT      300
TCAAATGTTG GCTTACATAA TCAATACGTG CATCATCATG AACTGTNTTT TCAGATTCAA      360
TAAATTCATC TTNATATCCT AAACCATNTT CAGTGATATA AATCTTGTA TAGGNTAGGA      420
TAATCTTTNA ACAACACGCA TGATTGGATC ATATAAACCT TGAGGATAGA TCATCCAGGT      480
CCAGGCTTGT GCGAGGTACG TCGACATCAA ATCA                                514

```

(2) INFORMATION FOR SEQ ID NO:1166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1166:

```

GCTCCTAAAA GGTACTCCA CCGGC                                25

```

WHAT IS CLAIMED IS:

1. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOS: 8, 10, 14, 19, 25, 27, 28, 30, 32 and 36.
2. An isolated nucleic acid encoding one of the amino acid sequences of
5 Claim 1 and nucleic acid sequences capable of hybridizing therewith under stringent conditions.
3. Recombinant vectors comprising the nucleic acid sequences of Claim 2 and host cells transformed or transfected therewith.
4. A method of identifying an antimicrobial compound comprising
10 contacting candidate compounds with a polypeptide of Claim 1 and selecting those compounds capable of inhibiting the bioactivity of said polypeptide.
5. Antimicrobial compounds identified by the method of Claim 4.
6. An isolated polypeptide comprising an acid sequence selected from the group consisting of SEQ ID NO:1 through SEQ ID NO:623.
- 15 7. An isolated nucleic acid encoding one of the amino acid sequences of Claim 6 and nucleic acid sequences capable of hybridizing therewith under stringent conditions.
8. An isolated polynucleotide comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 631, 633, 636, 641, 647, 649,
20 650, 652, 654 and 658.
9. An isolated polynucleotide comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:624 through SEQ ID NO:1165.
10. An antibody against the polypeptide of claim 6.

INTERNATIONAL SEARCH REPORT

International application No. -
PCT/US97/02318

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) : C07K 1/00, 16/00; C07H 21/04; C12N 15/00
US CL : 530/350, 387.9; 435/320.1, 325; 536/23.7

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 530/350, 387.9; 435/320.1, 325; 536/23.7

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS, MEDLINE, BIOSIS, EMBASE, CA, WPIDS
terms: antimicrobial, antibiotic, vector, antibody

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	US 4,431,739 A (RIGGS ET AL) 14 February 1984 (14/02/84), see entire document.	1-10
A	EP 0,233,715 A2 (BEECHAM GROUP PLC) 26 August 1987 (26/08/87), see entire document.	1-10
A	SEVIER et al. Monoclonal Antibodies in Clinical Immunology. Clinical Chemistry. November 1981, Vol. 27, No. 11, pages 1797-1806, see entire document.	10
A	AGA et al. Isolation and Identification of Antimicrobial Compounds in Brazilian Propolis. Biosci. Biotech. Biochem. May 1994, Vol. 58, No. 5, pages 945-946, see entire document.	4-5

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A" document defining the general state of the art which is not considered to be of particular relevance	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"E" earlier document published on or after the international filing date	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Z" document member of the same patent family
"O" document referring to an oral disclosure, use, exhibition or other means	
"P" document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

30 APRIL 1997

Date of mailing of the international search report

24 JUN 1997

Name and mailing address of the ISA/US
Commissioner of Patents and Trademarks
Box PCT
Washington, D.C. 20231

Facsimile No. (703) 305-3230

Authorized officer

MARK NAVARRO

Telephone No. (703) 308-0196

INTERNATIONAL SEARCH REPORT

International application No. -
PCT/US97/02318

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☒ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
1-10 and the species recited in claims 1 and 8.
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No. -
PCT/US97/02318

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING

This ISA found multiple inventions as follows:

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Group I, claims 1-4, and 6-10, drawn to DNA, proteins, and antibodies.

Group II, claims 5, drawn to antimicrobial compounds.

The inventions listed as Groups I and II do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: The special technical feature of Group I, drawn to polypeptides and DNA selected from SEQ ID NOS 8, 10, 14, 19, 25, 27, 28, 30, 32, 36, and 631, 633, 636, 641, 647, 649, 650, 652, 654, and 658 is that they are polypeptides which are required for bioactivity while the special technical feature of the Group II invention is that the compounds identified are capable of inhibiting the bioactivity of said polypeptides.

This application contains claims directed to more than one species of the generic invention. These species are deemed to lack Unity of Invention because they are not so linked to form a single inventive concept under PCT Rule 13.1. In order for more than one species to be searched, the appropriate additional search fees must be paid. The species are as follows:

Species 1, SEQ ID NOS 8, 10, 14, 19, 25, 27, 28, 30, 32, 36, and 631, 633, 636, 641, 647, 649, 650, 652, 654, and 658.

Species 2-154, The remaining SEQ ID NOS in groups of 4 peptides and their corresponding DNA sequences.

The species listed above do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, the species lack the same or corresponding special technical features for the following reasons: Each protein is a structurally distinct chemical compound and are unrelated to one another. Up to 10 independent and distinct peptides will be examined in a single application, and then up to 4 such additional sequences will constitute as an additional group.